



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 8, 2021 – 10:03 AM EST

PDB ID : 7RD3
Title : Crystal structure of PfCSP peptide 21 with vaccine-elicited human anti-malaria antibody m42.126
Authors : Xu, K.; Kwong, P.D.
Deposited on : 2021-07-09
Resolution : 1.81 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 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	:	2.24
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)	:	2.24

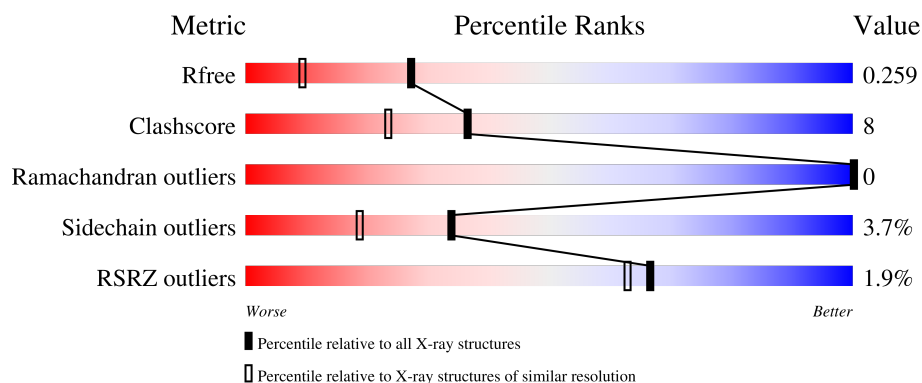
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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 $\leq 5\%$. 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	255	<div> <div>5%</div> <div>62%</div> <div>22%</div> <div>•</div> <div>16%</div> </div>
1	H	255	<div> <div>72%</div> <div>14%</div> <div>14%</div> </div>
2	B	220	<div> <div>87%</div> <div>11%</div> <div>•</div> </div>
2	L	220	<div> <div>86%</div> <div>12%</div> <div>•</div> </div>
3	C	15	<div> <div>20%</div> <div>67%</div> <div>33%</div> </div>

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Mol	Chain	Length	Quality of chain
3	D	15	 A horizontal bar chart showing the quality of chain D. The bar is divided into three segments: a green segment representing 87%, a yellow segment representing 7%, and a grey segment representing 7%. The percentages are labeled below the bar.

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7403 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 antibody m42.126 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1625	1027	273	316	9			
1	H	220	Total	C	N	O	S	0	0	0
			1659	1046	279	325	9			

- Molecule 2 is a protein called antibody m42.126 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	0	0
			1678	1053	280	340	5			
2	L	217	Total	C	N	O	S	0	0	0
			1678	1053	280	340	5			

- Molecule 3 is a protein called Circumsporozoite protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	0	0	0
			109	63	21	25			
3	D	14	Total	C	N	O	0	0	0
			101	59	19	23			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	86	Total	O	0	0
			86	86		
4	B	151	Total	O	0	0
			151	151		
4	H	140	Total	O	0	0
			140	140		
4	L	158	Total	O	0	0
			158	158		

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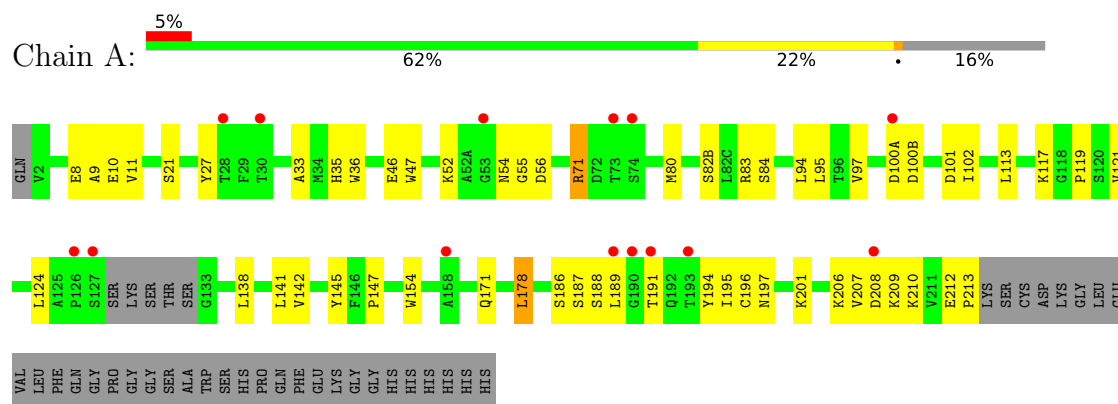
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	6	Total 6	O 6	0	0
4	D	12	Total 12	O 12	0	0

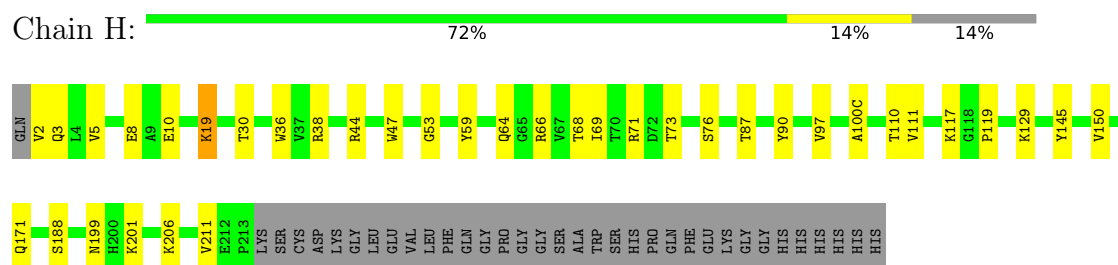
3 Residue-property plots [i](#)

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.

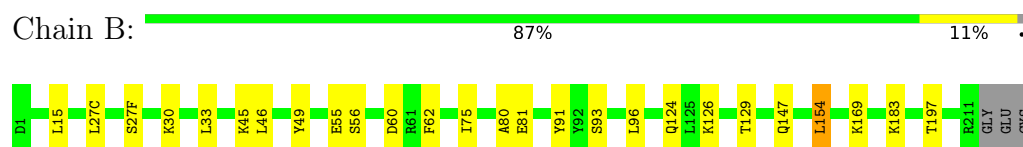
- Molecule 1: antibody m42.126 heavy chain



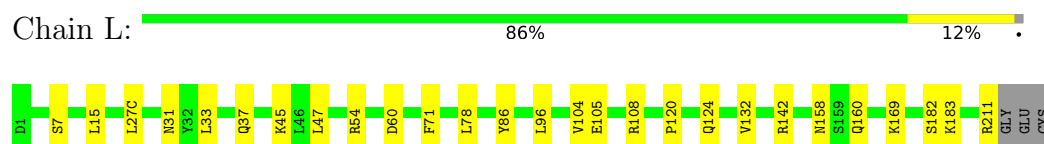
- Molecule 1: antibody m42.126 heavy chain



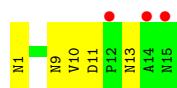
- Molecule 2: antibody m42.126 light chain



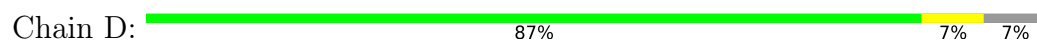
- Molecule 2: antibody m42.126 light chain



- Molecule 3: Circumsporozoite protein



- Molecule 3: Circumsporozoite protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.85Å 57.18Å 74.49Å 86.50° 76.86° 72.44°	Depositor
Resolution (Å)	44.38 – 1.81 44.38 – 1.81	Depositor EDS
% Data completeness (in resolution range)	86.0 (44.38-1.81) 86.1 (44.38-1.81)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.216 , 0.260 0.214 , 0.259	Depositor DCC
R_{free} test set	3245 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.801	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7403	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.09% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.29	0/1662	0.58	0/2263
1	H	0.30	0/1697	0.59	0/2311
2	B	0.32	0/1716	0.56	0/2333
2	L	0.32	0/1716	0.55	0/2333
3	C	0.30	0/112	0.52	0/157
3	D	0.30	0/104	0.49	0/146
All	All	0.31	0/7007	0.57	0/9543

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
2	L	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	108	ARG	Sidechain

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	1625	0	1603	39	0
1	H	1659	0	1639	33	0
2	B	1678	0	1626	20	0
2	L	1678	0	1626	16	0
3	C	109	0	93	5	0
3	D	101	0	87	1	0
4	A	86	0	0	12	0
4	B	151	0	0	8	1
4	C	6	0	0	2	0
4	D	12	0	0	0	0
4	H	140	0	0	16	1
4	L	158	0	0	3	0
All	All	7403	0	6674	107	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 8.

All (107) 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:H:8:GLU:OE1	4:H:301:HOH:O	1.85	0.94
1:A:46:GLU:OE2	4:A:302:HOH:O	1.88	0.91
1:A:171:GLN:O	4:A:303:HOH:O	1.98	0.82
3:C:11:ASP:OD2	4:C:102:HOH:O	1.97	0.81
1:H:76:SER:HB3	4:H:316:HOH:O	1.83	0.77
3:C:1:ASN:N	4:C:101:HOH:O	1.88	0.76
1:H:206:LYS:NZ	4:H:306:HOH:O	2.17	0.76
1:H:38:ARG:NH2	1:H:90:TYR:OH	2.17	0.74
1:A:33:ALA:HB2	1:A:52:LYS:HD2	1.70	0.73
1:A:189:LEU:HD12	1:A:213:PRO:HG3	1.69	0.73
1:H:73:THR:OG1	4:H:302:HOH:O	2.07	0.73
1:H:201:LYS:HA	4:H:318:HOH:O	1.90	0.70
1:A:71:ARG:NE	4:A:307:HOH:O	2.19	0.68
1:A:83:ARG:NH1	4:A:301:HOH:O	1.84	0.68
1:H:87:THR:HG23	1:H:110:THR:HA	1.75	0.67
2:L:158:ASN:OD1	4:L:301:HOH:O	2.13	0.65
1:H:2:VAL:N	4:H:311:HOH:O	2.29	0.65
1:H:117:LYS:NZ	4:H:313:HOH:O	2.30	0.64
2:B:27(C):LEU:O	4:B:301:HOH:O	2.14	0.64
4:A:305:HOH:O	2:B:46:LEU:N	2.31	0.63
1:A:210:LYS:HE3	1:A:212:GLU:HG2	1.79	0.62
2:B:80:ALA:HB1	4:B:304:HOH:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:171:GLN:HA	2:L:160:GLN:HE22	1.66	0.61
1:H:68:THR:O	4:H:304:HOH:O	2.16	0.60
2:B:30:LYS:HA	2:B:30:LYS:HE2	1.84	0.60
2:L:54:ARG:NH1	2:L:60:ASP:OD2	2.35	0.60
2:L:105:GLU:OE2	2:L:142:ARG:NH2	2.35	0.59
2:L:86:TYR:HE1	2:L:104:VAL:HG21	1.67	0.58
1:A:124:LEU:HD11	1:A:141:LEU:HB2	1.85	0.58
1:A:101:ASP:OD1	4:A:305:HOH:O	2.17	0.57
1:H:206:LYS:NZ	4:H:319:HOH:O	2.39	0.55
1:H:19:LYS:O	1:H:19:LYS:HD2	2.07	0.55
1:A:11:VAL:HB	1:A:147:PRO:HG3	1.88	0.54
1:A:119:PRO:HB3	1:A:145:TYR:HB3	1.90	0.54
1:A:121:VAL:HG11	1:A:207:VAL:HG11	1.88	0.54
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.91	0.53
2:L:124:GLN:NE2	4:L:307:HOH:O	2.37	0.53
1:A:154:TRP:CH2	1:A:196:CYS:HB3	2.44	0.53
2:L:86:TYR:CE1	2:L:104:VAL:HG21	2.44	0.52
2:L:120:PRO:HD3	2:L:132:VAL:HG22	1.92	0.52
1:A:54:ASN:O	4:A:306:HOH:O	2.19	0.51
2:L:37:GLN:HB3	2:L:47:LEU:HD21	1.93	0.51
1:H:111:VAL:O	4:H:307:HOH:O	2.19	0.51
1:H:5:VAL:O	4:H:308:HOH:O	2.19	0.50
1:H:8:GLU:HB2	1:H:201:LYS:HE2	1.93	0.50
1:A:187:SER:N	4:A:311:HOH:O	2.34	0.50
1:H:59:TYR:HB2	1:H:64:GLN:HG2	1.93	0.50
2:B:45:LYS:NZ	4:B:314:HOH:O	2.44	0.50
1:H:36:TRP:HD1	1:H:69:ILE:HD12	1.76	0.50
1:A:100(B):ASP:HA	4:A:366:HOH:O	2.11	0.49
1:H:44:ARG:NH1	4:H:317:HOH:O	2.37	0.49
1:A:35:HIS:HB2	1:A:95:LEU:HD23	1.93	0.49
2:B:93:SER:OG	4:B:302:HOH:O	2.18	0.49
1:A:194:TYR:H	1:A:210:LYS:NZ	2.11	0.49
1:A:36:TRP:CE2	1:A:80:MET:HB2	2.47	0.49
1:H:10:GLU:OE2	4:H:309:HOH:O	2.20	0.48
1:A:47:TRP:CD1	2:B:96:LEU:HD12	2.48	0.48
1:H:97:VAL:HA	3:D:9:ASN:HB3	1.96	0.48
2:B:169:LYS:N	2:B:169:LYS:HD2	2.28	0.48
2:L:211:ARG:O	4:L:302:HOH:O	2.20	0.48
2:L:86:TYR:HE1	2:L:104:VAL:CG2	2.27	0.48
2:L:37:GLN:CB	2:L:47:LEU:HD21	2.44	0.47
1:A:97:VAL:HA	3:C:9:ASN:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:110:THR:HG23	4:H:333:HOH:O	2.15	0.47
1:A:83:ARG:NH1	1:A:84:SER:H	2.13	0.47
1:A:97:VAL:HG22	3:C:9:ASN:HB3	1.96	0.46
1:A:10:GLU:OE1	4:A:308:HOH:O	2.21	0.46
1:A:27:TYR:CZ	1:A:94:LEU:HD11	2.50	0.46
1:A:194:TYR:H	1:A:210:LYS:HZ2	1.64	0.46
2:B:126:LYS:HA	2:B:126:LYS:HD3	1.70	0.46
1:H:59:TYR:CE2	1:H:69:ILE:HG22	2.51	0.46
1:A:188:SER:HA	1:A:191:THR:OG1	2.16	0.46
2:L:15:LEU:HD12	2:L:78:LEU:O	2.15	0.45
1:A:101:ASP:C	1:A:102:ILE:HD13	2.37	0.45
4:B:385:HOH:O	1:H:64:GLN:HG3	2.16	0.45
1:H:188:SER:HA	4:H:374:HOH:O	2.16	0.45
2:B:124:GLN:HG2	2:B:129:THR:O	2.17	0.45
1:A:35:HIS:CG	1:A:95:LEU:HD23	2.52	0.45
1:A:55:GLY:N	4:A:307:HOH:O	2.49	0.45
2:B:62:PHE:HE2	4:B:425:HOH:O	1.99	0.44
2:B:197:THR:HG23	4:B:340:HOH:O	2.18	0.43
1:A:186:SER:O	1:A:189:LEU:HB2	2.19	0.43
1:A:83:ARG:HG3	1:A:84:SER:N	2.33	0.43
1:H:188:SER:OG	4:H:305:HOH:O	2.17	0.43
1:A:142:VAL:HB	1:A:178:LEU:HD12	2.01	0.43
1:H:145:TYR:CE2	1:H:150:VAL:HG13	2.54	0.42
1:A:9:ALA:HB2	4:A:375:HOH:O	2.19	0.42
1:H:36:TRP:CD1	1:H:69:ILE:HD12	2.53	0.42
1:A:8:GLU:OE1	1:A:201:LYS:HB3	2.19	0.42
2:B:147:GLN:HB3	2:B:154:LEU:HD21	2.02	0.42
1:H:59:TYR:CZ	1:H:69:ILE:HG22	2.54	0.42
1:H:47:TRP:CD1	2:L:96:LEU:HD12	2.54	0.42
1:A:195:ILE:HG21	1:A:208:ASP:HB3	2.02	0.42
2:B:154:LEU:HD23	2:B:154:LEU:HA	1.81	0.42
2:B:55:GLU:HG3	2:B:56:SER:N	2.34	0.41
1:A:35:HIS:HB2	1:A:95:LEU:CD2	2.50	0.41
1:H:30:THR:HG22	1:H:53:GLY:HA2	2.00	0.41
2:B:91:TYR:CD2	3:C:10:VAL:HG21	2.56	0.41
1:A:100(A):ASP:OD2	1:A:100(A):ASP:N	2.45	0.41
2:B:15:LEU:HD11	4:B:310:HOH:O	2.20	0.41
1:A:209:LYS:HD2	1:A:209:LYS:HA	1.85	0.41
1:H:97:VAL:O	1:H:100(C):ALA:HA	2.21	0.41
2:B:75:ILE:N	2:B:75:ILE:HD12	2.36	0.40
2:L:33:LEU:HD22	2:L:71:PHE:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:TYR:HA	2:B:96:LEU:HD22	2.03	0.40
2:L:27(C):LEU:HB2	2:L:31:ASN:OD1	2.22	0.40
2:B:81:GLU:O	2:B:81:GLU:HG3	2.22	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)
4:B:447:HOH:O	4:H:406:HOH:O[1_644]	2.17	0.03

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	211/255 (83%)	207 (98%)	4 (2%)	0	100	100
1	H	218/255 (86%)	215 (99%)	3 (1%)	0	100	100
2	B	215/220 (98%)	211 (98%)	4 (2%)	0	100	100
2	L	215/220 (98%)	212 (99%)	3 (1%)	0	100	100
3	C	13/15 (87%)	12 (92%)	1 (8%)	0	100	100
3	D	12/15 (80%)	12 (100%)	0	0	100	100
All	All	884/980 (90%)	869 (98%)	15 (2%)	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	182/215 (85%)	172 (94%)	10 (6%)	21	8
1	H	187/215 (87%)	180 (96%)	7 (4%)	34	19
2	B	192/194 (99%)	186 (97%)	6 (3%)	40	25
2	L	192/194 (99%)	187 (97%)	5 (3%)	46	32
3	C	13/13 (100%)	12 (92%)	1 (8%)	13	3
3	D	12/13 (92%)	12 (100%)	0	100	100
All	All	778/844 (92%)	749 (96%)	29 (4%)	34	19

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	SER
1	A	56	ASP
1	A	71	ARG
1	A	82(B)	SER
1	A	113	LEU
1	A	117	LYS
1	A	138	LEU
1	A	178	LEU
1	A	197	ASN
1	A	206	LYS
2	B	27(F)	SER
2	B	33	LEU
2	B	49	TYR
2	B	60	ASP
2	B	154	LEU
2	B	183	LYS
1	H	3	GLN
1	H	19	LYS
1	H	66	ARG
1	H	71	ARG
1	H	129	LYS
1	H	199	ASN
1	H	211	VAL
2	L	7	SER
2	L	45	LYS
2	L	169	LYS
2	L	182	SER

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Mol	Chain	Res	Type
2	L	183	LYS
3	C	13	ASN

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

Mol	Chain	Res	Type
1	A	6	GLN
1	H	199	ASN
2	L	160	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 [i](#)

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	215/255 (84%)	0.42	14 (6%) 18 14	24, 42, 60, 69	0
1	H	220/255 (86%)	-0.15	0 100 100	22, 33, 49, 61	0
2	B	217/220 (98%)	-0.31	0 100 100	18, 28, 44, 59	0
2	L	217/220 (98%)	-0.30	0 100 100	20, 28, 47, 55	0
3	C	15/15 (100%)	0.38	3 (20%) 1 0	29, 34, 65, 68	0
3	D	14/15 (93%)	-0.33	0 100 100	23, 27, 36, 42	0
All	All	898/980 (91%)	-0.08	17 (1%) 66 63	18, 32, 53, 69	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	THR	3.4
1	A	189	LEU	3.3
1	A	74	SER	3.3
3	C	15	ASN	3.2
3	C	14	ALA	3.1
1	A	127	SER	2.8
1	A	100(A)	ASP	2.7
3	C	12	PRO	2.7
1	A	190	GLY	2.7
1	A	28	THR	2.6
1	A	53	GLY	2.5
1	A	30	THR	2.4
1	A	126	PRO	2.2
1	A	158	ALA	2.2
1	A	208	ASP	2.2
1	A	193	THR	2.1
1	A	73	THR	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.