Full wwPDB X-ray Structure Validation Report (i)

Aug 19, 2023 – 07:48 PM EDT

PDB ID	:	2H32
Title	:	Crystal structure of the pre-B cell receptor
Authors	:	Bankovich, A.J.
Deposited on	:	2006-05-22
Resolution	:	2.70 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 (i) 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 (1)) were used in the production of this report:

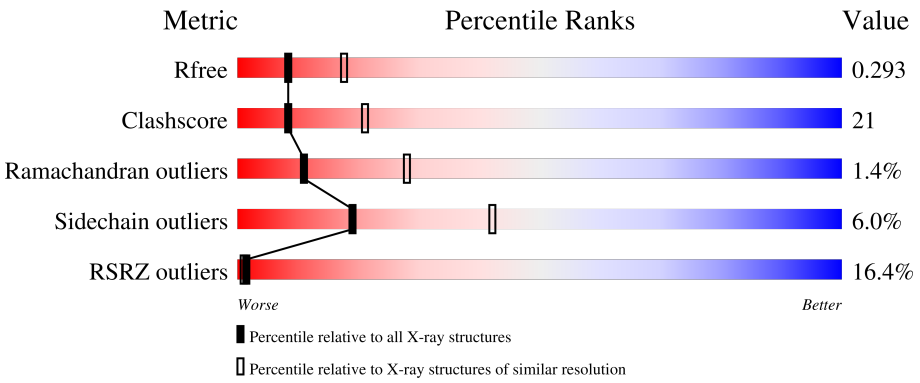
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

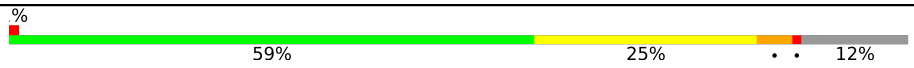
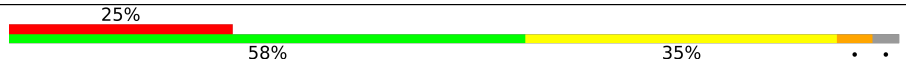
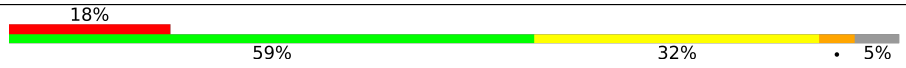
The reported resolution of this entry is 2.70 Å.

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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	126	
2	B	121	
3	H	223	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3535 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 Immunoglobulin iota chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	111	896	557	164	170	5	14	0	0

- Molecule 2 is a protein called Immunoglobulin omega chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	117	892	560	149	178	5	20	0	0

- Molecule 3 is a protein called Immunoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	211	1639	1048	268	314	9	26	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0
4	H	1	1	1	0	0

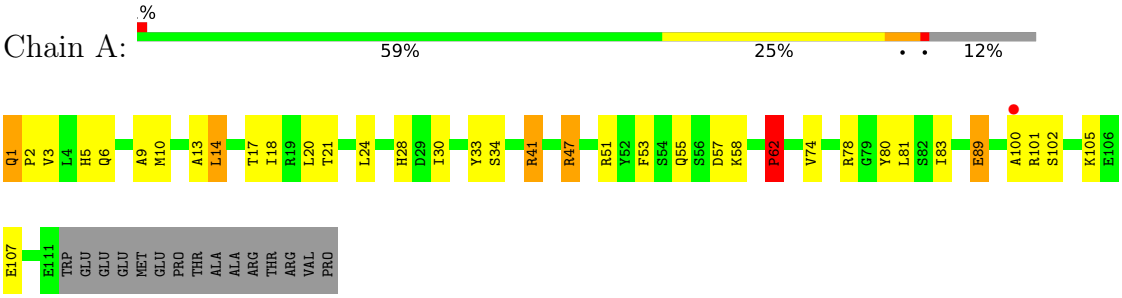
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	28	28	28	0	0
5	B	24	24	24	0	0
5	H	54	54	54	0	0

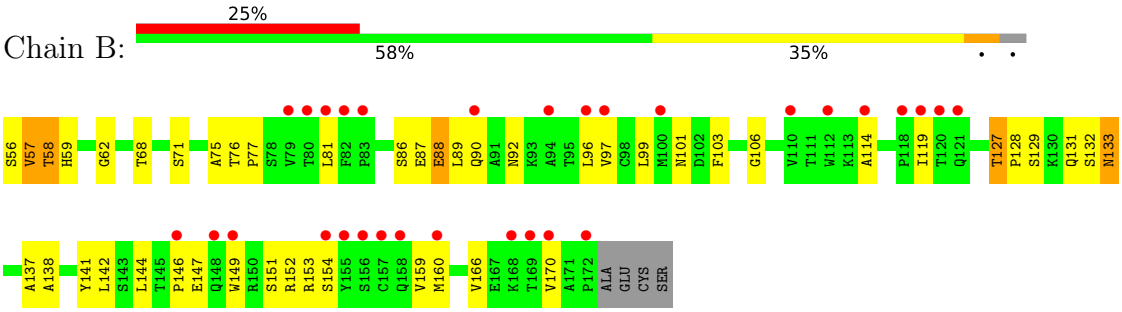
3 Residue-property plots (i)

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.

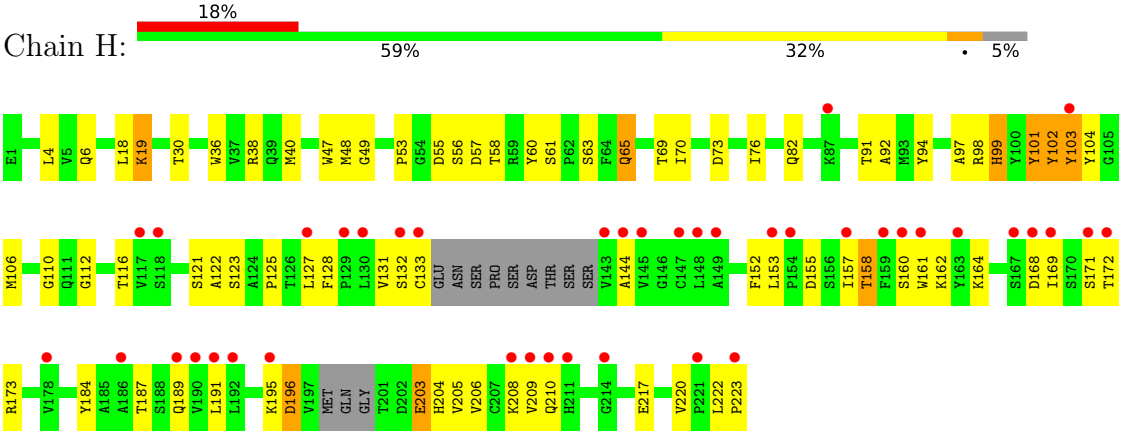
- Molecule 1: Immunoglobulin iota chain



- Molecule 2: Immunoglobulin omega chain



- Molecule 3: Immunoglobulin heavy chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	71.50Å 71.50Å 217.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 59.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-2.70) 99.6 (59.78-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	4.48 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019, CNS	Depositor
R, R_{free}	0.267 , 0.295 0.259 , 0.293	Depositor DCC
R_{free} test set	826 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	65.4	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 61.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3535	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.81	3/920 (0.3%)	0.76	0/1245
2	B	0.73	3/913 (0.3%)	0.62	0/1247
3	H	0.79	4/1685 (0.2%)	0.67	0/2289
All	All	0.78	10/3518 (0.3%)	0.68	0/4781

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	203	GLU	CD-OE1	9.97	1.36	1.25
3	H	203	GLU	CD-OE2	8.47	1.34	1.25
1	A	107	GLU	CB-CG	7.03	1.65	1.52
1	A	89	GLU	CD-OE2	6.83	1.33	1.25
2	B	87	GLU	CD-OE2	6.69	1.33	1.25
1	A	1	GLN	CB-CG	-6.52	1.34	1.52
3	H	168	ASP	CG-OD2	5.83	1.38	1.25
3	H	168	ASP	CG-OD1	5.78	1.38	1.25
2	B	88	GLU	CD-OE1	5.49	1.31	1.25
2	B	144	LEU	CB-CG	5.09	1.67	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	896	0	859	37	0
2	B	892	0	879	43	0
3	H	1639	0	1583	77	1
4	A	1	0	0	0	0
4	H	1	0	0	0	0
5	A	28	0	0	11	0
5	B	24	0	0	10	0
5	H	54	0	0	15	1
All	All	3535	0	3321	138	1

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 21.

All (138) 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:A:80:TYR:HD1	5:A:319:HOH:O	1.45	1.00
1:A:14:LEU:HD11	2:B:71:SER:HA	1.49	0.94
3:H:102:TYR:O	3:H:104:TYR:N	2.09	0.85
1:A:14:LEU:HD12	1:A:14:LEU:H	1.42	0.84
3:H:57:ASP:HA	5:H:341:HOH:O	1.76	0.84
1:A:24:LEU:HB3	5:A:314:HOH:O	1.77	0.83
3:H:69:THR:HB	5:H:321:HOH:O	1.83	0.79
1:A:6:GLN:HE21	2:B:62:GLY:HA3	1.46	0.79
3:H:158:THR:HG23	3:H:210:GLN:HB2	1.66	0.78
1:A:47:ARG:NH1	5:A:327:HOH:O	2.17	0.77
2:B:129:SER:HB3	5:B:192:HOH:O	1.83	0.77
3:H:103:TYR:O	3:H:104:TYR:HD1	1.68	0.76
3:H:65:GLN:HB3	5:H:348:HOH:O	1.86	0.75
1:A:33:TYR:CE2	1:A:100:ALA:HB2	2.24	0.73
2:B:59:HIS:CE1	3:H:104:TYR:CZ	2.77	0.72
3:H:220:VAL:HG13	5:H:353:HOH:O	1.89	0.72
2:B:96:LEU:HB2	2:B:142:LEU:HB3	1.72	0.71
2:B:132:SER:H	3:H:173:ARG:HH12	1.37	0.70
3:H:99:HIS:CE1	3:H:103:TYR:O	2.45	0.70
1:A:102:SER:O	5:A:307:HOH:O	2.09	0.70
3:H:173:ARG:HG3	5:H:355:HOH:O	1.91	0.69
1:A:13:ALA:HA	5:B:180:HOH:O	1.92	0.69
2:B:59:HIS:CE1	3:H:104:TYR:CE2	2.81	0.68
2:B:103:PHE:CE2	2:B:106:GLY:HA2	2.29	0.67
1:A:78:ARG:HD3	1:A:80:TYR:OH	1.93	0.67
1:A:41:ARG:HD2	5:A:317:HOH:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:6:GLN:HE21	3:H:110:GLY:HA3	1.60	0.65
1:A:101:ARG:HA	3:H:103:TYR:OH	1.98	0.64
2:B:153:ARG:HH11	2:B:154:SER:HB2	1.61	0.64
5:B:198:HOH:O	3:H:128:PHE:CB	2.46	0.64
3:H:123:SER:HB3	5:H:317:HOH:O	1.96	0.64
2:B:97:VAL:HG12	2:B:99:LEU:CD1	2.29	0.63
2:B:59:HIS:NE2	3:H:104:TYR:CZ	2.67	0.62
1:A:6:GLN:NE2	2:B:62:GLY:HA3	2.13	0.61
3:H:122:ALA:HA	3:H:153:LEU:HB3	1.83	0.61
3:H:6:GLN:NE2	3:H:112:GLY:H	2.00	0.59
2:B:132:SER:H	3:H:173:ARG:NH1	1.99	0.57
3:H:104:TYR:HB2	5:H:347:HOH:O	2.04	0.57
3:H:99:HIS:ND1	3:H:103:TYR:O	2.37	0.57
2:B:86:SER:C	2:B:88:GLU:H	2.09	0.56
2:B:89:LEU:HD11	2:B:149:TRP:HD1	1.71	0.56
3:H:144:ALA:HB2	3:H:191:LEU:HG	1.87	0.56
3:H:38:ARG:HD3	3:H:40:MET:HG3	1.87	0.55
3:H:101:TYR:CD2	3:H:102:TYR:HD2	2.24	0.55
3:H:203:GLU:HA	5:H:310:HOH:O	2.06	0.55
2:B:147:GLU:O	2:B:151:SER:HB3	2.07	0.55
1:A:53:PHE:HB3	1:A:57:ASP:HB3	1.88	0.55
1:A:21:THR:HG23	1:A:80:TYR:CE2	2.42	0.55
3:H:217:GLU:HG2	5:H:330:HOH:O	2.06	0.54
1:A:33:TYR:CD2	1:A:100:ALA:HB2	2.42	0.54
1:A:14:LEU:N	5:B:180:HOH:O	2.40	0.54
3:H:155:ASP:HB2	3:H:184:TYR:CE2	2.42	0.54
3:H:101:TYR:CD2	3:H:102:TYR:CD2	2.96	0.54
3:H:121:SER:HB3	5:H:323:HOH:O	2.07	0.54
2:B:97:VAL:HG11	3:H:187:THR:HG21	1.91	0.53
3:H:40:MET:HG2	3:H:92:ALA:HB2	1.89	0.53
2:B:92:ASN:HA	2:B:146:PRO:HG2	1.90	0.52
2:B:131:GLN:OE1	2:B:137:ALA:HB2	2.09	0.52
3:H:102:TYR:C	3:H:104:TYR:H	2.11	0.52
2:B:96:LEU:O	2:B:141:TYR:HA	2.09	0.52
2:B:81:LEU:HD23	2:B:170:VAL:HG22	1.92	0.51
1:A:9:ALA:O	1:A:10:MET:HG3	2.10	0.51
2:B:59:HIS:NE2	3:H:104:TYR:CE2	2.78	0.51
5:B:196:HOH:O	3:H:173:ARG:HB3	2.10	0.51
3:H:205:VAL:O	3:H:220:VAL:HB	2.10	0.51
3:H:160:SER:OG	3:H:208:LYS:HB2	2.11	0.51
3:H:208:LYS:HG2	3:H:217:GLU:CB	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:57:VAL:O	2:B:58:THR:O	2.29	0.50
2:B:132:SER:N	3:H:173:ARG:HH12	2.07	0.50
2:B:97:VAL:HG12	2:B:99:LEU:HD11	1.93	0.50
1:A:62:PRO:HD2	5:A:316:HOH:O	2.11	0.50
1:A:33:TYR:CE2	2:B:57:VAL:HG21	2.47	0.50
2:B:131:GLN:HB3	3:H:173:ARG:NH1	2.26	0.49
3:H:161:TRP:HB3	3:H:169:ILE:HD12	1.95	0.49
1:A:30:ILE:HB	5:A:314:HOH:O	2.14	0.48
2:B:75:ALA:CB	5:B:190:HOH:O	2.62	0.48
3:H:47:TRP:HE3	3:H:61:SER:HB2	1.77	0.48
3:H:164:LYS:NZ	3:H:204:HIS:HE1	2.12	0.48
1:A:55:GLN:O	1:A:58:LYS:HE3	2.14	0.48
2:B:103:PHE:HE2	2:B:106:GLY:HA2	1.79	0.48
2:B:159:VAL:HB	2:B:166:VAL:CG1	2.44	0.48
1:A:30:ILE:HD12	5:A:314:HOH:O	2.14	0.47
2:B:58:THR:O	2:B:59:HIS:HB2	2.15	0.47
3:H:169:ILE:HG22	3:H:171:SER:H	1.78	0.47
2:B:160:MET:HE3	5:B:197:HOH:O	2.15	0.47
3:H:6:GLN:HB3	5:H:335:HOH:O	2.14	0.47
3:H:73:ASP:HB3	3:H:76:ILE:HG12	1.96	0.47
2:B:114:ALA:HB2	2:B:119:ILE:HD11	1.97	0.47
3:H:164:LYS:HZ3	3:H:204:HIS:HE1	1.62	0.47
3:H:49:GLY:HA3	3:H:70:ILE:CD1	2.45	0.46
3:H:4:LEU:O	3:H:110:GLY:HA2	2.14	0.46
3:H:131:VAL:HG12	3:H:132:SER:N	2.31	0.46
3:H:63:SER:N	5:H:345:HOH:O	2.49	0.46
1:A:20:LEU:HD12	1:A:20:LEU:N	2.30	0.46
1:A:101:ARG:CA	3:H:103:TYR:OH	2.63	0.46
3:H:196:ASP:HB2	5:H:337:HOH:O	2.15	0.46
1:A:5:HIS:HA	5:A:322:HOH:O	2.15	0.46
2:B:128:PRO:HA	2:B:137:ALA:O	2.16	0.46
1:A:51:ARG:HD3	3:H:102:TYR:CG	2.51	0.45
3:H:161:TRP:CD1	3:H:172:THR:HG21	2.51	0.45
3:H:127:LEU:HD11	3:H:209:VAL:HG22	1.98	0.45
2:B:138:ALA:HA	5:B:178:HOH:O	2.17	0.45
1:A:41:ARG:NH1	5:A:305:HOH:O	2.46	0.45
3:H:65:GLN:HB3	3:H:65:GLN:HE21	1.60	0.45
1:A:28:HIS:ND1	1:A:33:TYR:OH	2.40	0.44
2:B:56:SER:O	5:B:186:HOH:O	2.21	0.44
1:A:105:LYS:HB2	1:A:105:LYS:HE3	1.73	0.44
3:H:102:TYR:C	3:H:104:TYR:N	2.67	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:THR:HG23	1:A:80:TYR:HE2	1.81	0.44
3:H:38:ARG:HG3	3:H:94:TYR:CE2	2.52	0.44
3:H:60:TYR:HB2	5:H:348:HOH:O	2.18	0.44
3:H:19:LYS:CG	3:H:82:GLN:HG3	2.48	0.44
2:B:127:THR:HG22	2:B:128:PRO:HD2	1.99	0.43
3:H:36:TRP:O	3:H:48:MET:HB2	2.18	0.43
3:H:6:GLN:HE21	3:H:110:GLY:CA	2.27	0.43
1:A:41:ARG:NE	1:A:89:GLU:O	2.50	0.43
3:H:30:THR:HA	3:H:53:PRO:HB2	1.99	0.43
1:A:102:SER:C	5:A:307:HOH:O	2.55	0.43
3:H:208:LYS:HG2	3:H:217:GLU:HB2	2.00	0.43
2:B:59:HIS:CE1	3:H:104:TYR:CE1	3.06	0.43
3:H:82:GLN:HB3	5:H:321:HOH:O	2.19	0.43
3:H:133:CYS:SG	3:H:223:PRO:HB3	2.59	0.43
2:B:57:VAL:O	2:B:58:THR:C	2.57	0.42
1:A:18:ILE:HD13	1:A:20:LEU:HD11	2.01	0.42
2:B:59:HIS:HE1	3:H:104:TYR:CE1	2.37	0.42
3:H:157:ILE:HG13	3:H:210:GLN:O	2.19	0.42
1:A:1:GLN:HA	1:A:2:PRO:HD3	1.91	0.42
2:B:133:ASN:H	3:H:173:ARG:HH22	1.68	0.42
3:H:125:PRO:HA	3:H:152:PHE:HB3	2.01	0.42
1:A:17:THR:HA	1:A:83:ILE:O	2.20	0.41
2:B:76:THR:CG2	2:B:77:PRO:HD2	2.51	0.41
1:A:13:ALA:CA	5:B:180:HOH:O	2.61	0.41
3:H:162:LYS:O	3:H:205:VAL:HG23	2.21	0.41
3:H:91:THR:HG23	3:H:116:THR:HA	2.02	0.41
3:H:55:ASP:O	3:H:56:SER:HB2	2.21	0.40
3:H:162:LYS:HB3	3:H:206:VAL:HB	2.03	0.40
2:B:101:ASN:HB2	2:B:131:GLN:OE1	2.22	0.40
3:H:97:ALA:HB1	3:H:106:MET:HB3	2.03	0.40

All (1) 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)
3:H:58:THR:O	5:H:341:HOH:O[8_555]	2.16	0.04

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	109/126 (86%)	97 (89%)	11 (10%)	1 (1%)	17	40
2	B	115/121 (95%)	98 (85%)	14 (12%)	3 (3%)	5	13
3	H	205/223 (92%)	181 (88%)	22 (11%)	2 (1%)	15	37
All	All	429/470 (91%)	376 (88%)	47 (11%)	6 (1%)	11	28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	58	THR
3	H	103	TYR
1	A	62	PRO
2	B	57	VAL
3	H	195	LYS
2	B	152	ARG

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	98/111 (88%)	90 (92%)	8 (8%)	11	26
2	B	104/107 (97%)	100 (96%)	4 (4%)	33	62
3	H	181/192 (94%)	170 (94%)	11 (6%)	18	41
All	All	383/410 (93%)	360 (94%)	23 (6%)	19	42

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	14	LEU
1	A	34	SER
1	A	41	ARG
1	A	47	ARG
1	A	62	PRO
1	A	74	VAL
1	A	81	LEU
2	B	68	THR
2	B	90	GLN
2	B	127	THR
2	B	133	ASN
3	H	18	LEU
3	H	19	LYS
3	H	65	GLN
3	H	98	ARG
3	H	99	HIS
3	H	101	TYR
3	H	102	TYR
3	H	158	THR
3	H	189	GLN
3	H	196	ASP
3	H	222	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	44	HIS
2	B	72	GLN
2	B	133	ASN
3	H	6	GLN
3	H	65	GLN
3	H	99	HIS
3	H	189	GLN
3	H	204	HIS
3	H	213	ASN

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)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	111/126 (88%)	0.47	1 (0%)	84	85	35, 50, 79, 86	3 (2%)
2	B	117/121 (96%)	1.45	30 (25%)	0	0	39, 94, 110, 115	5 (4%)
3	H	211/223 (94%)	1.09	41 (19%)	1	0	32, 60, 120, 122	4 (1%)
All	All	439/470 (93%)	1.03	72 (16%)	1	1	32, 62, 117, 122	12 (2%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	143	VAL	12.0
2	B	149	TRP	7.7
2	B	155	TYR	7.2
3	H	172	THR	6.6
2	B	156	SER	6.5
3	H	163	TYR	6.3
2	B	81	LEU	5.5
2	B	96	LEU	5.4
2	B	112	TRP	4.8
2	B	82	PHE	4.6
3	H	147	CYS	4.4
3	H	145	VAL	4.3
3	H	133	CYS	4.2
2	B	83	PRO	4.2
3	H	209	VAL	4.2
2	B	119	ILE	4.2
3	H	159	PHE	4.0
3	H	161	TRP	3.9
3	H	144	ALA	3.9
3	H	103	TYR	3.8
3	H	192	LEU	3.8
3	H	118	SER	3.7
1	A	100	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
3	H	211	HIS	3.6
2	B	146	PRO	3.6
3	H	208	LYS	3.6
2	B	97	VAL	3.5
2	B	90	GLN	3.5
3	H	191	LEU	3.5
3	H	189	GLN	3.4
2	B	80	THR	3.4
2	B	158	GLN	3.3
2	B	110	VAL	3.3
2	B	121	GLN	3.3
2	B	79	VAL	3.2
2	B	170	VAL	3.0
2	B	118	PRO	3.0
3	H	148	LEU	3.0
3	H	169	ILE	2.9
2	B	100	MET	2.9
2	B	120	THR	2.9
3	H	214	GLY	2.9
2	B	157	CYS	2.9
3	H	168	ASP	2.9
3	H	153	LEU	2.8
3	H	190	VAL	2.7
2	B	114	ALA	2.7
2	B	172	PRO	2.7
3	H	117	VAL	2.7
3	H	129	PRO	2.7
3	H	160	SER	2.7
2	B	94	ALA	2.6
2	B	154	SER	2.6
3	H	178	VAL	2.6
3	H	171	SER	2.5
3	H	149	ALA	2.5
3	H	130	LEU	2.5
3	H	132	SER	2.4
2	B	160	MET	2.3
2	B	169	THR	2.3
3	H	210	GLN	2.2
2	B	148	GLN	2.2
3	H	195	LYS	2.2
3	H	157	ILE	2.2
3	H	223	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
3	H	167	SER	2.2
2	B	168	LYS	2.1
3	H	154	PRO	2.1
3	H	221	PRO	2.1
3	H	127	LEU	2.1
3	H	87	LYS	2.1
3	H	186	ALA	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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	ZN	A	302	1/1	0.99	0.17	52,52,52,52	0
4	ZN	H	301	1/1	0.99	0.17	53,53,53,53	0

6.5 Other polymers (i)

There are no such residues in this entry.