Full wwPDB X-ray Structure Validation Report ⓘ

Feb 22, 2024 – 02:59 AM JST

PDB ID	:	8IJ7
Title	:	Crystal structure of alcohol dehydrogenase from Burkholderia gladioli
Authors	:	Han, X.; Mei, Z.L.; Liu, W.D.; Sun, Z.T.; Ma, J.A.
Deposited on	:	2023-02-26
Resolution	:	2.54 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:

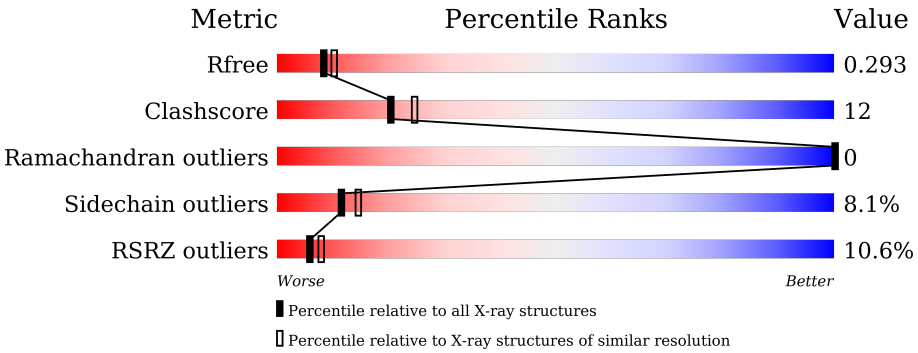
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 <=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	251	79% 20%
1	B	251	10% 75% 22%
1	C	251	16% 67% 32%
1	D	251	15% 61% 36%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7148 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 Putative short-chain dehydrogenases/reductase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1797	1116	322	357	2			
1	B	249	Total	C	N	O	S	0	0	0
			1793	1114	321	356	2			
1	C	248	Total	C	N	O	S	0	0	0
			1738	1084	298	354	2			
1	D	249	Total	C	N	O	S	0	0	0
			1743	1087	299	355	2			

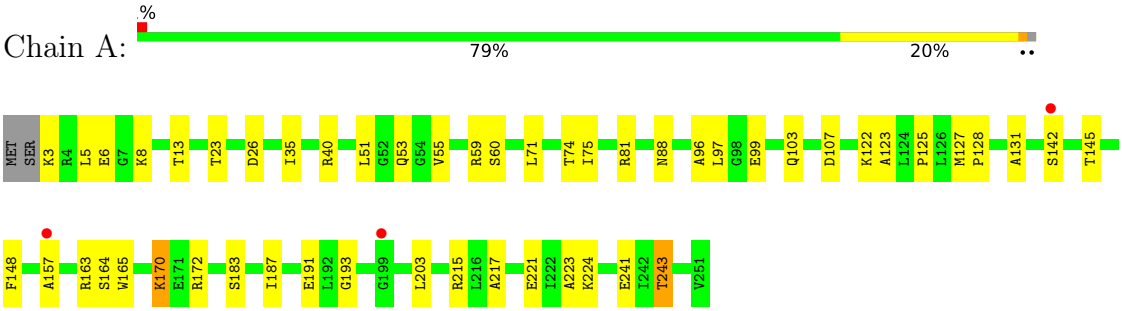
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	39	Total	O	0	0
			39	39		
2	B	14	Total	O	0	0
			14	14		
2	C	13	Total	O	0	0
			13	13		
2	D	11	Total	O	0	0
			11	11		

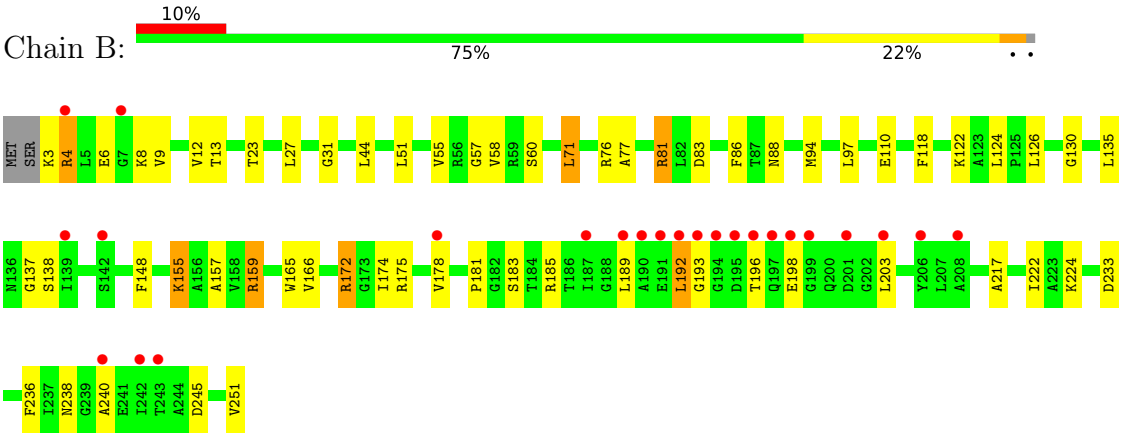
3 Residue-property plots (i)

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.

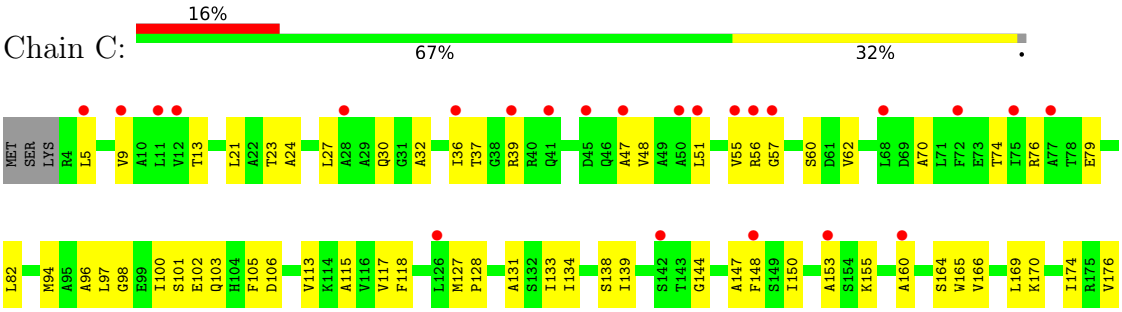
• Molecule 1: Putative short-chain dehydrogenases/reductase family protein

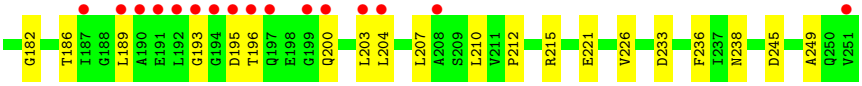


• Molecule 1: Putative short-chain dehydrogenases/reductase family protein

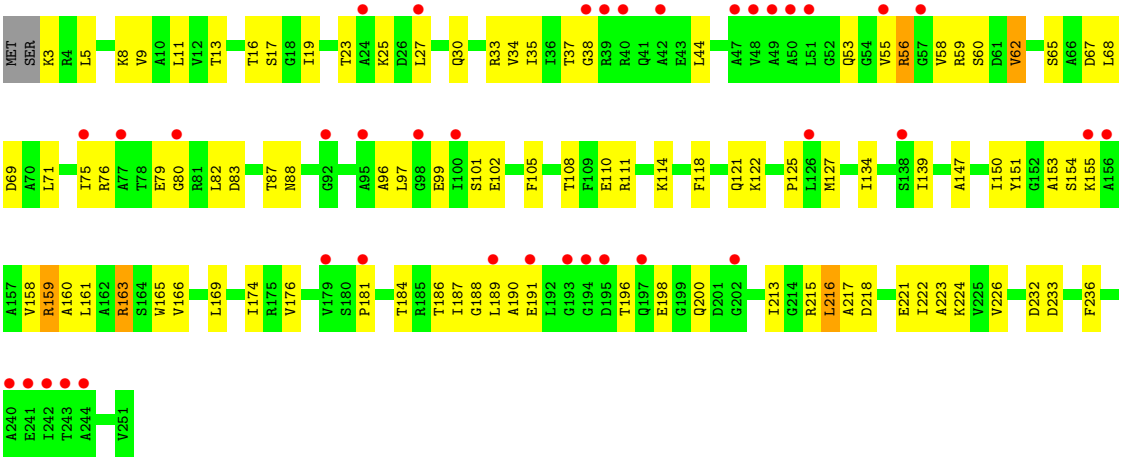


• Molecule 1: Putative short-chain dehydrogenases/reductase family protein





• Molecule 1: Putative short-chain dehydrogenases/reductase family protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	108.40Å 109.41Å 217.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.35 – 2.54 44.41 – 2.54	Depositor EDS
% Data completeness (in resolution range)	94.5 (27.35-2.54) 88.6 (44.41-2.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.10 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.246 , 0.294 0.253 , 0.293	Depositor DCC
R_{free} test set	2044 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	54.9	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 54.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.052 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7148	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.36	0/1814	0.61	0/2454
1	B	0.39	0/1810	0.64	0/2449
1	C	0.42	0/1755	0.66	0/2385
1	D	0.43	0/1760	0.63	0/2392
All	All	0.40	0/7139	0.63	0/9680

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1797	0	1822	25	0
1	B	1793	0	1816	39	0
1	C	1738	0	1717	63	0
1	D	1743	0	1719	77	0
2	A	39	0	0	1	0
2	B	14	0	0	0	0
2	C	13	0	0	0	0
2	D	11	0	0	2	0
All	All	7148	0	7074	176	0

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 12.

All (176) 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)
1:D:35:ILE:HD13	1:D:75:ILE:HG12	1.59	0.83
1:D:187:ILE:HD12	1:D:188:GLY:N	1.93	0.82
1:D:186:THR:HG22	1:D:188:GLY:H	1.44	0.82
1:D:34:VAL:HB	1:D:55:VAL:HG22	1.64	0.79
1:C:102:GLU:HA	1:D:118:PHE:HZ	1.48	0.78
1:D:60:SER:HB2	1:D:67:ASP:HB3	1.66	0.78
1:B:193:GLY:HA3	1:B:203:LEU:HG	1.65	0.78
1:C:56:ARG:HH22	1:C:74:THR:CB	1.99	0.74
1:C:13:THR:HA	1:C:37:THR:HB	1.70	0.73
1:C:9:VAL:HG12	1:C:82:LEU:HD12	1.71	0.72
1:D:187:ILE:HD12	1:D:188:GLY:H	1.52	0.71
1:C:56:ARG:HH22	1:C:74:THR:HB	1.56	0.71
1:C:100:ILE:H	1:D:121:GLN:HE22	1.37	0.70
1:D:76:ARG:HA	1:D:80:GLY:HA2	1.74	0.69
1:C:169:LEU:HD11	1:D:97:LEU:HD23	1.73	0.69
1:C:139:ILE:HD13	1:C:182:GLY:HA2	1.73	0.68
1:A:128:PRO:HD2	1:A:131:ALA:HB2	1.76	0.67
1:B:51:LEU:HD13	1:B:55:VAL:HG11	1.79	0.65
1:A:103:GLN:NE2	1:A:107:ASP:OD2	2.31	0.63
1:C:48:VAL:HG21	1:C:57:GLY:HA3	1.80	0.63
1:B:236:PHE:CZ	1:D:217:ALA:HB2	2.34	0.63
1:B:6:GLU:HG3	1:B:31:GLY:HA3	1.81	0.63
1:C:105:PHE:CE1	1:D:114:LYS:HG3	2.35	0.62
1:D:159:ARG:NH2	2:D:302:HOH:O	2.32	0.61
1:C:203:LEU:O	1:C:207:LEU:HD12	2.01	0.61
1:C:51:LEU:HB2	1:C:55:VAL:HG11	1.82	0.61
1:A:217:ALA:HB2	1:C:236:PHE:CE2	2.36	0.60
1:C:56:ARG:NH2	1:C:74:THR:OG1	2.34	0.60
1:C:98:GLY:H	1:D:121:GLN:HE21	1.49	0.60
1:C:113:VAL:O	1:C:117:VAL:HG23	2.02	0.59
1:D:5:LEU:HB2	1:D:30:GLN:HB2	1.83	0.59
1:C:62:VAL:HB	1:C:115:ALA:HB1	1.83	0.59
1:B:9:VAL:HG23	1:B:81:ARG:HE	1.67	0.59
1:D:151:TYR:CE1	1:D:155:LYS:HE2	2.37	0.59
1:C:56:ARG:NH2	1:C:74:THR:HB	2.17	0.58
1:C:23:THR:HG22	1:C:27:LEU:HD11	1.86	0.57
1:B:118:PHE:O	1:B:122:LYS:HG3	2.04	0.57
1:D:96:ALA:HA	1:D:147:ALA:HA	1.85	0.57
1:B:193:GLY:CA	1:B:203:LEU:HG	2.35	0.57
1:C:215:ARG:NH2	1:C:221:GLU:OE1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:23:THR:O	1:D:27:LEU:HD12	2.06	0.56
1:D:38:GLY:H	1:D:59:ARG:HA	1.71	0.56
1:D:218:ASP:HB3	1:D:221:GLU:HG3	1.87	0.56
1:C:70:ALA:O	1:C:74:THR:HG23	2.05	0.56
1:D:9:VAL:N	1:D:83:ASP:OD2	2.24	0.56
1:C:128:PRO:HD2	1:C:131:ALA:HB2	1.86	0.55
1:C:56:ARG:NH2	1:C:74:THR:CB	2.69	0.55
1:C:98:GLY:N	1:D:121:GLN:HE21	2.05	0.55
1:C:127:MET:HE1	1:C:133:ILE:HG12	1.88	0.55
1:A:96:ALA:O	1:A:99:GLU:HG2	2.07	0.54
1:B:181:PRO:HB3	1:B:222:ILE:HD12	1.88	0.54
1:D:110:GLU:HA	1:D:114:LYS:HB2	1.89	0.54
1:A:157:ALA:HB2	1:B:157:ALA:HB2	1.90	0.54
1:C:47:ALA:O	1:C:51:LEU:HD23	2.08	0.54
1:C:94:MET:HG2	1:C:148:PHE:CZ	2.43	0.54
1:C:102:GLU:HA	1:D:118:PHE:CZ	2.36	0.54
1:D:186:THR:HG22	1:D:188:GLY:N	2.19	0.54
1:C:36:ILE:HD11	1:C:48:VAL:HG23	1.89	0.53
1:D:151:TYR:CZ	1:D:155:LYS:HE2	2.43	0.53
1:B:137:GLY:O	1:B:181:PRO:HD2	2.09	0.53
1:C:21:LEU:HD11	1:C:51:LEU:HD21	1.90	0.53
1:C:134:ILE:HG21	1:C:226:VAL:HG13	1.89	0.53
1:C:103:GLN:HA	1:C:106:ASP:HB2	1.90	0.52
1:B:217:ALA:HB2	1:D:236:PHE:CZ	2.43	0.52
1:C:5:LEU:HB3	1:C:32:ALA:HB2	1.91	0.52
1:A:51:LEU:HD12	1:A:55:VAL:HG11	1.90	0.52
1:A:193:GLY:N	1:A:203:LEU:HD13	2.25	0.52
1:C:97:LEU:HA	1:C:100:ILE:HD12	1.90	0.52
1:C:9:VAL:HG21	1:C:79:GLU:HB3	1.92	0.52
1:D:53:GLN:N	1:D:53:GLN:OE1	2.42	0.52
1:D:169:LEU:HD13	1:D:174:ILE:HB	1.92	0.51
1:C:207:LEU:HA	1:C:210:LEU:HG	1.92	0.51
1:D:16:THR:CG2	1:D:38:GLY:HA2	2.40	0.51
1:B:23:THR:O	1:B:27:LEU:HG	2.10	0.51
1:C:166:VAL:HG22	1:C:238:ASN:OD1	2.10	0.51
1:C:196:THR:O	1:C:200:GLN:HG3	2.11	0.51
1:B:12:VAL:HG22	1:B:86:PHE:HB3	1.92	0.51
1:B:44:LEU:HD11	1:B:57:GLY:HA3	1.93	0.51
1:D:11:LEU:HD13	1:D:75:ILE:HD11	1.92	0.51
1:B:224:LYS:HB3	1:D:233:ASP:HB3	1.93	0.50
1:D:82:LEU:HG	1:D:127:MET:HE3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:PHE:HA	1:D:150:ILE:HG21	1.93	0.50
1:A:35:ILE:HD13	1:A:75:ILE:HG12	1.93	0.50
1:A:215:ARG:NH1	1:A:221:GLU:OE2	2.36	0.50
1:B:138:SER:HB3	1:B:155:LYS:HG3	1.92	0.50
1:D:8:LYS:O	1:D:33:ARG:N	2.46	0.49
1:D:154:SER:O	1:D:158:VAL:HG23	2.12	0.49
1:B:94:MET:HG2	1:B:148:PHE:CE1	2.47	0.49
1:B:217:ALA:HB2	1:D:236:PHE:CE2	2.47	0.49
1:D:19:ILE:O	1:D:23:THR:OG1	2.29	0.49
1:D:82:LEU:HB3	1:D:127:MET:HG2	1.93	0.49
1:C:118:PHE:HZ	1:D:102:GLU:HA	1.78	0.49
1:A:23:THR:HA	1:A:223:ALA:HB1	1.95	0.48
1:D:96:ALA:O	1:D:99:GLU:HG2	2.13	0.48
1:C:165:TRP:CD1	1:D:97:LEU:HD22	2.48	0.48
1:A:97:LEU:HG	1:B:124:LEU:HD11	1.95	0.48
1:D:181:PRO:HB3	1:D:222:ILE:HD12	1.96	0.48
1:B:135:LEU:HB2	1:B:178:VAL:HG22	1.96	0.48
1:B:240:ALA:HA	2:D:303:HOH:O	2.13	0.48
1:C:245:ASP:OD2	1:C:249:ALA:N	2.46	0.48
1:A:165:TRP:CD1	1:B:97:LEU:HD22	2.49	0.47
1:D:110:GLU:HG3	1:D:114:LYS:HD2	1.96	0.47
1:D:190:ALA:O	1:D:200:GLN:HG2	2.15	0.47
1:A:187:ILE:O	1:A:191:GLU:HG3	2.15	0.47
1:C:21:LEU:CD1	1:C:51:LEU:HD21	2.45	0.47
1:D:134:ILE:HD13	1:D:226:VAL:HG13	1.95	0.47
1:D:161:LEU:HD22	1:D:165:TRP:CZ2	2.50	0.47
1:A:5:LEU:O	1:A:8:LYS:HB2	2.15	0.46
1:B:130:GLY:O	1:B:175:ARG:NH2	2.48	0.46
1:D:216:LEU:HD22	1:D:216:LEU:HA	1.80	0.46
1:D:105:PHE:HD2	1:D:150:ILE:HD12	1.80	0.46
1:D:184:THR:O	1:D:189:LEU:HD22	2.16	0.46
1:A:13:THR:O	1:A:88:ASN:HB3	2.15	0.46
1:C:138:SER:HB3	1:C:155:LYS:HG3	1.98	0.46
1:D:56:ARG:NH1	1:D:79:GLU:OE1	2.49	0.46
1:B:172:ARG:HB3	1:B:174:ILE:HG13	1.98	0.46
1:D:139:ILE:HG23	1:D:181:PRO:O	2.15	0.46
1:D:65:SER:O	1:D:69:ASP:OD1	2.33	0.46
1:C:169:LEU:HD23	1:C:174:ILE:HB	1.98	0.45
1:C:100:ILE:H	1:D:121:GLN:NE2	2.11	0.45
1:B:245:ASP:OD2	1:B:245:ASP:N	2.50	0.45
1:B:236:PHE:CE2	1:D:217:ALA:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:PHE:HA	2:A:317:HOH:O	2.16	0.44
1:D:56:ARG:HH12	1:D:75:ILE:HA	1.82	0.44
1:A:97:LEU:HD22	1:B:165:TRP:CD1	2.52	0.44
1:A:224:LYS:HB3	1:C:233:ASP:HB3	1.99	0.44
1:C:48:VAL:HG13	1:C:55:VAL:HG13	1.99	0.44
1:D:23:THR:HA	1:D:223:ALA:HB1	1.98	0.44
1:B:233:ASP:HB3	1:D:224:LYS:HB3	1.99	0.44
1:C:200:GLN:O	1:C:204:LEU:HG	2.18	0.44
1:B:166:VAL:HG22	1:B:238:ASN:OD1	2.18	0.44
1:D:62:VAL:HG12	1:D:68:LEU:HD21	1.99	0.44
1:A:170:LYS:HD2	1:C:212:PRO:O	2.18	0.43
1:C:193:GLY:N	1:C:203:LEU:HD22	2.33	0.43
1:D:13:THR:O	1:D:88:ASN:HB3	2.17	0.43
1:D:37:THR:HA	1:D:58:VAL:O	2.18	0.43
1:B:4:ARG:HE	1:B:4:ARG:HB3	1.54	0.43
1:B:8:LYS:HA	1:B:83:ASP:OD1	2.19	0.43
1:C:203:LEU:HG	1:C:207:LEU:HD11	2.01	0.43
1:B:251:VAL:HG13	1:C:144:GLY:O	2.18	0.43
1:B:58:VAL:HB	1:B:71:LEU:HD12	1.99	0.43
1:C:160:ALA:HB3	1:D:153:ALA:HA	2.01	0.43
1:A:123:ALA:O	1:A:127:MET:HG3	2.19	0.43
1:C:96:ALA:HA	1:C:147:ALA:HA	2.01	0.43
1:B:189:LEU:HD23	1:B:189:LEU:HA	1.77	0.42
1:C:153:ALA:HA	1:D:160:ALA:HB3	1.99	0.42
1:B:13:THR:O	1:B:88:ASN:HB3	2.19	0.42
1:C:48:VAL:HG21	1:C:57:GLY:CA	2.49	0.42
1:C:150:ILE:HD13	1:C:150:ILE:HA	1.85	0.42
1:A:26:ASP:OD1	1:A:224:LYS:HE3	2.18	0.42
1:D:122:LYS:O	1:D:125:PRO:HD2	2.20	0.42
1:A:241:GLU:HG2	1:A:243:THR:HG22	2.00	0.42
1:C:24:ALA:HA	1:C:27:LEU:HD12	2.02	0.42
1:D:163:ARG:O	1:D:166:VAL:HG12	2.19	0.42
1:B:94:MET:HG3	1:B:192:LEU:HD21	2.02	0.42
1:C:82:LEU:O	1:C:127:MET:HG2	2.19	0.42
1:C:165:TRP:CE2	1:D:97:LEU:HD22	2.55	0.42
1:D:37:THR:HG22	1:D:71:LEU:HD11	2.02	0.41
1:B:159:ARG:HA	1:B:178:VAL:HG21	2.01	0.41
1:C:102:GLU:HG3	1:D:114:LYS:NZ	2.35	0.41
1:D:190:ALA:HB1	1:D:200:GLN:HG2	2.01	0.41
1:D:38:GLY:HA3	1:D:44:LEU:HB2	2.03	0.41
1:D:87:THR:O	1:D:87:THR:OG1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:163:ARG:H	1:D:163:ARG:HG3	1.68	0.41
1:C:97:LEU:HA	1:C:100:ILE:CD1	2.50	0.41
1:D:23:THR:HG22	1:D:27:LEU:HD11	2.03	0.41
1:A:122:LYS:O	1:A:125:PRO:HD2	2.21	0.41
1:D:189:LEU:HD12	1:D:189:LEU:HA	1.88	0.41
1:A:145:THR:HB	1:A:148:PHE:HB2	2.03	0.41
1:C:30:GLN:NE2	1:C:30:GLN:HA	2.36	0.40
1:D:187:ILE:H	1:D:187:ILE:HG13	1.62	0.40
1:A:203:LEU:C	1:A:203:LEU:HD23	2.42	0.40
1:B:76:ARG:HG3	1:B:77:ALA:N	2.35	0.40
1:D:16:THR:HG21	1:D:38:GLY:HA2	2.03	0.40
1:D:213:ILE:HG13	1:D:215:ARG:H	1.86	0.40
1:B:94:MET:HG2	1:B:148:PHE:CZ	2.56	0.40

There are no symmetry-related clashes.

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	247/251 (98%)	247 (100%)	0	0	100	100
1	B	247/251 (98%)	245 (99%)	2 (1%)	0	100	100
1	C	246/251 (98%)	243 (99%)	3 (1%)	0	100	100
1	D	247/251 (98%)	245 (99%)	2 (1%)	0	100	100
All	All	987/1004 (98%)	980 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	182/185 (98%)	166 (91%)	16 (9%)	10 12
1	B	181/185 (98%)	166 (92%)	15 (8%)	11 14
1	C	172/185 (93%)	162 (94%)	10 (6%)	20 26
1	D	172/185 (93%)	156 (91%)	16 (9%)	9 10
All	All	707/740 (96%)	650 (92%)	57 (8%)	11 14

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	6	GLU
1	A	40	ARG
1	A	53	GLN
1	A	59	ARG
1	A	60	SER
1	A	71	LEU
1	A	74	THR
1	A	81	ARG
1	A	142	SER
1	A	163	ARG
1	A	164	SER
1	A	170	LYS
1	A	172	ARG
1	A	183	SER
1	A	243	THR
1	B	3	LYS
1	B	4	ARG
1	B	60	SER
1	B	71	LEU
1	B	81	ARG
1	B	110	GLU
1	B	126	LEU
1	B	155	LYS

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Mol	Chain	Res	Type
1	B	159	ARG
1	B	172	ARG
1	B	183	SER
1	B	185	ARG
1	B	192	LEU
1	B	196	THR
1	B	198	GLU
1	C	39	ARG
1	C	60	SER
1	C	76	ARG
1	C	101	SER
1	C	164	SER
1	C	170	LYS
1	C	176	VAL
1	C	186	THR
1	C	189	LEU
1	C	195	ASP
1	D	3	LYS
1	D	17	SER
1	D	25	LYS
1	D	56	ARG
1	D	62	VAL
1	D	101	SER
1	D	108	THR
1	D	111	ARG
1	D	159	ARG
1	D	163	ARG
1	D	176	VAL
1	D	191	GLU
1	D	196	THR
1	D	198	GLU
1	D	216	LEU
1	D	232	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	30	GLN
1	C	41	GLN
1	D	41	GLN
1	D	46	GLN
1	D	121	GLN

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Mol	Chain	Res	Type
1	D	197	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	249/251 (99%)	0.13	3 (1%) 79 84	41, 54, 72, 89	0
1	B	249/251 (99%)	0.49	24 (9%) 8 10	40, 61, 100, 127	0
1	C	248/251 (98%)	0.94	40 (16%) 1 2	48, 77, 101, 132	0
1	D	249/251 (99%)	0.95	38 (15%) 2 2	55, 80, 107, 123	0
All	All	995/1004 (99%)	0.63	105 (10%) 6 8	40, 67, 100, 132	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	192	LEU	6.7
1	D	39	ARG	6.6
1	C	194	GLY	6.0
1	D	75	ILE	5.8
1	C	189	LEU	5.7
1	D	194	GLY	5.6
1	B	197	GLN	5.1
1	C	192	LEU	5.0
1	C	204	LEU	4.8
1	C	199	GLY	4.5
1	B	189	LEU	4.5
1	B	201	ASP	4.2
1	C	75	ILE	4.1
1	D	55	VAL	4.1
1	C	208	ALA	4.1
1	D	202	GLY	4.0
1	B	203	LEU	4.0
1	C	36	ILE	3.9
1	D	38	GLY	3.9
1	C	200	GLN	3.9
1	B	191	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	196	THR	3.8
1	B	198	GLU	3.8
1	D	193	GLY	3.8
1	D	189	LEU	3.8
1	B	193	GLY	3.7
1	D	191	GLU	3.7
1	C	195	ASP	3.6
1	D	51	LEU	3.5
1	B	195	ASP	3.4
1	C	196	THR	3.4
1	D	98	GLY	3.4
1	D	47	ALA	3.4
1	C	197	GLN	3.4
1	B	208	ALA	3.3
1	C	47	ALA	3.1
1	D	49	ALA	3.1
1	C	39	ARG	3.1
1	C	142	SER	3.1
1	B	242	ILE	3.1
1	C	72	PHE	3.1
1	C	191	GLU	3.1
1	B	194	GLY	3.1
1	C	57	GLY	3.0
1	C	77	ALA	3.0
1	C	28	ALA	3.0
1	D	100	ILE	3.0
1	B	206	TYR	3.0
1	C	11	LEU	3.0
1	C	55	VAL	2.9
1	B	243	THR	2.9
1	B	4	ARG	2.9
1	D	77	ALA	2.9
1	C	126	LEU	2.9
1	C	193	GLY	2.8
1	D	138	SER	2.8
1	D	156	ALA	2.8
1	C	153	ALA	2.8
1	C	251	VAL	2.7
1	D	27	LEU	2.7
1	B	190	ALA	2.7
1	C	187	ILE	2.7
1	C	56	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	40	ARG	2.7
1	C	68	LEU	2.7
1	D	80	GLY	2.7
1	C	203	LEU	2.6
1	C	51	LEU	2.6
1	B	178	VAL	2.6
1	B	199	GLY	2.6
1	D	242	ILE	2.6
1	D	57	GLY	2.6
1	C	45	ASP	2.5
1	D	195	ASP	2.5
1	C	9	VAL	2.5
1	C	5	LEU	2.4
1	D	197	GLN	2.4
1	D	240	ALA	2.4
1	D	24	ALA	2.4
1	B	139	ILE	2.4
1	B	240	ALA	2.4
1	C	41	GLN	2.4
1	C	190	ALA	2.3
1	D	241	GLU	2.3
1	D	243	THR	2.3
1	C	148	PHE	2.3
1	D	155	LYS	2.3
1	C	50	ALA	2.3
1	B	187	ILE	2.2
1	D	50	ALA	2.2
1	D	48	VAL	2.2
1	C	160	ALA	2.2
1	D	92	GLY	2.2
1	A	157	ALA	2.1
1	A	199	GLY	2.1
1	D	95	ALA	2.1
1	D	179	VAL	2.1
1	A	142	SER	2.1
1	B	142	SER	2.1
1	D	126	LEU	2.1
1	D	42	ALA	2.1
1	D	181	PRO	2.0
1	B	7	GLY	2.0
1	D	244	ALA	2.0
1	C	12	VAL	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.