Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 06:13 AM EDT

PDB ID	:	6BAN
Title	:	Potent and Selective Antitumor Activity of a T-Cell Engaging Bispecific Antibody Targeting a Membrane-Proximal Epitope of ROR1
Authors	:	Park, H.; Rader, C.
Deposited on	:	2017-10-14
Resolution	:	1.95 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:

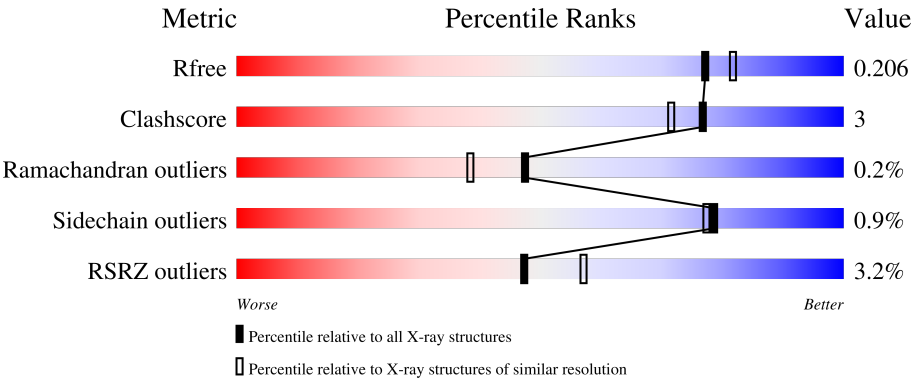
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	114	93%
1	C	114	96%
1	E	114	95%
1	G	114	95%
2	B	117	4% 89% 8%

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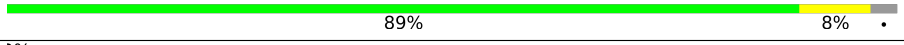
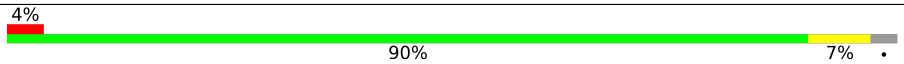
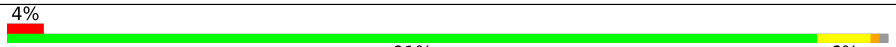
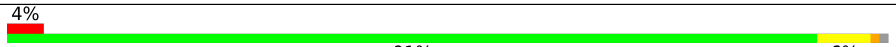
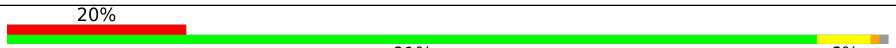
Mol	Chain	Length	Quality of chain
2	D	117	
2	F	117	
2	H	117	
3	M	82	
3	N	82	
3	O	82	
3	P	82	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10703 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 Variable domain of R11 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	0	0	0
			810	501	140	166	3			
1	C	111	Total	C	N	O	S	0	0	0
			813	503	140	166	4			
1	E	111	Total	C	N	O	S	0	0	0
			813	503	140	166	4			
1	G	111	Total	C	N	O	S	0	0	0
			813	503	140	166	4			

- Molecule 2 is a protein called Variable domain R11 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			
2	D	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			
2	F	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			
2	H	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			

- Molecule 3 is a protein called Inactive tyrosine-protein kinase transmembrane receptor ROR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	81	Total	C	N	O	S	0	0	0
			641	398	115	122	6			
3	N	81	Total	C	N	O	S	0	0	0
			641	398	115	122	6			
3	O	81	Total	C	N	O	S	0	0	0
			646	401	117	122	6			
3	P	81	Total	C	N	O	S	0	0	0
			641	398	115	122	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	310	MET	-	initiating methionine	UNP Q01973
N	310	MET	-	initiating methionine	UNP Q01973
O	310	MET	-	initiating methionine	UNP Q01973
P	310	MET	-	initiating methionine	UNP Q01973

- Molecule 4 is water.

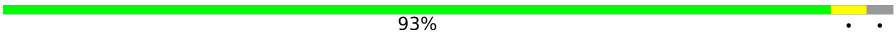
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	133	Total O 133 133	0	0
4	B	123	Total O 123 123	0	0
4	C	152	Total O 152 152	0	0
4	D	137	Total O 137 137	0	0
4	E	146	Total O 146 146	0	0
4	F	116	Total O 116 116	0	0
4	G	149	Total O 149 149	0	0
4	H	119	Total O 119 119	0	0
4	M	102	Total O 102 102	0	0
4	N	118	Total O 118 118	0	0
4	O	77	Total O 77 77	0	0
4	P	53	Total O 53 53	0	0

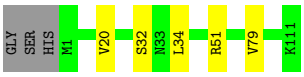
3 Residue-property plots (i)

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: Variable domain of R11 Light Chain

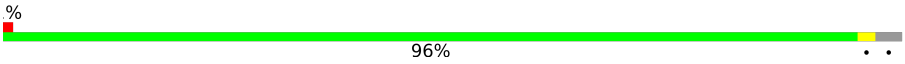
Chain A:

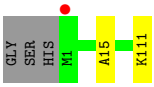




• Molecule 1: Variable domain of R11 Light Chain

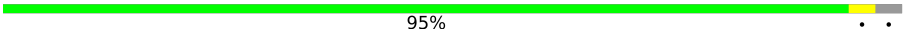
Chain C:

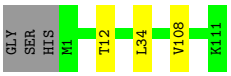




• Molecule 1: Variable domain of R11 Light Chain

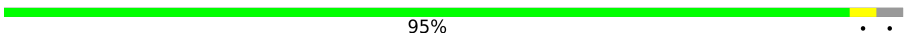
Chain E:

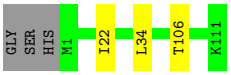




• Molecule 1: Variable domain of R11 Light Chain

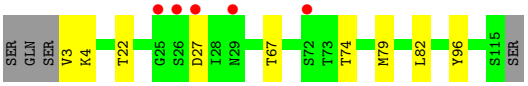
Chain G:





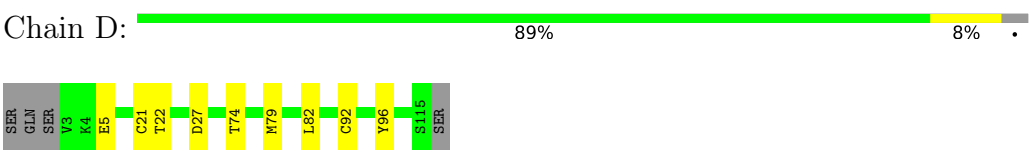
• Molecule 2: Variable domain R11 Heavy chain

Chain B:



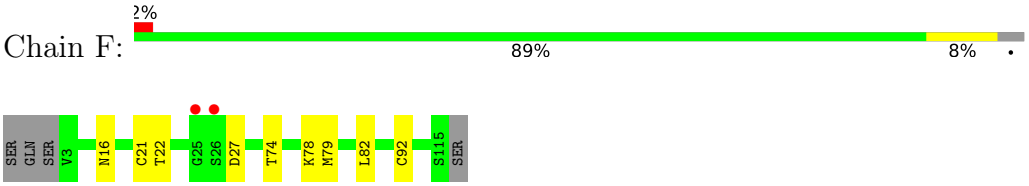
• Molecule 2: Variable domain R11 Heavy chain

Chain D:



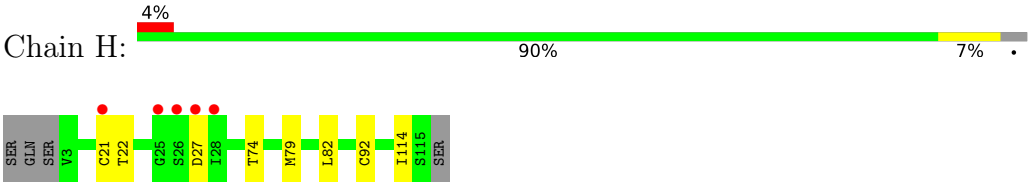
• Molecule 2: Variable domain R11 Heavy chain

Chain F:



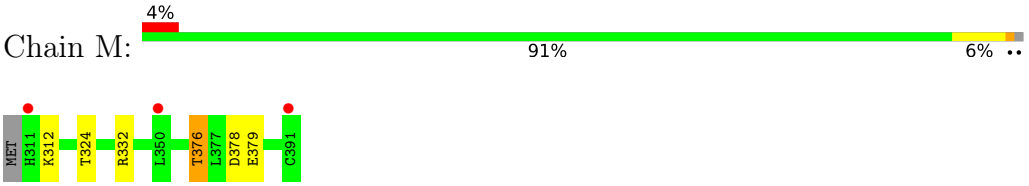
• Molecule 2: Variable domain R11 Heavy chain

Chain H:



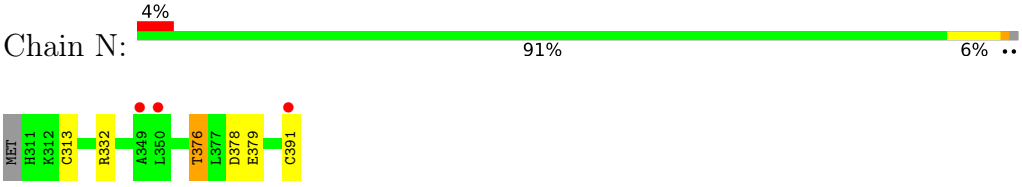
• Molecule 3: Inactive tyrosine-protein kinase transmembrane receptor ROR1

Chain M:



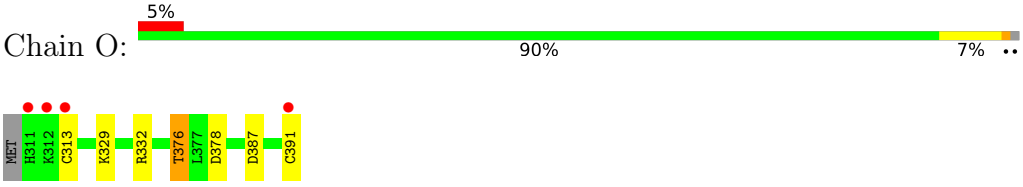
• Molecule 3: Inactive tyrosine-protein kinase transmembrane receptor ROR1

Chain N:



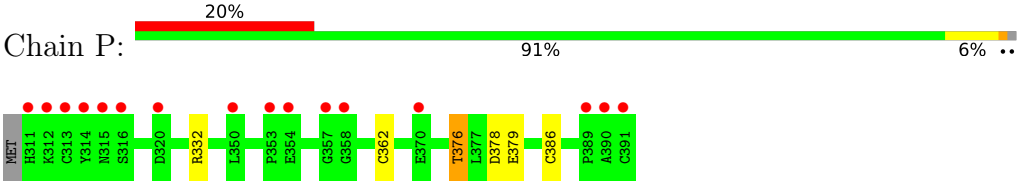
• Molecule 3: Inactive tyrosine-protein kinase transmembrane receptor ROR1

Chain O:



• Molecule 3: Inactive tyrosine-protein kinase transmembrane receptor ROR1

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	86.79Å 84.36Å 102.74Å 90.00° 113.88° 90.00°	Depositor
Resolution (Å)	41.04 – 1.95 41.04 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.04-1.95) 99.8 (41.04-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.57 (at 1.95Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.160 , 0.196 0.168 , 0.206	Depositor DCC
R_{free} test set	4839 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	17.7	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 56.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10703	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.18% 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	0.52	0/824	0.67	0/1121
1	C	0.52	0/827	0.65	0/1124
1	E	0.48	0/827	0.66	0/1124
1	G	0.50	0/827	0.65	0/1124
2	B	0.52	0/888	0.64	0/1214
2	D	0.55	0/888	0.65	0/1214
2	F	0.52	0/888	0.64	0/1214
2	H	0.48	0/888	0.62	0/1214
3	M	0.54	0/661	0.62	1/899 (0.1%)
3	N	0.57	0/661	0.62	1/899 (0.1%)
3	O	0.46	0/667	0.65	0/907
3	P	0.48	0/661	0.59	0/899
All	All	0.51	0/9507	0.64	2/12953 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	N	376	THR	N-CA-CB	-5.70	99.47	110.30
3	M	376	THR	N-CA-CB	-5.36	100.11	110.30

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	810	0	790	2	0
1	C	813	0	797	1	0
1	E	813	0	795	1	0
1	G	813	0	797	1	0
2	B	865	0	824	4	0
2	D	865	0	824	4	0
2	F	865	0	824	7	0
2	H	865	0	824	5	0
3	M	641	0	582	6	0
3	N	641	0	582	5	0
3	O	646	0	587	5	0
3	P	641	0	584	6	0
4	A	133	0	0	0	0
4	B	123	0	0	1	0
4	C	152	0	0	0	0
4	D	137	0	0	0	0
4	E	146	0	0	0	0
4	F	116	0	0	2	0
4	G	149	0	0	0	0
4	H	119	0	0	0	0
4	M	102	0	0	0	0
4	N	118	0	0	0	0
4	O	77	0	0	0	0
4	P	53	0	0	0	0
All	All	10703	0	8810	46	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 3.

All (46) 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)
2:D:21:CYS:HG	2:D:92:CYS:HG	1.14	0.92
2:F:21:CYS:HG	2:F:92:CYS:HG	1.29	0.70
2:H:21:CYS:HG	2:H:92:CYS:HG	1.47	0.61
1:A:20:VAL:HG23	1:A:79:VAL:HG21	1.82	0.61
3:O:376:THR:HG23	3:O:378:ASP:H	1.66	0.60
3:P:376:THR:HG23	3:P:378:ASP:H	1.65	0.59
2:H:22:THR:HG22	2:H:74:THR:HG22	1.84	0.59
2:F:22:THR:HG22	2:F:74:THR:HG22	1.86	0.58
2:F:79:MET:HB2	2:F:82:LEU:HD21	1.85	0.58
2:B:22:THR:HG22	2:B:74:THR:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:332:ARG:HD3	3:O:376:THR:HG21	1.87	0.57
2:D:22:THR:HG22	2:D:74:THR:HG22	1.87	0.56
2:F:78:LYS:HE3	4:F:235:HOH:O	2.07	0.53
3:M:376:THR:CG2	3:M:378:ASP:H	2.21	0.52
2:D:5:GLU:OE1	2:F:21:CYS:SG	2.68	0.52
3:N:376:THR:CG2	3:N:378:ASP:H	2.23	0.52
2:B:3:VAL:HG13	2:B:4:LYS:HG2	1.93	0.51
3:M:376:THR:HG22	3:M:378:ASP:H	1.75	0.51
3:N:332:ARG:HD3	3:N:376:THR:HG21	1.92	0.51
2:F:16:ASN:HB2	4:F:235:HOH:O	2.11	0.50
3:M:332:ARG:HD3	3:M:376:THR:HG21	1.94	0.50
3:N:376:THR:HG22	3:N:378:ASP:H	1.77	0.50
3:P:376:THR:CG2	3:P:378:ASP:H	2.26	0.48
3:P:362:CYS:SG	3:P:386:CYS:CB	3.00	0.48
2:H:82:LEU:HB3	2:H:114:ILE:HG12	1.95	0.48
3:P:332:ARG:HD3	3:P:376:THR:HG21	1.96	0.47
2:B:79:MET:HB3	2:B:82:LEU:HD21	1.96	0.47
1:C:15:ALA:HA	1:C:111:LYS:HG3	1.97	0.47
2:H:79:MET:HB3	2:H:82:LEU:HD21	1.97	0.46
3:N:313:CYS:SG	3:N:391:CYS:HB2	2.56	0.46
3:O:376:THR:CG2	3:O:378:ASP:H	2.29	0.46
2:B:67:THR:HG22	4:B:282:HOH:O	2.17	0.45
3:O:313:CYS:SG	3:O:391:CYS:SG	3.05	0.45
2:H:21:CYS:SG	2:H:92:CYS:SG	3.06	0.45
3:M:379:GLU:CD	3:M:379:GLU:H	2.21	0.45
3:M:312:LYS:HZ1	3:M:324:THR:H	1.65	0.44
1:E:12:THR:HG22	1:E:108:VAL:HG22	1.98	0.44
3:N:379:GLU:CD	3:N:379:GLU:H	2.21	0.43
3:M:312:LYS:NZ	3:M:324:THR:H	2.16	0.43
2:F:79:MET:HG3	2:F:82:LEU:HD11	2.01	0.42
3:P:379:GLU:H	3:P:379:GLU:CD	2.22	0.42
2:D:79:MET:HB3	2:D:82:LEU:HD21	2.01	0.42
1:A:32:SER:O	1:A:51:ARG:HA	2.21	0.41
1:G:22:ILE:HG12	1:G:106:THR:HG21	2.02	0.41
3:O:329:LYS:HA	3:O:387:ASP:HB2	2.03	0.41
3:P:362:CYS:CB	3:P:386:CYS:SG	3.09	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	109/114 (96%)	104 (95%)	5 (5%)	0	100	100
1	C	109/114 (96%)	103 (94%)	6 (6%)	0	100	100
1	E	109/114 (96%)	104 (95%)	5 (5%)	0	100	100
1	G	109/114 (96%)	104 (95%)	5 (5%)	0	100	100
2	B	111/117 (95%)	109 (98%)	1 (1%)	1 (1%)	17	8
2	D	111/117 (95%)	109 (98%)	1 (1%)	1 (1%)	17	8
2	F	111/117 (95%)	107 (96%)	4 (4%)	0	100	100
2	H	111/117 (95%)	109 (98%)	2 (2%)	0	100	100
3	M	79/82 (96%)	78 (99%)	1 (1%)	0	100	100
3	N	79/82 (96%)	78 (99%)	1 (1%)	0	100	100
3	O	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
3	P	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
All	All	1196/1252 (96%)	1159 (97%)	35 (3%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	96	TYR
2	D	96	TYR

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	89/92 (97%)	88 (99%)	1 (1%)	73	71
1	C	90/92 (98%)	90 (100%)	0	100	100
1	E	90/92 (98%)	89 (99%)	1 (1%)	73	71
1	G	90/92 (98%)	89 (99%)	1 (1%)	73	71
2	B	94/98 (96%)	93 (99%)	1 (1%)	73	71
2	D	94/98 (96%)	93 (99%)	1 (1%)	73	71
2	F	94/98 (96%)	93 (99%)	1 (1%)	73	71
2	H	94/98 (96%)	93 (99%)	1 (1%)	73	71
3	M	71/73 (97%)	71 (100%)	0	100	100
3	N	71/73 (97%)	71 (100%)	0	100	100
3	O	72/73 (99%)	71 (99%)	1 (1%)	67	62
3	P	71/73 (97%)	70 (99%)	1 (1%)	67	62
All	All	1020/1052 (97%)	1011 (99%)	9 (1%)	78	77

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LEU
2	B	27	ASP
2	D	27	ASP
1	E	34	LEU
2	F	27	ASP
1	G	34	LEU
2	H	27	ASP
3	O	376	THR
3	P	376	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	16	ASN
3	M	359	HIS
3	O	315	ASN

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	111/114 (97%)	-0.59	0 100 100	9, 19, 37, 61	0
1	C	111/114 (97%)	-0.54	1 (0%) 84 89	9, 16, 33, 66	0
1	E	111/114 (97%)	-0.52	0 100 100	12, 21, 34, 69	0
1	G	111/114 (97%)	-0.57	0 100 100	12, 20, 36, 66	0
2	B	113/117 (96%)	-0.13	5 (4%) 34 44	8, 19, 48, 59	0
2	D	113/117 (96%)	-0.29	0 100 100	7, 16, 40, 51	0
2	F	113/117 (96%)	-0.28	2 (1%) 68 76	11, 20, 48, 56	0
2	H	113/117 (96%)	-0.24	5 (4%) 34 44	12, 22, 50, 64	0
3	M	81/82 (98%)	-0.41	3 (3%) 41 51	9, 17, 48, 84	0
3	N	81/82 (98%)	-0.25	3 (3%) 41 51	8, 17, 45, 72	0
3	O	81/82 (98%)	-0.05	4 (4%) 29 39	16, 29, 68, 109	0
3	P	81/82 (98%)	0.67	16 (19%) 1 1	16, 34, 72, 123	0
All	All	1220/1252 (97%)	-0.29	39 (3%) 47 57	7, 21, 50, 123	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	P	391	CYS	6.1
3	P	311	HIS	6.0
2	H	26	SER	5.4
3	N	391	CYS	4.4
3	P	357	GLY	4.4
3	P	313	CYS	4.2
3	O	391	CYS	4.2
3	P	358	GLY	3.9
3	O	311	HIS	3.7
3	P	350	LEU	3.7
2	F	25	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
3	P	316	SER	3.3
2	B	27	ASP	3.1
2	H	27	ASP	3.0
3	M	391	CYS	3.0
3	P	315	ASN	2.9
1	C	1	MET	2.9
2	B	26	SER	2.8
3	P	390	ALA	2.8
3	P	389	PRO	2.8
3	P	320	ASP	2.8
3	O	313	CYS	2.6
2	F	26	SER	2.6
3	M	350	LEU	2.6
3	P	312	LYS	2.5
3	P	370	GLU	2.5
3	O	312	LYS	2.5
2	H	28	ILE	2.4
3	P	314	TYR	2.4
2	H	21	CYS	2.3
2	B	25	GLY	2.3
3	M	311	HIS	2.2
2	B	72	SER	2.2
3	P	354	GLU	2.1
3	N	349	ALA	2.1
2	B	29	ASN	2.1
3	N	350	LEU	2.1
3	P	353	PRO	2.1
2	H	25	GLY	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.