



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:23 AM UTC

PDB ID : 6C6X / pdb_00006c6x
Title : Crystal structure of Middle-East Respiratory Syndrome (MERS) coronavirus neutralizing antibody JC57-14 isolated from a vaccinated rhesus macaque.
Authors : Joyce, M.G.; Mascola, J.R.; Graham, B.S.; Kwong, P.D.
Deposited on : 2018-01-19
Resolution : 1.99 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

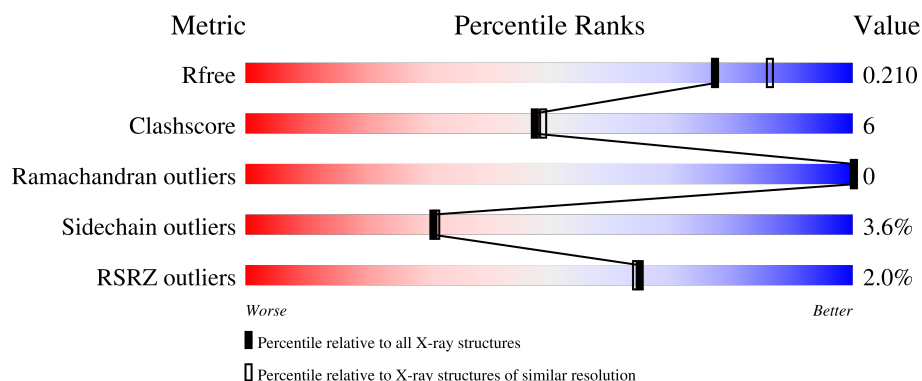
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	225	 87% 7% 6%
1	C	225	 84% 10% 5%
1	E	225	 4% 80% 14% . .
1	H	225	 4% 80% 14% . .
2	B	214	 % 85% 12% .

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Mol	Chain	Length	Quality of chain
2	D	214	% 85% 13%
2	F	214	2% 83% 16%
2	L	214	2% 88% 12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13929 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 JC57-14 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1582	998	262	318	4			
1	C	213	Total	C	N	O	S	0	0	0
			1588	1001	263	320	4			
1	E	215	Total	C	N	O	S	0	0	0
			1601	1008	265	324	4			
1	H	215	Total	C	N	O	S	0	0	0
			1600	1007	265	324	4			

- Molecule 2 is a protein called JC57-14 Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1650	1030	275	340	5			
2	D	214	Total	C	N	O	S	0	0	0
			1656	1033	276	341	6			
2	F	214	Total	C	N	O	S	0	0	0
			1656	1033	276	341	6			
2	L	214	Total	C	N	O	S	0	0	0
			1656	1033	276	341	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	131	Total	O	0	0
			131	131		
3	B	86	Total	O	0	0
			86	86		
3	C	180	Total	O	0	0
			180	180		
3	D	129	Total	O	0	0
			129	129		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	108	Total 108	O 108	0	0
3	F	92	Total 92	O 92	0	0
3	H	98	Total 98	O 98	0	0
3	L	116	Total 116	O 116	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.

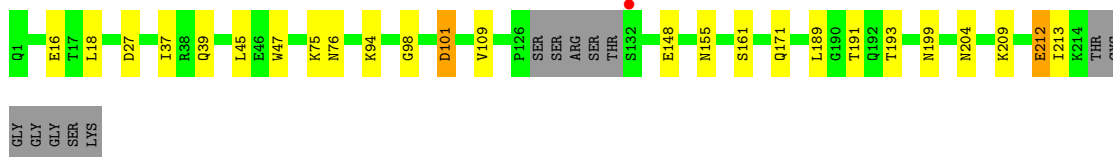
- Molecule 1: JC57-14 Heavy chain

Chain A: 



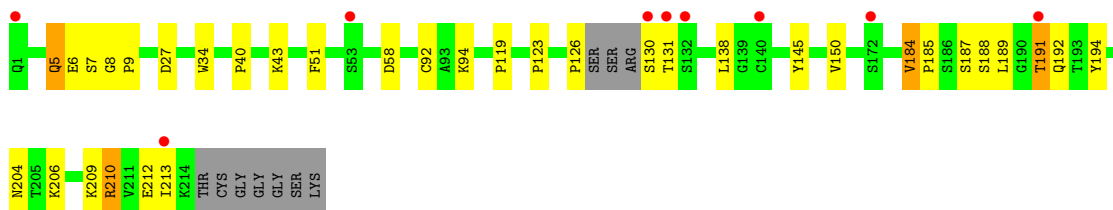
- Molecule 1: JC57-14 Heavy chain

Chain C: 



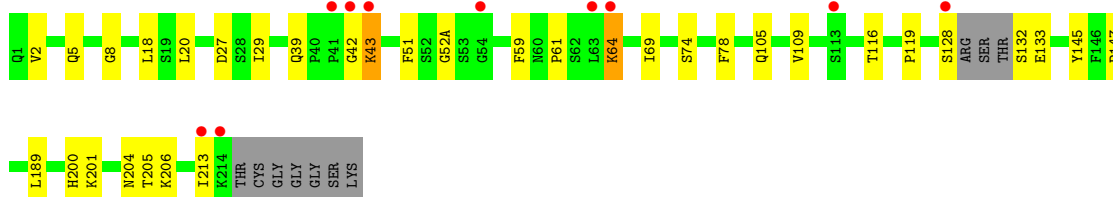
- Molecule 1: JC57-14 Heavy chain

Chain E: 

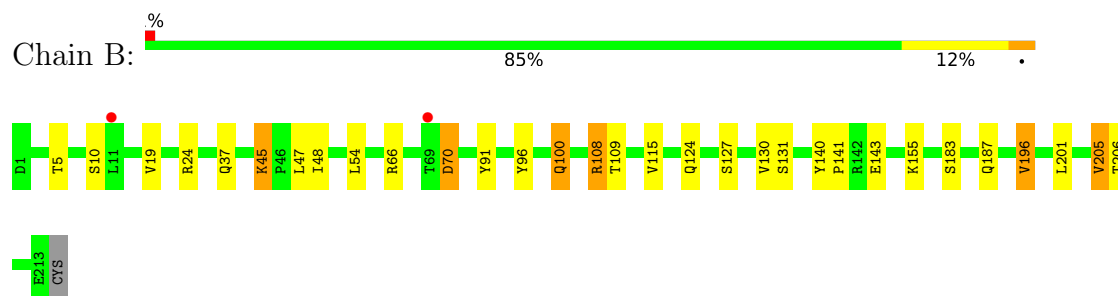


- Molecule 1: JC57-14 Heavy chain

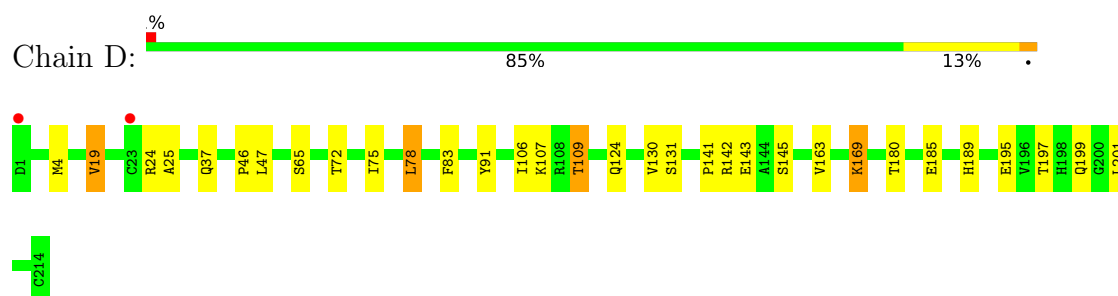
Chain H: 



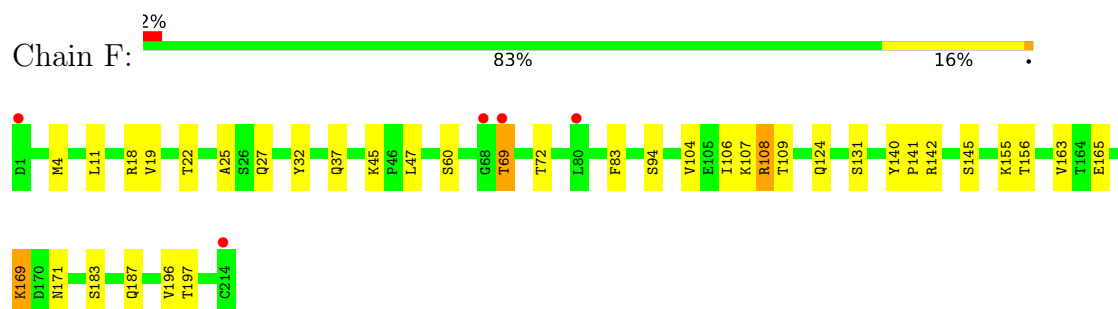
• Molecule 2: JC57-14 Light chain



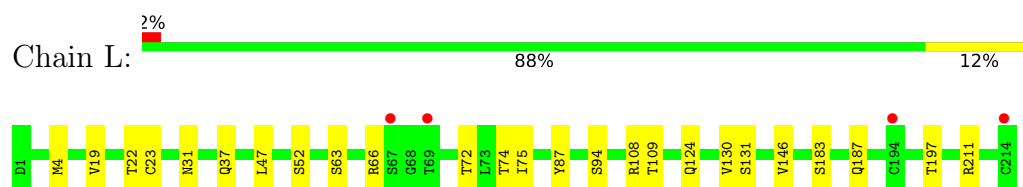
• Molecule 2: JC57-14 Light chain



• Molecule 2: JC57-14 Light chain



• Molecule 2: JC57-14 Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.70Å 129.80Å 84.00Å 90.00° 110.01° 90.00°	Depositor
Resolution (Å)	41.28 – 1.99 41.28 – 1.99	Depositor EDS
% Data completeness (in resolution range)	89.8 (41.28-1.99) 89.8 (41.28-1.99)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.176 , 0.208 0.178 , 0.210	Depositor DCC
R_{free} test set	5059 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.066 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13929	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.05% 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

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	0.25	0/1620	0.40	0/2213
1	C	0.25	0/1626	0.41	0/2221
1	E	0.53	5/1639 (0.3%)	0.54	4/2239 (0.2%)
1	H	0.16	0/1638	0.41	0/2237
2	B	0.32	0/1686	0.46	0/2292
2	D	0.18	0/1692	0.42	0/2300
2	F	0.48	2/1692 (0.1%)	0.48	0/2300
2	L	0.30	1/1692 (0.1%)	0.42	0/2300
All	All	0.33	8/13285 (0.1%)	0.44	4/18102 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	19	VAL	C-O	-6.30	1.17	1.24
2	F	32	TYR	C-O	-6.00	1.17	1.23
1	E	8	GLY	C-N	5.60	1.40	1.33
1	E	8	GLY	C-O	-5.43	1.16	1.24
2	L	52	SER	C-O	-5.39	1.17	1.24
1	E	184	VAL	C-N	5.26	1.40	1.33
1	E	185	PRO	N-CD	5.06	1.54	1.47
1	E	9	PRO	N-CD	5.03	1.54	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	8	GLY	CA-C-N	-5.76	114.04	120.14
1	E	8	GLY	C-N-CA	-5.76	114.04	120.14
1	E	184	VAL	CA-C-N	-5.68	113.91	119.76
1	E	184	VAL	C-N-CA	-5.68	113.91	119.76

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	1582	0	1544	10	0
1	C	1588	0	1549	20	0
1	E	1601	0	1561	25	0
1	H	1600	0	1559	22	0
2	B	1650	0	1591	18	0
2	D	1656	0	1596	22	0
2	F	1656	0	1596	21	0
2	L	1656	0	1596	13	0
3	A	131	0	0	3	0
3	B	86	0	0	3	0
3	C	180	0	0	9	0
3	D	129	0	0	8	0
3	E	108	0	0	7	0
3	F	92	0	0	5	0
3	H	98	0	0	4	0
3	L	116	0	0	4	0
All	All	13929	0	12592	143	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 6.

All (143) 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:42:GLY:O	1:H:43:LYS:NZ	1.99	0.96
1:C:161:SER:OG	3:C:301:HOH:O	1.88	0.89
1:E:27:ASP:OD2	1:E:94:LYS:NZ	2.09	0.85
2:D:180:THR:OG1	3:D:301:HOH:O	1.93	0.84
1:A:1:GLN:N	3:A:301:HOH:O	2.09	0.84
2:D:24:ARG:NH1	3:D:304:HOH:O	2.11	0.83
1:H:133:GLU:OE2	3:H:301:HOH:O	2.02	0.77
1:E:189:LEU:HD13	1:E:213:ILE:HD11	1.65	0.77
2:F:83:PHE:HB3	2:F:106:ILE:HG12	1.69	0.74
1:E:123:PRO:HB3	1:E:209:LYS:HZ1	1.52	0.74
1:H:189:LEU:HB3	1:H:213:ILE:HD11	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:143:GLU:OE2	3:D:303:HOH:O	2.07	0.72
2:D:107:LYS:O	3:D:302:HOH:O	2.07	0.72
1:E:212:GLU:N	1:E:212:GLU:OE2	2.22	0.69
2:L:22:THR:HG22	2:L:72:THR:HG22	1.74	0.69
1:C:75:LYS:NZ	3:C:304:HOH:O	2.26	0.68
2:F:165:GLU:OE1	3:F:301:HOH:O	2.11	0.67
2:B:10:SER:OG	3:B:301:HOH:O	2.13	0.67
2:F:22:THR:HG22	2:F:72:THR:HG22	1.78	0.66
2:D:83:PHE:HB3	2:D:106:ILE:HG12	1.78	0.65
2:F:142:ARG:HD2	2:F:163:VAL:HG11	1.78	0.65
2:D:143:GLU:O	3:D:305:HOH:O	2.15	0.64
1:E:5:GLN:OE1	3:E:301:HOH:O	2.14	0.64
2:L:63:SER:OG	3:L:301:HOH:O	2.15	0.64
2:B:24:ARG:NH1	2:B:24:ARG:HB3	2.13	0.63
2:B:24:ARG:HB3	2:B:24:ARG:HH11	1.63	0.63
1:C:18:LEU:HD13	1:C:109:VAL:HG11	1.82	0.62
1:E:123:PRO:HB3	1:E:209:LYS:NZ	2.13	0.62
2:D:195:GLU:O	3:D:306:HOH:O	2.16	0.61
2:F:124:GLN:OE1	2:F:131:SER:N	2.32	0.61
2:F:37:GLN:HB2	2:F:47:LEU:HD11	1.83	0.60
2:F:107:LYS:O	3:F:302:HOH:O	2.16	0.59
1:C:171:GLN:HG3	3:C:306:HOH:O	2.02	0.58
2:B:124:GLN:NE2	3:B:304:HOH:O	2.35	0.58
2:D:169:LYS:HB2	2:D:169:LYS:NZ	2.18	0.58
2:B:24:ARG:HG2	2:B:70:ASP:OD1	2.03	0.58
1:C:193:THR:HG22	3:C:471:HOH:O	2.02	0.58
2:F:108:ARG:HD3	2:F:109:THR:O	2.03	0.58
2:L:183:SER:O	2:L:187:GLN:HG3	2.04	0.58
1:H:29:ILE:O	1:H:52(A):GLY:HA3	2.03	0.57
2:B:124:GLN:OE1	2:B:131:SER:N	2.35	0.57
2:B:183:SER:O	2:B:187:GLN:HG3	2.06	0.56
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.88	0.56
1:H:39:GLN:NE2	3:H:304:HOH:O	2.37	0.56
1:A:16:GLU:OE2	3:A:302:HOH:O	2.18	0.55
1:C:16:GLU:OE2	3:C:302:HOH:O	2.18	0.55
1:C:189:LEU:HB3	1:C:213:ILE:HD13	1.88	0.54
1:E:40:PRO:HG2	1:E:43:LYS:HB2	1.89	0.54
1:H:43:LYS:HG2	2:L:87:TYR:OH	2.08	0.54
2:B:45:LYS:HB2	2:B:45:LYS:NZ	2.24	0.53
1:E:5:GLN:CD	3:E:301:HOH:O	2.52	0.53
1:H:8:GLY:HA3	1:H:20:LEU:HD23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:108:ARG:HD3	2:B:109:THR:O	2.10	0.52
1:C:27:ASP:O	1:C:76:ASN:ND2	2.40	0.52
2:D:124:GLN:OE1	2:D:131:SER:N	2.42	0.52
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.91	0.52
2:D:109:THR:HG23	3:D:401:HOH:O	2.11	0.51
1:E:188:SER:HA	1:E:191:THR:HG23	1.91	0.51
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.92	0.51
1:C:27:ASP:OD2	1:C:94:LYS:NZ	2.31	0.51
2:B:127:SER:O	3:B:302:HOH:O	2.19	0.50
1:C:171:GLN:NE2	3:C:310:HOH:O	2.43	0.50
1:E:130:SER:N	3:E:308:HOH:O	2.44	0.50
2:B:48:ILE:HG12	2:B:54:LEU:HD23	1.94	0.49
2:F:27:GLN:NE2	3:F:306:HOH:O	2.33	0.49
2:D:145:SER:HB3	2:D:197:THR:HB	1.95	0.49
1:E:131:THR:N	3:E:308:HOH:O	2.46	0.49
2:F:183:SER:O	2:F:187:GLN:HG3	2.13	0.49
1:E:191:THR:HG1	1:E:192:GLN:HE21	1.59	0.48
1:C:212:GLU:CD	1:C:212:GLU:H	2.20	0.48
1:A:1:GLN:HB2	3:E:365:HOH:O	2.14	0.48
1:H:2:VAL:HG22	1:H:27:ASP:HB2	1.96	0.48
2:L:19:VAL:HG22	2:L:75:ILE:HB	1.96	0.48
1:H:61:PRO:HA	1:H:64:LYS:HG3	1.96	0.47
1:E:210:ARG:N	1:E:210:ARG:HD3	2.27	0.47
1:H:105:GLN:OE1	3:H:302:HOH:O	2.20	0.47
1:H:51:PHE:CD1	1:H:69:ILE:HD13	2.50	0.47
2:D:169:LYS:HB2	2:D:169:LYS:HZ2	1.80	0.47
2:D:37:GLN:HB2	2:D:47:LEU:HD11	1.97	0.47
2:F:145:SER:HB3	2:F:197:THR:OG1	2.15	0.47
2:D:189:HIS:HE1	3:D:310:HOH:O	1.97	0.46
2:L:108:ARG:HH21	2:L:109:THR:HG23	1.81	0.46
1:A:39:GLN:HB2	1:A:45:LEU:HD23	1.96	0.46
1:E:209:LYS:HE3	1:E:209:LYS:HB3	1.78	0.46
1:H:119:PRO:HD2	1:H:205:THR:HG21	1.96	0.46
1:C:155:ASN:HA	3:C:454:HOH:O	2.14	0.46
1:H:18:LEU:HD13	1:H:109:VAL:HG11	1.96	0.46
1:A:57:THR:OG1	3:A:303:HOH:O	2.21	0.46
1:H:59:PHE:O	1:H:64:LYS:NZ	2.48	0.46
1:C:75:LYS:NZ	1:E:7:SER:HB2	2.31	0.46
1:E:204:ASN:ND2	1:E:204:ASN:O	2.49	0.46
2:F:169:LYS:NZ	3:F:308:HOH:O	2.49	0.45
1:C:148:GLU:OE2	3:C:303:HOH:O	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:31:ASN:OD1	2:L:66:ARG:NH1	2.44	0.45
2:F:11:LEU:HD11	2:F:104:VAL:HG13	1.99	0.45
2:D:142:ARG:HE	2:D:163:VAL:HG11	1.82	0.44
1:H:116:THR:HG22	1:H:147:PRO:HD3	1.99	0.44
2:L:211:ARG:NH2	3:L:313:HOH:O	2.51	0.44
1:A:50:ARG:NH2	1:A:97:SER:O	2.51	0.44
1:E:34:TRP:HB2	1:E:51:PHE:CE1	2.53	0.44
1:E:119:PRO:HB3	1:E:145:TYR:HB3	1.99	0.44
1:H:201:LYS:HE2	1:H:201:LYS:HA	2.00	0.44
2:F:4:MET:HE1	2:F:25:ALA:HB2	1.99	0.43
1:E:126:PRO:HD3	1:E:138:LEU:HD23	2.00	0.43
1:A:34:TRP:HB2	1:A:51:PHE:CE1	2.53	0.43
2:L:146:VAL:HB	3:L:318:HOH:O	2.17	0.43
2:D:4:MET:HE1	2:D:25:ALA:HB2	2.00	0.43
2:B:100:GLN:H	2:B:100:GLN:CD	2.25	0.43
1:C:37:ILE:HD13	1:C:47:TRP:HA	2.01	0.43
2:D:141:PRO:HD3	2:D:199:GLN:NE2	2.33	0.43
1:E:5:GLN:HG3	3:E:301:HOH:O	2.18	0.43
2:L:124:GLN:OE1	2:L:131:SER:N	2.43	0.43
1:A:64:LYS:HE2	1:A:64:LYS:HB3	1.70	0.43
1:A:98:GLY:HA3	2:B:91:TYR:CD2	2.54	0.42
2:B:115:VAL:HG21	2:B:196:VAL:HG11	2.01	0.42
1:C:98:GLY:HA3	2:D:91:TYR:CD2	2.54	0.42
1:C:101:ASP:HA	2:D:46:PRO:HG3	2.01	0.42
2:F:106:ILE:HB	2:F:171:ASN:ND2	2.34	0.42
1:H:200:HIS:HB3	1:H:205:THR:HB	2.01	0.42
1:E:58:ASP:OD2	2:F:94:SER:OG	2.28	0.42
2:L:94:SER:OG	3:L:302:HOH:O	2.21	0.42
1:E:5:GLN:CG	3:E:301:HOH:O	2.68	0.42
2:D:19:VAL:CG1	2:D:78:LEU:HG	2.49	0.42
2:F:69:THR:HG21	1:H:5:GLN:CD	2.45	0.42
2:B:201:LEU:HD13	2:B:205:VAL:HG13	2.01	0.42
2:F:140:TYR:CG	2:F:141:PRO:HA	2.55	0.42
2:F:45:LYS:NZ	3:F:310:HOH:O	2.45	0.41
1:E:6:GLU:HG3	1:E:92:CYS:SG	2.60	0.41
1:H:133:GLU:HB3	3:H:301:HOH:O	2.21	0.41
1:H:51:PHE:HZ	1:H:78:PHE:CE1	2.38	0.41
2:B:140:TYR:CG	2:B:141:PRO:HA	2.55	0.41
1:C:39:GLN:HB2	1:C:45:LEU:HD23	2.03	0.41
1:E:184:VAL:HG11	1:E:194:TYR:CE1	2.56	0.41
1:A:8:GLY:HA3	1:A:20:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:LEU:HD22	1:C:213:ILE:HD11	2.02	0.41
1:E:126:PRO:O	1:E:130:SER:N	2.54	0.41
2:F:106:ILE:HB	2:F:171:ASN:HD22	1.86	0.41
1:C:209:LYS:NZ	3:C:311:HOH:O	2.44	0.41
2:D:75:ILE:HG21	2:D:78:LEU:HD23	2.03	0.41
2:B:91:TYR:HA	2:B:96:TYR:HD1	1.86	0.40
2:D:65:SER:OG	2:D:72:THR:OG1	2.38	0.40
2:L:4:MET:HE3	2:L:23:CYS:SG	2.62	0.40
2:F:69:THR:HG21	1:H:5:GLN:OE1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	208/225 (92%)	204 (98%)	4 (2%)	0	100	100
1	C	209/225 (93%)	204 (98%)	5 (2%)	0	100	100
1	E	211/225 (94%)	201 (95%)	10 (5%)	0	100	100
1	H	211/225 (94%)	208 (99%)	3 (1%)	0	100	100
2	B	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
2	D	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
2	F	212/214 (99%)	208 (98%)	4 (2%)	0	100	100
2	L	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
All	All	1686/1756 (96%)	1645 (98%)	41 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	183/194 (94%)	178 (97%)	5 (3%)	39	42
1	C	184/194 (95%)	179 (97%)	5 (3%)	39	42
1	E	186/194 (96%)	180 (97%)	6 (3%)	34	35
1	H	186/194 (96%)	179 (96%)	7 (4%)	29	29
2	B	191/192 (100%)	178 (93%)	13 (7%)	14	11
2	D	192/192 (100%)	185 (96%)	7 (4%)	31	31
2	F	192/192 (100%)	184 (96%)	8 (4%)	26	25
2	L	192/192 (100%)	189 (98%)	3 (2%)	55	62
All	All	1506/1544 (98%)	1452 (96%)	54 (4%)	31	31

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASP
1	A	50	ARG
1	A	68	THR
1	A	73	THR
1	A	99	THR
2	B	5	THR
2	B	19	VAL
2	B	45	LYS
2	B	66	ARG
2	B	70	ASP
2	B	100	GLN
2	B	108	ARG
2	B	130	VAL
2	B	143	GLU
2	B	155	LYS
2	B	196	VAL
2	B	205	VAL
2	B	206	THR
1	C	101	ASP

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Mol	Chain	Res	Type
1	C	191	THR
1	C	199	ASN
1	C	204	ASN
1	C	212	GLU
2	D	19	VAL
2	D	78	LEU
2	D	109	THR
2	D	130	VAL
2	D	169	LYS
2	D	185	GLU
2	D	201	LEU
1	E	5	GLN
1	E	150	VAL
1	E	187	SER
1	E	191	THR
1	E	206	LYS
1	E	210	ARG
2	F	18	ARG
2	F	60	SER
2	F	69	THR
2	F	108	ARG
2	F	155	LYS
2	F	156	THR
2	F	169	LYS
2	F	196	VAL
1	H	43	LYS
1	H	64	LYS
1	H	74	SER
1	H	128	SER
1	H	132	SER
1	H	204	ASN
1	H	206	LYS
2	L	74	THR
2	L	130	VAL
2	L	197	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	30	ASN
2	D	92	ASN
2	D	187	GLN

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Mol	Chain	Res	Type
2	D	199	GLN
2	F	30	ASN
2	F	92	ASN
2	F	171	ASN
1	H	39	GLN
2	L	30	ASN
2	L	38	GLN
2	L	92	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 oligosaccharides 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	212/225 (94%)	-0.04	1 (0%) 87 87	21, 33, 57, 78	0
1	C	213/225 (94%)	-0.06	1 (0%) 87 87	19, 30, 53, 121	0
1	E	215/225 (95%)	0.26	9 (4%) 40 39	18, 39, 78, 97	0
1	H	215/225 (95%)	0.24	10 (4%) 36 35	24, 38, 66, 121	0
2	B	213/214 (99%)	0.31	2 (0%) 81 80	26, 46, 69, 95	0
2	D	214/214 (100%)	0.03	2 (0%) 81 80	23, 39, 56, 71	0
2	F	214/214 (100%)	0.24	5 (2%) 61 60	23, 44, 67, 82	0
2	L	214/214 (100%)	0.02	4 (1%) 66 66	24, 36, 59, 93	0
All	All	1710/1756 (97%)	0.13	34 (1%) 65 64	18, 38, 65, 121	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	130	SER	4.9
2	B	11	LEU	4.2
2	L	214	CYS	4.1
1	E	131	THR	3.7
1	H	42	GLY	3.5
1	H	128	SER	3.4
1	H	213	ILE	2.9
2	L	69	THR	2.8
1	E	53	SER	2.8
1	E	213	ILE	2.8
1	E	132	SER	2.7
2	L	194	CYS	2.7
1	H	41	PRO	2.6
1	C	132	SER	2.6
1	H	64	LYS	2.6
2	F	80	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	1	GLN	2.5
2	F	1	ASP	2.5
2	F	68	GLY	2.4
1	H	63	LEU	2.3
1	H	214	LYS	2.3
1	H	54	GLY	2.3
2	D	23	CYS	2.3
2	B	69	THR	2.2
2	D	1	ASP	2.2
1	H	43	LYS	2.2
2	F	69	THR	2.1
1	E	191	THR	2.1
1	H	113	SER	2.1
1	E	140	CYS	2.1
2	F	214	CYS	2.1
1	A	213	ILE	2.0
2	L	67	SER	2.0
1	E	172	SER	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 oligosaccharides 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.