Full wwPDB X-ray Structure Validation Report (i)

Oct 10, 2023 – 10:14 AM EDT

PDB ID	:	7L79
Title	:	Crystal structure of broadly HIV-1-neutralizing antibody VRC40.01
Authors	:	Zhou, T.; Kwong, P.D.
Deposited on	:	2020-12-27
Resolution	:	2.83 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:

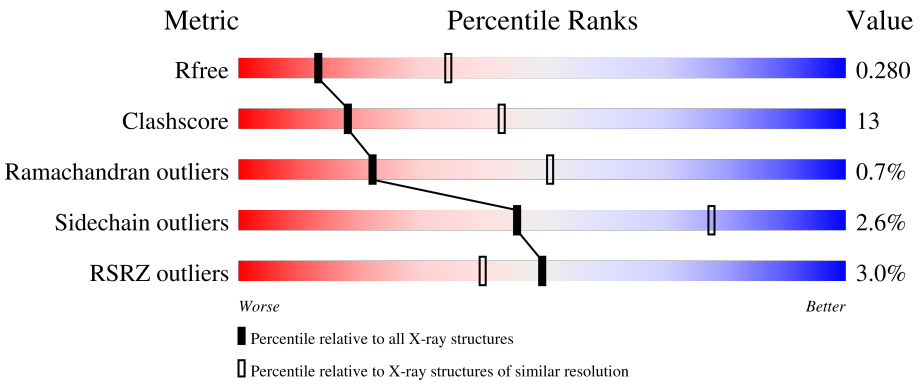
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.83 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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	230	5% 73% 26% •
1	H	230	3% 66% 32% •
2	B	214	2% 74% 23% •
2	L	214	% 76% 22% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9872 atoms, of which 2987 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 Heavy chain of VRC40.01.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	H	229	2444	1102	715	297	324	6	0	0	0
1	A	229	2425	1102	696	297	324	6	0	0	0

- Molecule 2 is a protein called Light chain of VRC40.01.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	L	214	2447	1036	788	286	330	7	0	0	0
2	B	214	2447	1036	788	286	330	7	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	H	1	1	1	0	0
3	L	5	5	5	0	0
3	B	3	3	3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	H	22	22	22	0	0
4	L	37	37	37	0	0
4	A	20	20	20	0	0

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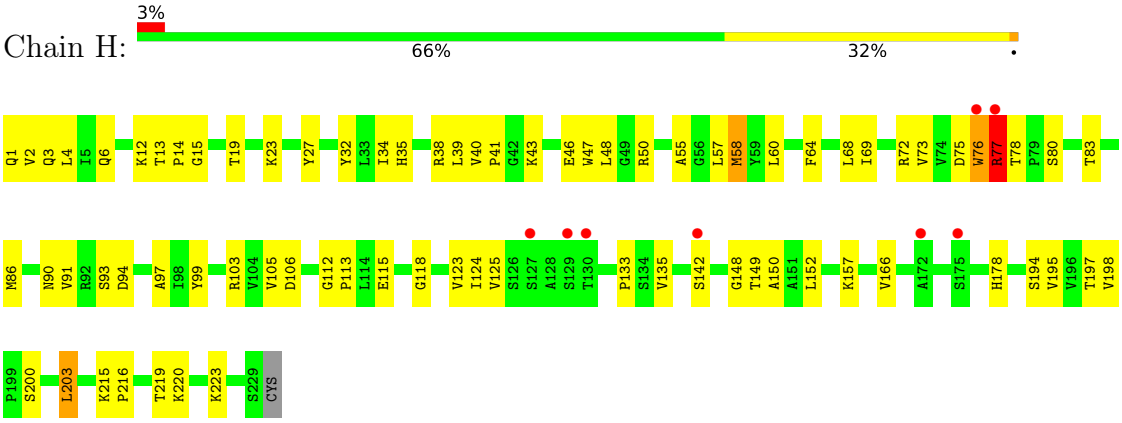
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	B	21	21	21	0	0

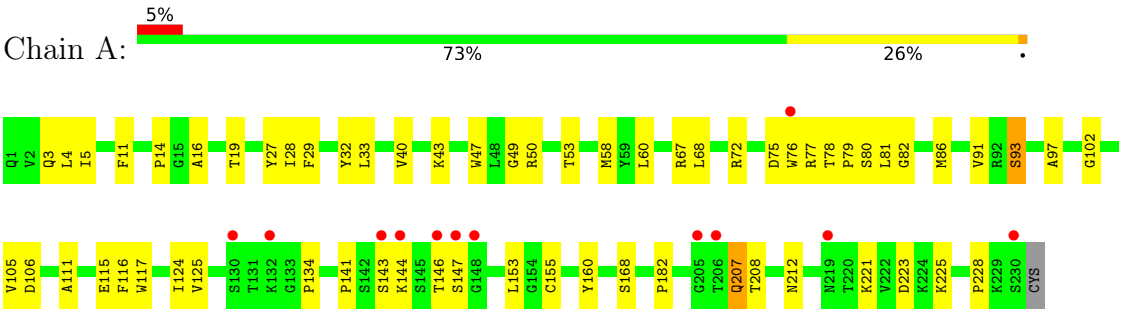
3 Residue-property plots (i)

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.

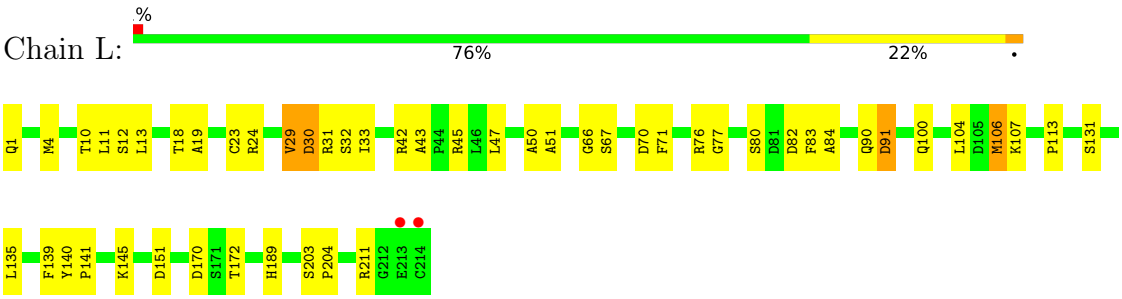
• Molecule 1: Heavy chain of VRC40.01



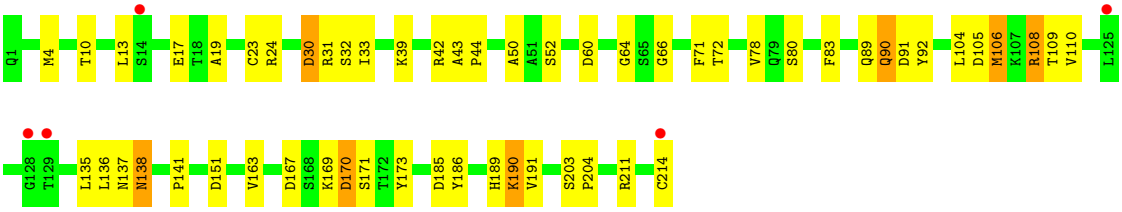
• Molecule 1: Heavy chain of VRC40.01



• Molecule 2: Light chain of VRC40.01



• Molecule 2: Light chain of VRC40.01


Q1
M4
T10
L13
S14
E17
T18
A19
C23
R24
D30
R31
S32
I33
K39
R42
A43
P44
A50
A51
S52
D60
G64
S65
G66
F71
T72
V78
Q79
S80
F83
Q89
Q90
D91
Y92
L104
D105
M106
K107
R108
T109
V110
L125
G128
T129
L135
L136
N137
N138
P141
D151
V163
D167
S168
K169
D170
S171
T172
Y173
D185
Y186
H189
K190
V191
S203
P204
R211
C214

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	62.79Å 135.95Å 136.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.92 – 2.83 36.92 – 2.83	Depositor EDS
% Data completeness (in resolution range)	97.0 (36.92-2.83) 97.0 (36.92-2.83)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.81Å)	Xtriage
Refinement program	PHENIX V1.1	Depositor
R, R_{free}	0.220 , 0.280 0.220 , 0.280	Depositor DCC
R_{free} test set	1394 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	55.3	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 34.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	9872	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2064e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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	0.47	1/1773 (0.1%)	0.63	2/2416 (0.1%)
1	H	0.37	0/1773	0.57	0/2416
2	B	0.40	0/1695	0.60	3/2301 (0.1%)
2	L	0.38	0/1695	0.57	0/2301
All	All	0.41	1/6936 (0.0%)	0.59	5/9434 (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	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	155	CYS	CB-SG	-12.12	1.61	1.82

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	75	ASP	CB-CG-OD2	-8.61	110.55	118.30
2	B	60	ASP	CB-CG-OD1	7.62	125.16	118.30
1	A	75	ASP	CB-CG-OD1	7.36	124.93	118.30
2	B	30	ASP	CB-CG-OD1	5.38	123.14	118.30
2	B	185	ASP	CB-CG-OD2	5.29	123.06	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	75	ASP	Peptide

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	1729	696	1731	50	0
1	H	1729	715	1730	52	2
2	B	1659	788	1608	39	0
2	L	1659	788	1607	45	0
3	B	3	0	0	0	0
3	H	1	0	0	0	0
3	L	5	0	0	0	0
4	A	20	0	0	1	0
4	B	21	0	0	7	0
4	H	22	0	0	1	0
4	L	37	0	0	10	0
All	All	6885	2987	6676	181	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 (181) 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:B:151:ASP:OD2	4:B:401:HOH:O	1.84	0.95
2:L:18:THR:HG23	2:L:76:ARG:HA	1.47	0.93
2:L:151:ASP:OD2	4:L:401:HOH:O	1.91	0.89
2:L:30:ASP:HB3	4:L:413:HOH:O	1.74	0.87
2:L:12:SER:HB3	2:L:107:LYS:HD2	1.55	0.86
2:B:13:LEU:HD12	2:B:104:LEU:HD11	1.56	0.86
2:L:100:GLN:OE1	4:L:402:HOH:O	1.92	0.85
1:A:40:VAL:CG2	1:A:43:LYS:HB2	2.06	0.84
1:A:40:VAL:HG23	1:A:43:LYS:HB2	1.61	0.82
1:H:76:TRP:O	1:H:77:ARG:HB2	1.78	0.82
2:L:145:LYS:NZ	4:L:403:HOH:O	2.12	0.81
1:A:58:MET:HE1	1:A:60:LEU:HD11	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:149:THR:HG21	1:H:197:THR:HG22	1.63	0.79
1:A:40:VAL:HG12	1:A:97:ALA:HB2	1.65	0.77
2:B:50:ALA:O	4:B:402:HOH:O	2.04	0.76
2:B:17:GLU:O	2:B:78:VAL:HG23	1.85	0.75
2:B:52:SER:OG	4:B:402:HOH:O	2.03	0.74
1:H:47:TRP:HZ2	1:H:50:ARG:HG2	1.53	0.73
2:L:76:ARG:HG3	2:L:77:GLY:H	1.54	0.73
2:L:80:SER:HA	2:L:83:PHE:CE1	2.25	0.71
1:A:27:TYR:O	1:A:80:SER:HA	1.92	0.70
1:H:148:GLY:O	1:H:200:SER:OG	2.08	0.70
1:A:58:MET:CE	1:A:60:LEU:HD11	2.22	0.69
2:L:45:ARG:HG2	4:L:422:HOH:O	1.92	0.69
1:A:58:MET:HE3	1:A:60:LEU:HD21	1.75	0.68
2:L:47:LEU:HD23	4:L:422:HOH:O	1.93	0.67
2:B:190:LYS:HD2	2:B:191:VAL:HG23	1.76	0.67
2:L:12:SER:CB	2:L:107:LYS:HD2	2.25	0.67
1:A:58:MET:CE	1:A:60:LEU:HD21	2.25	0.66
2:B:10:THR:HG22	4:B:410:HOH:O	1.96	0.66
2:B:4:MET:HE2	2:B:23:CYS:SG	2.36	0.66
1:A:144:LYS:O	1:A:146:THR:N	2.26	0.66
2:L:131:SER:O	4:L:404:HOH:O	2.13	0.65
2:L:4:MET:O	4:L:402:HOH:O	2.15	0.64
1:H:195:VAL:HG21	2:L:135:LEU:HD22	1.78	0.64
1:H:27:TYR:O	1:H:80:SER:HA	1.98	0.63
1:A:3:GLN:O	1:A:4:LEU:HD23	1.99	0.63
2:L:66:GLY:HA3	2:L:71:PHE:HA	1.80	0.63
1:H:152:LEU:HD23	1:H:203:LEU:HD21	1.79	0.62
1:H:34:ILE:HD13	1:H:103:ARG:HB3	1.81	0.62
1:A:28:ILE:HD12	1:A:79:PRO:HB2	1.82	0.62
1:A:72:ARG:O	1:A:72:ARG:HD2	2.00	0.61
1:A:76:TRP:O	1:A:77:ARG:HB3	2.00	0.61
1:A:19:THR:HA	1:A:86:MET:O	2.00	0.61
2:L:189:HIS:O	2:L:211:ARG:NH1	2.34	0.61
2:L:170:ASP:HB2	2:L:172:THR:HG23	1.82	0.61
1:A:47:TRP:HZ2	1:A:50:ARG:HG2	1.66	0.61
2:B:108:ARG:HD2	4:B:405:HOH:O	1.99	0.60
1:H:68:LEU:HD11	1:H:86:MET:HG3	1.82	0.60
1:A:143:SER:HB3	1:A:147:SER:OG	2.02	0.59
1:H:133:PRO:HD2	1:H:219:THR:HG21	1.85	0.58
1:A:16:ALA:O	1:A:91:VAL:HG22	2.03	0.58
1:H:40:VAL:HG13	1:H:41:PRO:HD2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:58:MET:HE1	1:H:69:ILE:HG23	1.84	0.58
1:H:15:GLY:HA2	1:H:90:ASN:OD1	2.04	0.58
1:A:32:TYR:HE2	1:A:106:ASP:HA	1.70	0.57
2:L:82:ASP:O	2:L:104:LEU:HD23	2.05	0.57
1:A:40:VAL:HG12	1:A:97:ALA:CB	2.34	0.56
2:B:13:LEU:HD12	2:B:104:LEU:CD1	2.33	0.56
1:A:14:PRO:HA	1:A:91:VAL:O	2.06	0.56
1:A:117:TRP:CZ3	2:B:44:PRO:HG2	2.41	0.55
1:H:55:ALA:HB3	1:H:57:LEU:HD12	1.88	0.54
2:L:189:HIS:ND1	4:L:401:HOH:O	2.26	0.54
2:B:137:ASN:ND2	2:B:138:ASN:OD1	2.41	0.53
1:H:47:TRP:CZ2	1:H:50:ARG:HG2	2.41	0.53
2:L:29:VAL:O	2:L:30:ASP:C	2.47	0.53
2:L:24:ARG:HH21	2:L:24:ARG:HG3	1.72	0.53
1:H:55:ALA:HB3	1:H:57:LEU:CD1	2.37	0.53
1:H:105:VAL:HG22	1:H:115:GLU:HB2	1.91	0.53
1:A:11:PHE:CE2	1:A:124:ILE:HD13	2.44	0.53
1:A:29:PHE:CD1	1:A:82:GLY:HA3	2.43	0.53
1:A:68:LEU:HD11	1:A:86:MET:HG3	1.90	0.52
1:A:3:GLN:C	1:A:4:LEU:HD23	2.31	0.51
1:H:19:THR:HA	1:H:86:MET:O	2.11	0.51
1:A:47:TRP:CZ2	1:A:49:GLY:HA2	2.45	0.51
1:A:153:LEU:C	1:A:153:LEU:HD12	2.31	0.51
1:H:38:ARG:HD3	1:H:99:TYR:CE2	2.46	0.50
2:L:113:PRO:HB3	2:L:139:PHE:HB3	1.92	0.50
2:L:203:SER:HB2	2:L:204:PRO:HD2	1.93	0.50
1:H:32:TYR:HE2	1:H:106:ASP:HA	1.76	0.50
2:L:12:SER:O	2:L:13:LEU:HG	2.11	0.50
2:B:110:VAL:HG22	2:B:141:PRO:HD3	1.93	0.50
1:H:149:THR:HG23	1:H:198:VAL:O	2.11	0.50
1:A:72:ARG:HD2	1:A:72:ARG:C	2.32	0.50
1:H:3:GLN:C	1:H:4:LEU:HD12	2.33	0.50
2:B:135:LEU:C	2:B:136:LEU:HD12	2.32	0.50
2:L:83:PHE:O	2:L:84:ALA:HB2	2.13	0.49
1:A:141:PRO:HD2	1:A:228:PRO:HA	1.95	0.49
1:H:35:HIS:CE1	1:H:50:ARG:HD3	2.48	0.49
2:B:108:ARG:NE	2:B:109:THR:O	2.45	0.49
1:A:29:PHE:CE2	1:A:53:THR:HB	2.48	0.48
1:A:58:MET:HE2	1:A:60:LEU:HG	1.95	0.48
1:H:13:THR:OG1	1:H:14:PRO:HD2	2.12	0.48
1:H:73:VAL:O	1:H:73:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:THR:HG23	1:A:225:LYS:HE2	1.95	0.48
1:H:166:VAL:HG11	1:H:194:SER:CB	2.43	0.48
2:L:170:ASP:OD1	2:L:170:ASP:N	2.34	0.48
1:H:6:GLN:OE1	1:H:118:GLY:HA3	2.14	0.48
1:H:38:ARG:HD3	1:H:99:TYR:CZ	2.49	0.48
2:L:24:ARG:HG3	2:L:24:ARG:NH2	2.30	0.47
1:A:58:MET:HE2	1:A:60:LEU:CG	2.43	0.47
2:L:32:SER:HB3	2:L:91:ASP:OD1	2.14	0.47
1:H:124:ILE:HD12	1:H:124:ILE:N	2.29	0.47
1:A:5:ILE:HD12	1:A:5:ILE:N	2.30	0.46
1:A:143:SER:HB3	1:A:147:SER:CB	2.46	0.46
2:B:80:SER:HA	2:B:83:PHE:CE1	2.50	0.46
2:L:10:THR:HG22	2:L:11:LEU:N	2.30	0.46
2:B:13:LEU:CD1	2:B:19:ALA:HB2	2.44	0.46
2:B:189:HIS:ND1	4:B:401:HOH:O	2.28	0.46
1:H:91:VAL:HB	1:H:125:VAL:HG21	1.97	0.46
1:H:123:VAL:HG13	1:H:123:VAL:O	2.16	0.46
2:B:105:ASP:OD2	2:B:173:TYR:OH	2.32	0.46
2:L:24:ARG:NH2	2:L:70:ASP:OD1	2.49	0.46
2:B:30:ASP:HB2	2:B:92:TYR:CE1	2.51	0.46
1:H:112:GLY:N	1:H:113:PRO:CD	2.79	0.45
1:H:149:THR:CG2	1:H:150:ALA:N	2.79	0.45
1:H:12:LYS:O	1:H:125:VAL:HA	2.16	0.45
2:L:76:ARG:HG3	2:L:77:GLY:N	2.27	0.45
2:B:39:LYS:HD2	2:B:42:ARG:NH2	2.31	0.45
2:B:64:GLY:HA2	2:B:72:THR:O	2.17	0.45
2:B:186:TYR:CZ	2:B:211:ARG:HG3	2.51	0.45
2:L:80:SER:HA	2:L:83:PHE:CD1	2.51	0.45
1:H:1:GLN:HG3	1:H:2:VAL:H	1.81	0.45
2:B:30:ASP:HB3	2:B:31:ARG:H	1.63	0.45
1:H:94:ASP:OD1	4:H:401:HOH:O	2.21	0.45
1:H:48:LEU:HD23	1:H:64:PHE:CE2	2.52	0.45
2:L:1:GLN:HA	2:L:1:GLN:OE1	2.16	0.44
1:H:135:VAL:O	1:H:223:LYS:HE3	2.16	0.44
1:H:195:VAL:HG21	2:L:135:LEU:CD2	2.45	0.44
1:A:33:LEU:HD23	1:A:50:ARG:HD2	1.99	0.44
2:B:203:SER:HB2	2:B:204:PRO:HD2	1.99	0.44
1:A:78:THR:HG21	1:A:81:LEU:HD12	1.99	0.44
2:B:13:LEU:HD13	2:B:19:ALA:HB2	1.98	0.44
1:A:111:ALA:HB1	2:B:91:ASP:OD2	2.17	0.44
1:H:39:LEU:O	1:H:97:ALA:HB1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:32:TYR:CD2	1:H:103:ARG:NH1	2.82	0.44
1:H:77:ARG:HB3	1:H:78:THR:HG23	1.99	0.44
1:A:80:SER:O	1:A:81:LEU:HD23	2.18	0.44
2:L:13:LEU:HD13	2:L:19:ALA:HB2	1.98	0.44
2:B:32:SER:HB3	2:B:91:ASP:OD2	2.18	0.43
1:A:134:PRO:HB3	1:A:160:TYR:HB3	2.00	0.43
2:B:24:ARG:HG3	2:B:24:ARG:HH21	1.83	0.43
2:B:33:ILE:HG13	2:B:71:PHE:CE1	2.54	0.43
2:B:42:ARG:HG2	2:B:43:ALA:N	2.33	0.43
1:H:38:ARG:HH21	1:H:46:GLU:CD	2.21	0.43
2:B:66:GLY:HA3	2:B:71:PHE:HA	2.01	0.43
1:H:32:TYR:CE2	1:H:106:ASP:HA	2.54	0.43
1:A:67:ARG:HD3	4:A:310:HOH:O	2.19	0.43
1:H:40:VAL:CG1	1:H:41:PRO:HD2	2.49	0.42
1:A:168:SER:HB2	1:A:212:ASN:HB2	2.01	0.42
1:A:207:GLN:HG3	1:A:208:THR:N	2.35	0.42
2:B:108:ARG:CD	4:B:405:HOH:O	2.63	0.42
2:B:167:ASP:O	2:B:171:SER:HA	2.20	0.42
1:H:58:MET:HG3	1:H:60:LEU:HD21	2.01	0.42
1:A:102:GLY:HA2	1:A:116:PHE:O	2.20	0.42
1:H:40:VAL:HG22	1:H:97:ALA:HB2	2.00	0.42
1:H:178:HIS:CE1	4:L:410:HOH:O	2.73	0.42
2:L:13:LEU:CD1	2:L:19:ALA:HB2	2.50	0.42
2:L:140:TYR:CG	2:L:141:PRO:HA	2.55	0.42
1:A:105:VAL:HG22	1:A:115:GLU:HB2	2.01	0.42
2:B:89:GLN:HG2	2:B:90:GLN:N	2.34	0.42
2:B:106:MET:HE2	2:B:106:MET:HB2	1.98	0.41
2:L:30:ASP:HB3	2:L:31:ARG:H	1.68	0.41
2:L:4:MET:HE3	2:L:23:CYS:SG	2.61	0.41
2:L:106:MET:HE2	2:L:106:MET:HB2	1.96	0.41
2:L:203:SER:HB2	2:L:204:PRO:CD	2.50	0.41
2:B:80:SER:HA	2:B:83:PHE:CD1	2.55	0.41
1:H:149:THR:HG21	1:H:197:THR:CG2	2.41	0.41
1:A:182:PRO:HG2	2:B:163:VAL:O	2.20	0.41
2:B:108:ARG:NH2	2:B:170:ASP:O	2.53	0.41
2:L:33:ILE:HG13	2:L:71:PHE:CE1	2.56	0.41
1:A:93:SER:HA	1:A:125:VAL:HB	2.02	0.41
2:L:13:LEU:HD12	2:L:104:LEU:HD11	2.02	0.41
1:A:212:ASN:HA	1:A:223:ASP:OD2	2.20	0.41
1:H:215:LYS:N	1:H:216:PRO:CD	2.83	0.40
1:A:28:ILE:CD1	1:A:79:PRO:HB2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:LYS:HA	1:A:144:LYS:HD3	1.87	0.40
1:H:99:TYR:CE1	1:H:123:VAL:CG1	3.05	0.40
2:L:42:ARG:HG2	2:L:43:ALA:N	2.36	0.40
2:L:50:ALA:O	2:L:51:ALA:HB3	2.20	0.40
1:H:23:LYS:HG2	1:H:83:THR:HG23	2.04	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)
1:H:142:SER:O	1:H:220:LYS:HZ2[4_555]	1.25	0.35
1:H:142:SER:O	1:H:220:LYS:NZ[4_555]	1.86	0.34

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	227/230 (99%)	210 (92%)	17 (8%)	0	100	100
1	H	227/230 (99%)	212 (93%)	12 (5%)	3 (1%)	12	34
2	B	212/214 (99%)	194 (92%)	17 (8%)	1 (0%)	29	59
2	L	212/214 (99%)	195 (92%)	15 (7%)	2 (1%)	17	44
All	All	878/888 (99%)	811 (92%)	61 (7%)	6 (1%)	22	51

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	76	TRP
1	H	77	ARG
2	B	138	ASN
1	H	43	LYS

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Mol	Chain	Res	Type
2	L	30	ASP
2	L	29	VAL

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	195/196 (100%)	192 (98%)	3 (2%)	65	88
1	H	195/196 (100%)	189 (97%)	6 (3%)	40	72
2	B	186/186 (100%)	179 (96%)	7 (4%)	33	65
2	L	186/186 (100%)	182 (98%)	4 (2%)	52	81
All	All	762/764 (100%)	742 (97%)	20 (3%)	46	78

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	58	MET
1	H	72	ARG
1	H	77	ARG
1	H	93	SER
1	H	157	LYS
1	H	203	LEU
2	L	67	SER
2	L	90	GLN
2	L	91	ASP
2	L	106	MET
1	A	93	SER
1	A	207	GLN
1	A	221	LYS
2	B	90	GLN
2	B	106	MET
2	B	108	ARG
2	B	169	LYS
2	B	170	ASP
2	B	190	LYS

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Mol	Chain	Res	Type
2	B	214	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	1	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)

Of 9 ligands modelled in this entry, 9 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	229/230 (99%)	0.29	12 (5%)	27	18	29, 49, 87, 125	0
1	H	229/230 (99%)	0.16	8 (3%)	44	34	28, 47, 98, 131	0
2	B	214/214 (100%)	0.28	5 (2%)	60	50	28, 43, 72, 117	0
2	L	214/214 (100%)	0.24	2 (0%)	84	80	25, 43, 82, 134	0
All	All	886/888 (99%)	0.24	27 (3%)	50	40	25, 45, 85, 134	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	214	CYS	14.6
2	B	214	CYS	9.1
1	H	76	TRP	4.9
1	H	172	ALA	3.8
1	A	76	TRP	3.5
2	B	14	SER	3.4
1	A	144	LYS	3.2
1	A	143	SER	3.2
1	A	206	THR	3.0
1	A	147	SER	3.0
2	L	213	GLU	2.9
1	H	142	SER	2.9
2	B	125	LEU	2.8
1	A	230	SER	2.6
2	B	129	THR	2.4
1	A	130	SER	2.4
1	A	146	THR	2.4
1	H	77	ARG	2.4
1	H	129	SER	2.3
1	H	175	SER	2.2
1	A	148	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	130	THR	2.1
1	A	132	LYS	2.1
1	H	127	SER	2.1
1	A	205	GLY	2.0
1	A	219	ASN	2.0
2	B	128	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)

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
3	ZN	L	304	1/1	0.74	0.23	110,110,110,110	0
3	ZN	L	305	1/1	0.91	0.26	89,89,89,89	0
3	ZN	L	303	1/1	0.92	0.09	53,53,53,53	0
3	ZN	L	302	1/1	0.93	0.07	61,61,61,61	0
3	ZN	B	303	1/1	0.93	0.07	47,47,47,47	0
3	ZN	H	301	1/1	0.94	0.06	54,54,54,54	0
3	ZN	B	302	1/1	0.97	0.07	40,40,40,40	0
3	ZN	L	301	1/1	0.98	0.05	41,41,41,41	0
3	ZN	B	301	1/1	0.98	0.07	59,59,59,59	0

6.5 Other polymers (i)

There are no such residues in this entry.