



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 02:18 PM EDT

PDB ID : 2VLK
Title : The Structural Dynamics and Energetics of an Immunodominant T-cell Receptor are Programmed by its Vbeta Domain
Authors : Ishizuka, J.; Stewart-Jones, G.; Van Der Merwe, A.; Bell, J.; Mcmichael, A.; Jones, Y.
Deposited on : 2008-01-15
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

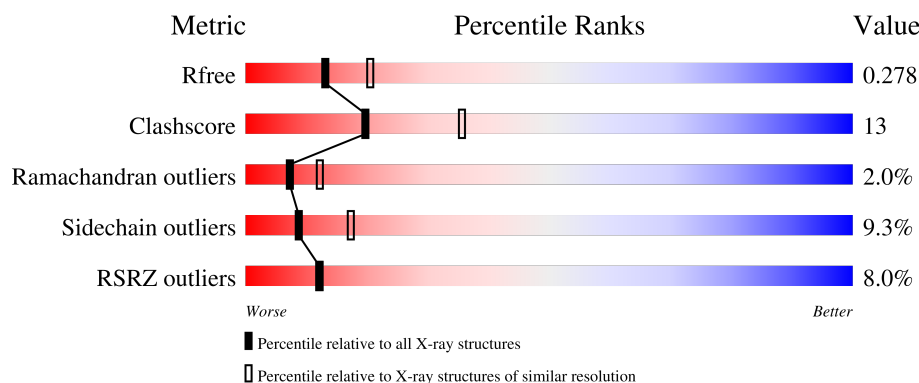
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	276	<div> <div>10%</div> <div>74%</div> <div>21%</div> <div>• •</div> </div>
2	B	100	<div> <div>5%</div> <div>85%</div> <div>12%</div> <div>•</div> </div>
3	C	9	<div> <div>89%</div> <div>11%</div> </div>
4	D	201	<div> <div>9%</div> <div>76%</div> <div>17%</div> <div>6%</div> <div>•</div> </div>
5	E	244	<div> <div>6%</div> <div>73%</div> <div>19%</div> <div>5%</div> <div>• •</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6833 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2252	1407	410	426	9			

- Molecule 2 is a protein called BETA-2-MICROGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			836	533	141	158	4			

- Molecule 3 is a protein called FLU MATRIX PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			68	49	9	10			

- Molecule 4 is a protein called JM22 TCR ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	199	Total	C	N	O	S	0	0	0
			1530	959	255	310	6			

- Molecule 5 is a protein called JM22 TCR BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	240	Total	C	N	O	S	0	0	0
			1932	1218	334	375	5			

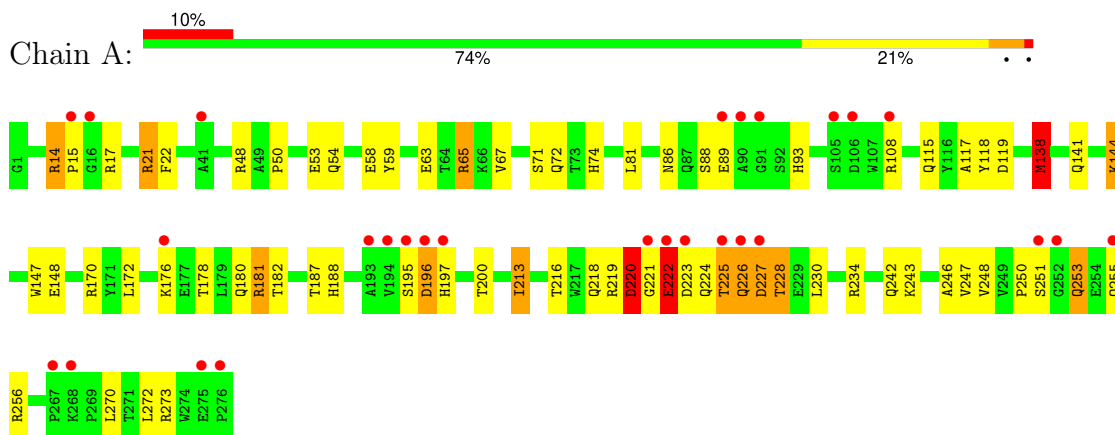
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	75	Total 75	O 75	0	0
6	B	31	Total 31	O 31	0	0
6	C	2	Total 2	O 2	0	0
6	D	47	Total 47	O 47	0	0
6	E	60	Total 60	O 60	0	0

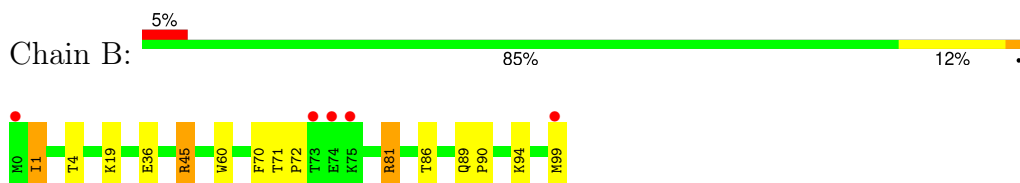
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

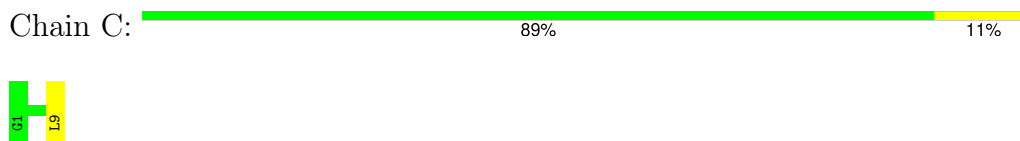
- Molecule 1: HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN



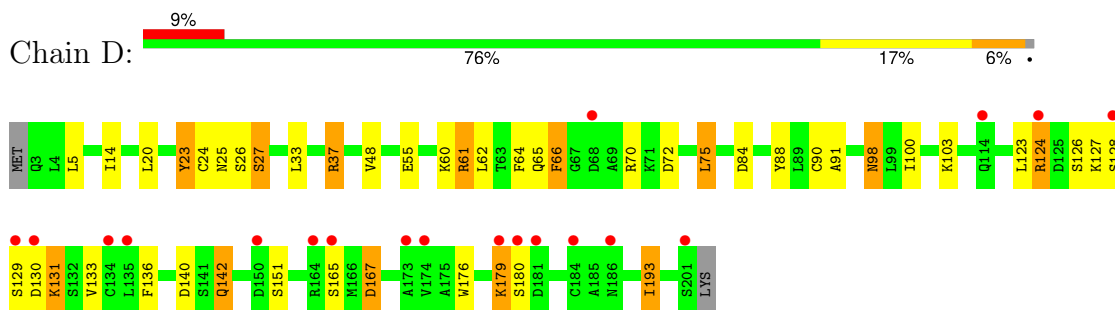
- Molecule 2: BETA-2-MICROGLOBULIN



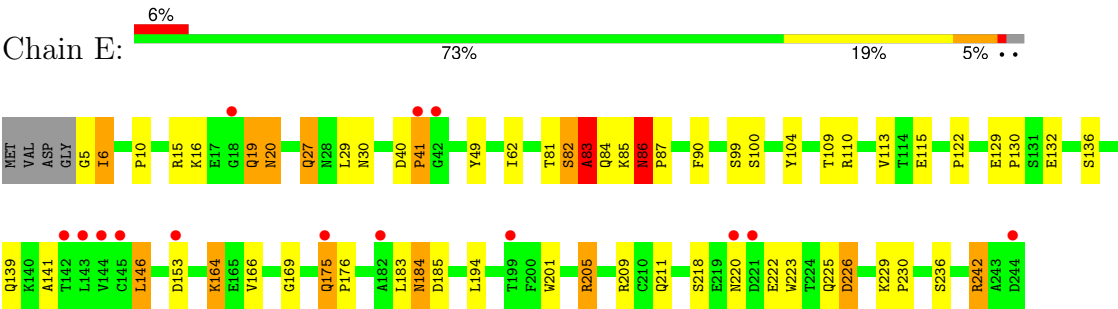
- Molecule 3: FLU MATRIX PEPTIDE



- Molecule 4: JM22 TCR ALPHA CHAIN



● Molecule 5: JM22 TCR BETA CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	210.80Å 47.89Å 112.82Å 90.00° 112.34° 90.00°	Depositor
Resolution (Å)	104.26 – 2.50 26.72 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (104.26-2.50) 99.8 (26.72-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.218 , 0.288 0.210 , 0.278	Depositor DCC
R_{free} test set	1827 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6833	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.75	1/2317 (0.0%)	0.79	1/3145 (0.0%)
2	B	0.75	0/859	0.73	0/1162
3	C	0.97	0/69	0.67	0/92
4	D	0.73	0/1560	0.80	3/2113 (0.1%)
5	E	0.75	0/1985	0.79	1/2700 (0.0%)
All	All	0.75	1/6790 (0.0%)	0.78	5/9212 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
5	E	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	138	MET	CB-CG	6.29	1.71	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	MET	CB-CG-SD	6.32	131.37	112.40
5	E	146	LEU	CA-CB-CG	6.25	129.69	115.30
4	D	123	LEU	CA-CB-CG	5.30	127.48	115.30
4	D	61	ARG	NE-CZ-NH1	-5.27	117.66	120.30
4	D	37	ARG	NE-CZ-NH2	-5.21	117.69	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	226	GLN	Peptide
1	A	227	ASP	Peptide
5	E	83	ALA	Peptide
5	E	86	ASN	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2252	0	2098	61	0
2	B	836	0	803	12	0
3	C	68	0	75	2	0
4	D	1530	0	1480	39	0
5	E	1932	0	1829	54	0
6	A	75	0	0	14	1
6	B	31	0	0	4	1
6	C	2	0	0	0	0
6	D	47	0	0	6	1
6	E	60	0	0	8	0
All	All	6833	0	6285	164	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (164) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:86:ASN:HA	6:E:2029:HOH:O	1.26	1.28
4:D:142:GLN:HG3	6:D:2041:HOH:O	1.41	1.18
4:D:61:ARG:NH1	4:D:84:ASP:OD2	1.86	1.08
5:E:183:LEU:HG	5:E:185:ASP:H	1.23	1.02
1:A:21:ARG:HG2	1:A:21:ARG:HH11	1.27	0.97
4:D:124:ARG:HD2	4:D:124:ARG:H	1.26	0.97
1:A:225:THR:HA	1:A:228:THR:HG22	1.46	0.96
5:E:84:GLN:HE21	5:E:85:LYS:H	1.05	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:45:ARG:HD2	6:B:2016:HOH:O	1.66	0.95
4:D:61:ARG:HH12	4:D:84:ASP:CG	1.69	0.95
4:D:124:ARG:H	4:D:124:ARG:CD	1.81	0.92
4:D:14:ILE:HG22	6:D:2005:HOH:O	1.73	0.86
5:E:183:LEU:HG	5:E:185:ASP:N	1.95	0.81
1:A:74:HIS:CD2	6:A:2025:HOH:O	2.33	0.81
1:A:221:GLY:HA2	6:A:2058:HOH:O	1.81	0.80
1:A:225:THR:HA	1:A:228:THR:CG2	2.11	0.80
5:E:139:GLN:HE21	5:E:139:GLN:HA	1.46	0.80
5:E:86:ASN:H	5:E:87:PRO:HD3	1.46	0.79
5:E:139:GLN:HA	5:E:139:GLN:NE2	1.99	0.77
1:A:178:THR:O	1:A:181:ARG:HD2	1.85	0.77
5:E:5:GLY:CA	6:E:2004:HOH:O	2.34	0.76
1:A:234:ARG:HE	1:A:242:GLN:HE21	1.32	0.76
1:A:93:HIS:HD2	1:A:119:ASP:OD2	1.68	0.76
1:A:15:PRO:HD2	6:A:2005:HOH:O	1.87	0.74
1:A:200:THR:HG22	1:A:248:VAL:HG22	1.67	0.74
2:B:99:MET:SD	6:B:2031:HOH:O	2.46	0.73
1:A:65:ARG:HH11	1:A:65:ARG:CG	2.00	0.73
1:A:234:ARG:HE	1:A:242:GLN:NE2	1.87	0.73
5:E:183:LEU:CG	5:E:185:ASP:H	2.00	0.73
5:E:84:GLN:HE21	5:E:85:LYS:N	1.85	0.72
1:A:21:ARG:HH11	1:A:21:ARG:CG	2.00	0.71
1:A:21:ARG:HG2	1:A:21:ARG:NH1	2.00	0.71
5:E:183:LEU:HD12	5:E:184:ASN:H	1.56	0.70
5:E:183:LEU:HD12	5:E:184:ASN:N	2.07	0.70
1:A:138:MET:HG2	1:A:141:GLN:HG3	1.74	0.69
1:A:65:ARG:HB2	1:A:65:ARG:NH1	2.07	0.69
1:A:147:TRP:CZ2	3:C:9:LEU:HD23	2.27	0.69
1:A:65:ARG:HH11	1:A:65:ARG:HG3	1.58	0.67
5:E:86:ASN:N	5:E:87:PRO:HD3	2.11	0.66
2:B:4:THR:HG22	2:B:86:THR:OG1	1.96	0.66
5:E:222:GLU:O	6:E:2055:HOH:O	2.15	0.65
4:D:64:PHE:CE1	4:D:75:LEU:CD2	2.80	0.64
4:D:64:PHE:CE1	4:D:75:LEU:HD23	2.32	0.64
4:D:64:PHE:HE1	4:D:75:LEU:HD23	1.63	0.64
2:B:81:ARG:HD3	6:B:2028:HOH:O	1.99	0.62
5:E:175:GLN:HG3	5:E:176:PRO:HD2	1.81	0.62
5:E:242:ARG:CG	5:E:242:ARG:HH11	2.13	0.62
4:D:75:LEU:C	4:D:75:LEU:CD1	2.69	0.61
4:D:133:VAL:HG12	4:D:176:TRP:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:180:SER:HA	6:D:2046:HOH:O	2.01	0.61
5:E:5:GLY:HA3	6:E:2004:HOH:O	1.99	0.60
5:E:19:GLN:O	5:E:20:ASN:O	2.20	0.59
1:A:228:THR:HA	1:A:246:ALA:O	2.03	0.58
4:D:124:ARG:HD2	4:D:124:ARG:N	2.07	0.58
1:A:65:ARG:NH1	1:A:65:ARG:CB	2.67	0.57
1:A:219:ARG:C	1:A:221:GLY:H	2.08	0.57
1:A:65:ARG:HG2	6:A:2023:HOH:O	2.04	0.56
4:D:37:ARG:HD2	4:D:88:TYR:CZ	2.41	0.56
1:A:88:SER:HA	6:A:2030:HOH:O	2.05	0.56
5:E:183:LEU:HD21	5:E:185:ASP:HB2	1.88	0.55
1:A:65:ARG:HH11	1:A:65:ARG:HB2	1.71	0.55
4:D:25:ASN:ND2	4:D:72:ASP:OD1	2.33	0.55
1:A:50:PRO:O	1:A:53:GLU:HG3	2.07	0.55
5:E:40:ASP:HB3	5:E:41:PRO:HD2	1.87	0.55
5:E:139:GLN:HE21	5:E:139:GLN:CA	2.15	0.54
1:A:65:ARG:HH11	1:A:65:ARG:CB	2.20	0.54
2:B:36:GLU:HG2	2:B:81:ARG:NH2	2.23	0.54
4:D:75:LEU:C	4:D:75:LEU:HD13	2.27	0.54
4:D:165:SER:O	6:D:2044:HOH:O	2.18	0.54
5:E:164:LYS:HE3	5:E:166:VAL:HG12	1.89	0.54
1:A:250:PRO:HG2	1:A:253:GLN:NE2	2.22	0.54
1:A:65:ARG:CG	1:A:65:ARG:NH1	2.70	0.53
5:E:40:ASP:CB	5:E:41:PRO:HD2	2.37	0.53
5:E:62:ILE:HG13	5:E:62:ILE:O	2.09	0.53
4:D:66:PHE:CE2	4:D:70:ARG:HG2	2.44	0.53
5:E:132:GLU:OE1	5:E:132:GLU:N	2.41	0.53
1:A:219:ARG:C	1:A:221:GLY:N	2.63	0.52
5:E:226:ASP:N	5:E:226:ASP:OD1	2.42	0.52
1:A:187:THR:O	1:A:188:HIS:HB3	2.10	0.52
5:E:84:GLN:HG3	5:E:86:ASN:HB3	1.91	0.52
5:E:169:GLY:O	5:E:194:LEU:HA	2.09	0.52
4:D:127:LYS:O	4:D:128:SER:HB3	2.10	0.51
1:A:223:ASP:HB3	6:A:2064:HOH:O	2.11	0.51
4:D:98:ASN:HD22	4:D:98:ASN:C	2.14	0.51
4:D:64:PHE:CE1	4:D:75:LEU:HD22	2.45	0.50
5:E:153:ASP:OD2	5:E:153:ASP:O	2.29	0.50
5:E:6:ILE:HD11	5:E:104:TYR:HB3	1.93	0.50
4:D:124:ARG:CD	4:D:124:ARG:N	2.56	0.49
5:E:81:THR:O	5:E:83:ALA:N	2.46	0.49
5:E:242:ARG:HH11	5:E:242:ARG:HG2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:23:TYR:CD1	4:D:23:TYR:N	2.80	0.49
1:A:93:HIS:CD2	1:A:119:ASP:OD2	2.59	0.49
1:A:234:ARG:HH21	1:A:242:GLN:NE2	2.11	0.48
5:E:225:GLN:HG3	6:E:2057:HOH:O	2.12	0.48
1:A:253:GLN:HA	6:A:2072:HOH:O	2.12	0.48
5:E:129:GLU:HG2	5:E:201:TRP:CH2	2.49	0.48
5:E:86:ASN:N	5:E:87:PRO:CD	2.75	0.47
4:D:5:LEU:HD13	4:D:90:CYS:SG	2.54	0.47
4:D:91:ALA:HA	4:D:100:ILE:O	2.14	0.47
1:A:14:ARG:HA	1:A:15:PRO:HD3	1.50	0.47
5:E:27:GLN:HE21	5:E:29:LEU:H	1.62	0.47
1:A:21:ARG:CG	1:A:21:ARG:NH1	2.70	0.47
4:D:14:ILE:HD11	4:D:20:LEU:HD23	1.97	0.47
4:D:126:SER:HA	5:E:129:GLU:OE2	2.15	0.46
2:B:94:LYS:HG3	6:B:2026:HOH:O	2.16	0.46
5:E:115:GLU:HB2	6:E:2038:HOH:O	2.15	0.46
2:B:36:GLU:HG2	2:B:81:ARG:HH22	1.80	0.46
5:E:10:PRO:O	5:E:109:THR:HG23	2.15	0.46
5:E:27:GLN:NE2	5:E:29:LEU:H	2.14	0.46
1:A:81:LEU:HD13	1:A:118:TYR:CD1	2.51	0.46
4:D:14:ILE:CG2	6:D:2005:HOH:O	2.46	0.46
5:E:122:PRO:HD3	5:E:230:PRO:HB3	1.98	0.46
1:A:50:PRO:HD3	6:A:2018:HOH:O	2.16	0.46
4:D:5:LEU:HD23	4:D:26:SER:HB2	1.97	0.46
1:A:220:ASP:OD1	1:A:256:ARG:HA	2.16	0.45
1:A:144:LYS:O	1:A:148:GLU:HG3	2.16	0.45
4:D:98:ASN:ND2	6:D:2031:HOH:O	2.47	0.45
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.52	0.45
1:A:224:GLN:C	1:A:226:GLN:H	2.21	0.45
1:A:220:ASP:HB3	6:A:2057:HOH:O	2.17	0.45
5:E:15:ARG:O	5:E:113:VAL:HA	2.17	0.45
5:E:130:PRO:HG3	5:E:141:ALA:HB1	1.99	0.45
1:A:181:ARG:NE	6:A:2051:HOH:O	2.49	0.44
1:A:181:ARG:CZ	6:A:2051:HOH:O	2.65	0.44
1:A:219:ARG:HH21	1:A:221:GLY:HA3	1.82	0.44
2:B:4:THR:CG2	2:B:86:THR:OG1	2.65	0.44
4:D:140:ASP:OD1	4:D:142:GLN:NE2	2.50	0.44
5:E:242:ARG:CG	5:E:242:ARG:NH1	2.79	0.44
1:A:176:LYS:NZ	1:A:176:LYS:CB	2.81	0.44
1:A:181:ARG:NH2	6:A:2051:HOH:O	2.51	0.44
5:E:5:GLY:O	5:E:27:GLN:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:20:ASN:N	6:E:2008:HOH:O	2.50	0.44
4:D:130:ASP:OD2	4:D:131:LYS:N	2.48	0.44
5:E:99:SER:O	5:E:100:SER:HB2	2.17	0.44
1:A:176:LYS:NZ	1:A:176:LYS:HB2	2.33	0.43
5:E:205:ARG:HA	5:E:205:ARG:HD3	1.75	0.43
5:E:225:GLN:CG	6:E:2057:HOH:O	2.67	0.43
1:A:147:TRP:HZ2	3:C:9:LEU:HD23	1.79	0.43
1:A:234:ARG:NE	1:A:242:GLN:HE21	2.09	0.43
5:E:29:LEU:O	5:E:30:ASN:CB	2.65	0.43
4:D:167:ASP:N	4:D:167:ASP:OD1	2.52	0.42
2:B:89:GLN:O	2:B:90:PRO:C	2.57	0.42
5:E:209:ARG:NH2	5:E:211:GLN:OE1	2.53	0.42
1:A:176:LYS:HB2	1:A:176:LYS:HZ2	1.84	0.42
1:A:213:ILE:CG2	1:A:243:LYS:HD3	2.50	0.42
5:E:223:TRP:CD1	5:E:229:LYS:HB3	2.55	0.42
1:A:222:GLU:HB3	1:A:223:ASP:H	1.73	0.42
4:D:136:PHE:CE2	4:D:193:ILE:HD11	2.55	0.42
4:D:179:LYS:HB3	4:D:180:SER:H	1.54	0.42
5:E:153:ASP:O	5:E:153:ASP:CG	2.58	0.42
4:D:5:LEU:HD13	4:D:24:CYS:SG	2.61	0.41
5:E:90:PHE:CD2	5:E:110:ARG:HG2	2.56	0.41
1:A:22:PHE:CD2	1:A:71:SER:HB2	2.55	0.41
2:B:71:THR:HA	2:B:72:PRO:HD2	1.85	0.41
1:A:72:GLN:NE2	6:A:2024:HOH:O	2.47	0.41
1:A:59:TYR:O	1:A:63:GLU:HG2	2.21	0.41
1:A:218:GLN:HG2	1:A:223:ASP:OD2	2.21	0.41
1:A:48:ARG:HA	1:A:48:ARG:HD2	1.80	0.40
4:D:98:ASN:C	4:D:98:ASN:ND2	2.74	0.40
4:D:14:ILE:CD1	4:D:20:LEU:HD23	2.52	0.40
1:A:108:ARG:HD2	6:A:2034:HOH:O	2.20	0.40
1:A:172:LEU:O	1:A:180:GLN:NE2	2.42	0.40
2:B:1:ILE:HD12	2:B:1:ILE:HA	1.87	0.40
4:D:26:SER:OG	4:D:27:SER:N	2.54	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:2003:HOH:O	6:D:2003:HOH:O[2_654]	1.01	1.19
6:A:2063:HOH:O	6:B:2025:HOH:O[1_565]	2.11	0.09

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/276 (99%)	251 (92%)	15 (6%)	8 (3%)	4	6
2	B	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	197/201 (98%)	187 (95%)	8 (4%)	2 (1%)	15	28
5	E	238/244 (98%)	218 (92%)	14 (6%)	6 (2%)	5	8
All	All	814/830 (98%)	757 (93%)	41 (5%)	16 (2%)	7	12

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86	ASN
1	A	222	GLU
1	A	227	ASP
4	D	179	LYS
5	E	20	ASN
5	E	83	ALA
5	E	86	ASN
1	A	195	SER
1	A	197	HIS
1	A	220	ASP
4	D	131	LYS
5	E	41	PRO
5	E	82	SER
1	A	196	ASP
1	A	17	ARG
5	E	220	ASN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	231/232 (100%)	203 (88%)	28 (12%)	5	9
2	B	95/95 (100%)	90 (95%)	5 (5%)	22	43
3	C	7/7 (100%)	7 (100%)	0	100	100
4	D	175/177 (99%)	157 (90%)	18 (10%)	7	14
5	E	212/215 (99%)	196 (92%)	16 (8%)	13	26
All	All	720/726 (99%)	653 (91%)	67 (9%)	9	17

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	21	ARG
1	A	54	GLN
1	A	58	GLU
1	A	65	ARG
1	A	67	VAL
1	A	89	GLU
1	A	115	GLN
1	A	138	MET
1	A	144	LYS
1	A	170	ARG
1	A	181	ARG
1	A	182	THR
1	A	196	ASP
1	A	213	ILE
1	A	216	THR
1	A	220	ASP
1	A	222	GLU
1	A	225	THR
1	A	228	THR
1	A	230	LEU
1	A	247	VAL
1	A	251	SER
1	A	253	GLN
1	A	255	GLN
1	A	270	LEU
1	A	272	LEU

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Mol	Chain	Res	Type
1	A	273	ARG
2	B	1	ILE
2	B	19	LYS
2	B	45	ARG
2	B	70	PHE
2	B	81	ARG
4	D	23	TYR
4	D	27	SER
4	D	33	LEU
4	D	48	VAL
4	D	55	GLU
4	D	60	LYS
4	D	62	LEU
4	D	65	GLN
4	D	66	PHE
4	D	75	LEU
4	D	98	ASN
4	D	103	LYS
4	D	124	ARG
4	D	129	SER
4	D	142	GLN
4	D	151	SER
4	D	167	ASP
4	D	193	ILE
5	E	6	ILE
5	E	16	LYS
5	E	19	GLN
5	E	27	GLN
5	E	49	TYR
5	E	82	SER
5	E	136	SER
5	E	146	LEU
5	E	164	LYS
5	E	175	GLN
5	E	184	ASN
5	E	205	ARG
5	E	218	SER
5	E	226	ASP
5	E	236	SER
5	E	242	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	72	GLN
1	A	93	HIS
1	A	141	GLN
1	A	242	GLN
1	A	253	GLN
1	A	260	HIS
2	B	83	ASN
2	B	89	GLN
4	D	15	GLN
4	D	76	HIS
4	D	98	ASN
4	D	112	ASN
4	D	115	ASN
5	E	19	GLN
5	E	27	GLN
5	E	84	GLN
5	E	139	GLN
5	E	233	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	276/276 (100%)	0.53	28 (10%) 7 6	20, 35, 59, 76	0
2	B	100/100 (100%)	0.13	5 (5%) 28 30	19, 31, 48, 60	0
3	C	9/9 (100%)	1.06	0 100 100	20, 21, 25, 29	0
4	D	199/201 (99%)	0.52	19 (9%) 8 8	18, 36, 55, 58	0
5	E	240/244 (98%)	0.37	14 (5%) 23 24	19, 35, 50, 59	0
All	All	824/830 (99%)	0.44	66 (8%) 12 12	18, 34, 55, 76	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	129	SER	7.8
1	A	195	SER	6.8
1	A	196	ASP	6.3
1	A	276	PRO	5.5
1	A	227	ASP	5.4
4	D	130	ASP	5.2
1	A	226	GLN	5.1
1	A	221	GLY	5.1
1	A	225	THR	4.7
5	E	41	PRO	4.6
4	D	135	LEU	4.6
5	E	220	ASN	4.5
1	A	223	ASP	4.5
4	D	164	ARG	4.4
1	A	251	SER	4.1
4	D	184	CYS	4.0
4	D	150	ASP	3.9
1	A	193	ALA	3.9
1	A	16	GLY	3.7
5	E	144	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	194	VAL	3.4
1	A	275	GLU	3.3
1	A	89	GLU	3.2
4	D	181	ASP	3.2
5	E	42	GLY	3.2
2	B	99	MET	3.1
1	A	222	GLU	3.1
1	A	197	HIS	3.1
5	E	182	ALA	3.1
4	D	174	VAL	3.0
1	A	91	GLY	3.0
5	E	244	ASP	3.0
1	A	90	ALA	3.0
4	D	114	GLN	2.9
2	B	0	MET	2.9
1	A	15	PRO	2.8
4	D	179	LYS	2.8
4	D	68	ASP	2.8
4	D	201	SER	2.7
5	E	142	THR	2.7
1	A	176	LYS	2.7
4	D	134	CYS	2.6
1	A	252	GLY	2.6
4	D	165	SER	2.6
4	D	124	ARG	2.6
4	D	180	SER	2.6
1	A	255	GLN	2.5
2	B	75	LYS	2.5
5	E	18	GLY	2.5
1	A	108	ARG	2.5
1	A	41	ALA	2.5
1	A	267	PRO	2.5
5	E	143	LEU	2.4
4	D	186	ASN	2.4
4	D	128	SER	2.3
1	A	268	LYS	2.3
5	E	145	CYS	2.2
2	B	74	GLU	2.2
1	A	106	ASP	2.1
2	B	73	THR	2.1
1	A	105	SER	2.1
5	E	221	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
5	E	175	GLN	2.1
4	D	173	ALA	2.1
5	E	199	THR	2.0
5	E	153	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.