



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2021 – 11:24 AM EDT

PDB ID : 3KYO
Title : Crystal structure of HLA-G presenting KLPAQFYIL peptide
Authors : Walpole, N.G.; Rossjohn, J.; Clements, C.S.
Deposited on : 2009-12-06
Resolution : 1.70 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 ⓘ 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 : 2.23.2
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) : 2.23.2

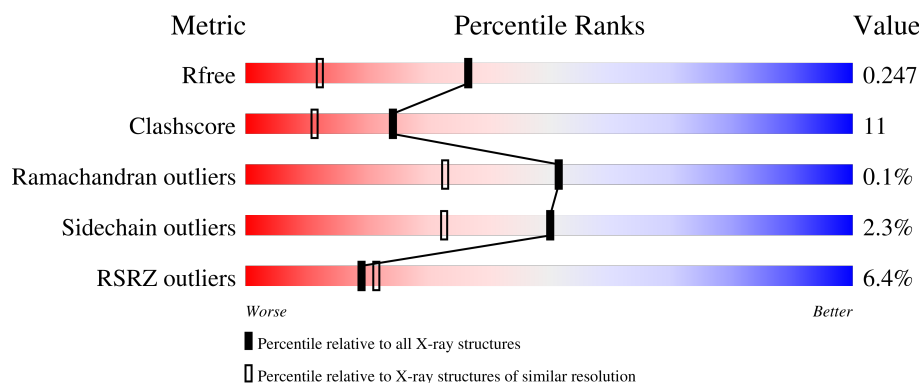
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 $\leq 5\%$. 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	273	<div> <div>5%</div> <div>84%</div> <div>15%</div> <div>.</div> </div>
1	C	273	<div> <div>8%</div> <div>83%</div> <div>15%</div> <div>.</div> </div>
2	B	100	<div> <div>6%</div> <div>90%</div> <div>10%</div> </div>
2	D	100	<div> <div>5%</div> <div>80%</div> <div>19%</div> <div>.</div> </div>
3	P	9	<div> <div>78%</div> <div>22%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	9	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7283 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2224	1386	400	426	12			
1	C	273	Total	C	N	O	S	0	1	0
			2227	1389	400	426	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	SER	CYS	engineered mutation	UNP Q9MYA2
C	42	SER	CYS	engineered mutation	UNP Q9MYA2

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	1	0
			840	537	141	158	4			
2	D	100	Total	C	N	O	S	0	1	0
			841	537	141	159	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
D	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called KLPAQFYIL peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	9	Total	C	N	O	0	0	0
			78	55	11	12			
3	Q	9	Total	C	N	O	0	0	0
			78	55	11	12			

- Molecule 4 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Co 1	0	0
4	D	1	Total 1	Co 1	0	0

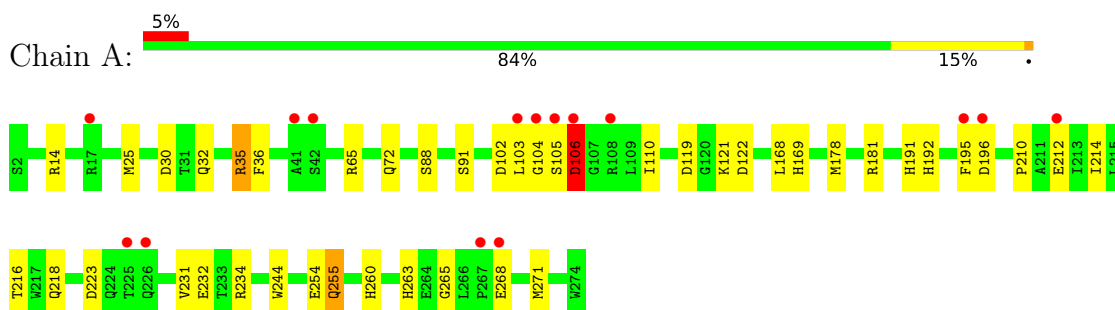
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	343	Total 343	O 343	0	0
5	B	166	Total 166	O 166	0	0
5	C	315	Total 315	O 315	0	0
5	D	155	Total 155	O 155	0	0
5	P	6	Total 6	O 6	0	0
5	Q	8	Total 8	O 8	0	0

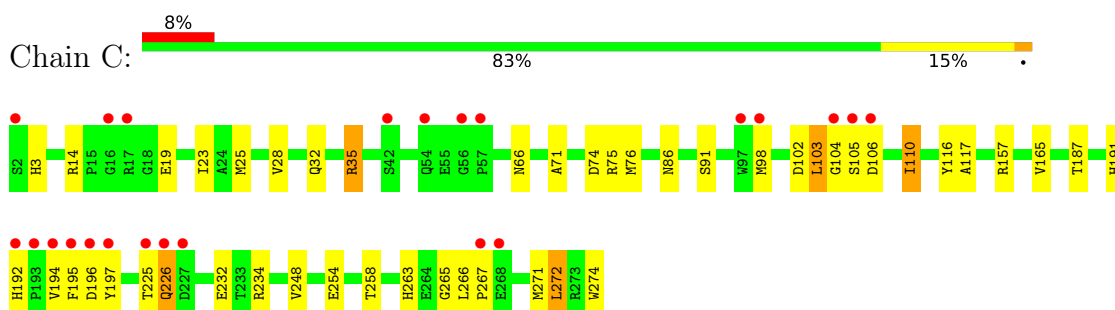
3 Residue-property plots [i](#)

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.

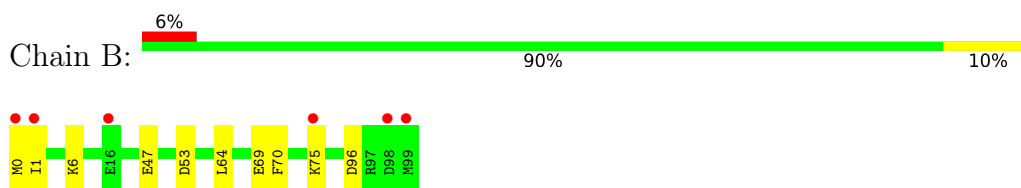
- Molecule 1: MHC class I antigen



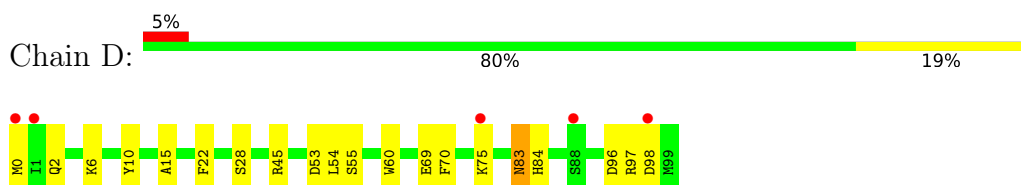
- Molecule 1: MHC class I antigen




- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: KLPAQFYIL peptide

Chain P:  78% 22%



- Molecule 3: KLPAQFYIL peptide

Chain Q:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.61Å 85.98Å 111.57Å 90.00° 95.61° 90.00°	Depositor
Resolution (Å)	43.00 – 1.70 43.01 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.00-1.70) 99.1 (43.01-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.70Å)	Xtriage
Refinement program	CNS, REFMAC 5.2.0019	Depositor
R, R_{free}	0.182 , 0.226 0.211 , 0.247	Depositor DCC
R_{free} test set	5992 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.424	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7283	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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 29.75 % 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 1.4693e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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

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	1.06	0/2285	0.98	4/3101 (0.1%)
1	C	1.03	1/2291 (0.0%)	0.99	8/3111 (0.3%)
2	B	1.09	1/866 (0.1%)	1.01	2/1172 (0.2%)
2	D	1.01	1/867 (0.1%)	0.95	0/1172
3	P	1.15	0/80	1.04	0/106
3	Q	1.26	0/80	1.16	0/106
All	All	1.05	3/6469 (0.0%)	0.99	14/8768 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	10	TYR	CD2-CE2	5.44	1.47	1.39
1	C	116	TYR	CE2-CZ	-5.18	1.31	1.38
2	B	47	GLU	CB-CG	5.00	1.61	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	104	GLY	N-CA-C	-5.92	98.31	113.10
1	A	234	ARG	NE-CZ-NH1	5.85	123.22	120.30
1	C	74	ASP	CB-CG-OD1	5.76	123.48	118.30
2	B	64	LEU	CA-CB-CG	5.70	128.41	115.30
1	A	122	ASP	CB-CG-OD1	5.63	123.37	118.30
2	B	96	ASP	CB-CG-OD1	5.62	123.35	118.30
1	C	157	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	C	14	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	C	28	VAL	CB-CA-C	-5.41	101.11	111.40
1	C	226	GLN	CB-CA-C	5.33	121.07	110.40
1	C	234	ARG	NE-CZ-NH1	5.31	122.96	120.30
1	C	14	ARG	NE-CZ-NH1	5.28	122.94	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	272	LEU	CA-CB-CG	5.17	127.20	115.30
1	A	106	ASP	CB-CA-C	5.16	120.71	110.40

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	2224	0	2075	60	0
1	C	2227	0	2082	54	0
2	B	840	0	812	9	0
2	D	841	0	812	21	0
3	P	78	0	86	2	0
3	Q	78	0	86	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	343	0	0	28	0
5	B	166	0	0	5	0
5	C	315	0	0	18	0
5	D	155	0	0	5	0
5	P	6	0	0	0	0
5	Q	8	0	0	0	0
All	All	7283	0	5953	135	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 11.

All (135) 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:91:SER:HB3	5:A:686:HOH:O	1.42	1.16
1:A:223:ASP:HB3	5:A:959:HOH:O	1.59	1.02
1:C:76:MET:HB3	5:C:419:HOH:O	1.64	0.96
1:C:76:MET:SD	5:C:965:HOH:O	2.24	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:MET:SD	5:C:962:HOH:O	2.24	0.93
1:C:32:GLN:HE22	1:C:35:ARG:HD2	1.34	0.93
1:A:102:ASP:O	1:A:110:ILE:HG22	1.73	0.86
1:A:196:ASP:HB2	5:A:974:HOH:O	1.77	0.85
1:A:32:GLN:HE22	1:A:35:ARG:HE	1.22	0.85
1:C:194:VAL:HG12	1:C:195:PHE:H	1.42	0.82
1:C:194:VAL:HG12	1:C:195:PHE:N	1.96	0.80
1:A:212:GLU:HG3	5:A:818:HOH:O	1.84	0.77
1:C:98:MET:SD	5:D:454:HOH:O	2.43	0.75
2:B:75:LYS:HE3	5:B:976:HOH:O	1.87	0.75
2:D:2:GLN:NE2	5:D:942:HOH:O	2.21	0.73
1:A:232:GLU:OE1	2:B:6:LYS:NZ	2.23	0.71
1:A:32:GLN:NE2	1:A:35:ARG:HE	1.89	0.70
1:C:104:GLY:O	1:C:106:ASP:HA	1.91	0.70
1:A:103:LEU:HA	5:A:378:HOH:O	1.93	0.69
1:C:19:GLU:CD	1:C:75:ARG:NH1	2.47	0.69
1:C:105:SER:HA	1:C:106:ASP:OD1	1.93	0.69
1:A:169:HIS:NE2	5:A:879:HOH:O	2.24	0.68
1:C:103:LEU:C	1:C:110:ILE:HG22	2.14	0.68
1:C:86:ASN:HB3	5:C:885:HOH:O	1.92	0.68
1:A:105:SER:HA	1:A:106:ASP:CB	2.22	0.68
1:A:32:GLN:HE22	1:A:35:ARG:NE	1.92	0.67
1:C:35:ARG:NH2	2:D:54:LEU:O	2.28	0.67
1:C:263:HIS:CD2	1:C:265:GLY:H	2.13	0.67
1:C:225:THR:O	1:C:226:GLN:HG3	1.95	0.67
1:C:91:SER:HB3	5:C:415:HOH:O	1.95	0.66
1:C:19:GLU:OE1	1:C:75:ARG:NH1	2.29	0.65
1:C:274:TRP:C	5:C:925:HOH:O	2.35	0.65
1:A:191:HIS:HE1	1:A:254:GLU:OE2	1.80	0.65
1:A:105:SER:HA	1:A:106:ASP:HB2	1.79	0.64
1:C:23:ILE:HD12	1:C:35:ARG:NH2	2.13	0.64
1:C:32:GLN:NE2	1:C:35:ARG:HD2	2.10	0.63
2:D:83:ASN:HD22	2:D:84:HIS:H	1.46	0.63
1:C:91:SER:HA	5:C:415:HOH:O	1.98	0.62
1:C:271:MET:HB3	5:C:662:HOH:O	1.99	0.62
1:C:194:VAL:CG1	1:C:195:PHE:H	2.10	0.61
1:A:216:THR:HG23	5:A:407:HOH:O	2.01	0.61
1:C:71:ALA:O	1:C:75:ARG:HG3	2.00	0.61
1:A:102:ASP:O	1:A:110:ILE:CG2	2.47	0.60
1:A:263:HIS:CD2	1:A:265:GLY:H	2.19	0.60
2:D:97:ARG:O	2:D:98:ASP:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:69:GLU:HG3	5:B:320:HOH:O	2.01	0.60
1:A:30:ASP:HB2	5:A:678:HOH:O	2.02	0.59
2:D:97:ARG:HB2	5:D:699:HOH:O	2.02	0.59
2:D:96:ASP:OD1	2:D:97:ARG:O	2.21	0.58
1:C:194:VAL:CG1	1:C:195:PHE:N	2.65	0.58
1:A:195:PHE:HB3	5:A:973:HOH:O	2.02	0.58
1:A:102:ASP:C	1:A:110:ILE:HG22	2.23	0.58
1:A:35:ARG:HG3	1:A:36:PHE:N	2.19	0.57
1:C:103:LEU:HD11	1:C:165:VAL:HG13	1.86	0.57
1:C:248:VAL:HG12	5:C:412:HOH:O	2.04	0.57
1:C:102:ASP:O	1:C:110:ILE:CG2	2.52	0.57
1:C:192:HIS:NE2	2:D:98:ASP:O	2.37	0.57
1:A:169:HIS:HE1	5:A:747:HOH:O	1.87	0.57
1:C:258:THR:HB	1:C:271:MET:HE3	1.88	0.56
5:C:377:HOH:O	2:D:0:MET:HE1	2.06	0.55
1:C:191:HIS:HD2	5:C:670:HOH:O	1.89	0.55
2:D:22:PHE:CZ	2:D:69:GLU:HG2	2.41	0.54
1:A:169:HIS:CE1	5:A:747:HOH:O	2.61	0.54
1:A:14:ARG:NH2	5:A:345:HOH:O	2.40	0.54
1:C:91:SER:CA	5:C:415:HOH:O	2.55	0.54
2:D:75:LYS:HB3	5:D:676:HOH:O	2.08	0.54
2:B:75:LYS:HB2	5:B:977:HOH:O	2.08	0.53
1:A:192:HIS:HD2	5:A:382:HOH:O	1.92	0.53
1:C:263:HIS:HD2	1:C:265:GLY:H	1.57	0.53
1:C:102:ASP:O	1:C:110:ILE:HG23	2.10	0.52
1:A:169:HIS:CE1	5:A:879:HOH:O	2.60	0.52
1:C:117:ALA:HB2	2:D:60:TRP:CE2	2.45	0.51
1:C:192:HIS:CE1	2:D:98:ASP:O	2.62	0.51
1:A:103:LEU:N	1:A:103:LEU:CD1	2.74	0.51
1:A:121:LYS:HD3	5:B:899:HOH:O	2.11	0.50
1:A:105:SER:HB3	5:A:886:HOH:O	2.12	0.50
5:A:840:HOH:O	3:P:7:TYR:HB2	2.12	0.50
1:A:105:SER:CB	5:A:886:HOH:O	2.60	0.50
1:A:263:HIS:HD2	1:A:265:GLY:H	1.57	0.50
1:A:105:SER:CA	1:A:106:ASP:CB	2.89	0.50
1:A:231:VAL:HG13	1:A:244:TRP:CZ2	2.46	0.50
1:C:76:MET:HE2	5:C:980:HOH:O	2.12	0.50
1:C:19:GLU:CD	1:C:75:ARG:HH11	2.15	0.49
1:A:65:ARG:HD2	5:A:671:HOH:O	2.12	0.49
1:C:102:ASP:O	1:C:110:ILE:HG22	2.13	0.49
1:A:255:GLN:H	1:A:255:GLN:NE2	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:97:ARG:O	2:D:98:ASP:CB	2.60	0.48
1:A:32:GLN:NE2	1:A:35:ARG:HH21	2.12	0.48
1:C:35:ARG:HD3	2:D:53:ASP:CG	2.34	0.47
1:A:91:SER:CB	5:A:686:HOH:O	2.25	0.47
5:A:981:HOH:O	3:P:1:LYS:HE2	2.14	0.47
1:C:187:THR:HB	1:C:272:LEU:HD21	1.97	0.47
2:D:15:ALA:HB3	2:D:97:ARG:HD3	1.97	0.47
2:D:22:PHE:CE1	2:D:69:GLU:HG2	2.50	0.47
1:A:72:GLN:NE2	5:A:326:HOH:O	2.48	0.46
1:A:178:MET:CG	5:A:328:HOH:O	2.63	0.46
1:C:91:SER:CB	5:C:415:HOH:O	2.57	0.46
1:A:178:MET:HB2	5:A:304:HOH:O	2.14	0.46
1:A:102:ASP:HB2	1:A:110:ILE:HG23	1.98	0.45
1:A:231:VAL:CG1	1:A:244:TRP:CZ2	3.00	0.45
1:A:121:LYS:HG3	2:B:1:ILE:HG12	1.97	0.45
2:D:55:SER:OG	5:D:673:HOH:O	2.21	0.45
1:A:178:MET:HG2	5:A:328:HOH:O	2.16	0.45
1:A:35:ARG:CZ	2:B:53:ASP:HB3	2.46	0.45
1:A:103:LEU:HD13	1:A:168:LEU:HD23	1.98	0.45
1:C:103:LEU:C	1:C:110:ILE:CG2	2.83	0.45
1:C:76:MET:CE	5:C:980:HOH:O	2.64	0.45
1:C:191:HIS:HE1	1:C:254:GLU:OE2	1.99	0.45
1:C:266:LEU:HA	1:C:267:PRO:HD2	1.87	0.44
1:A:106:ASP:O	5:A:700:HOH:O	2.21	0.44
5:A:384:HOH:O	2:D:45:ARG:HD2	2.18	0.44
1:C:110:ILE:HD13	1:C:110:ILE:HG21	1.69	0.44
1:A:119:ASP:HB3	2:B:0:MET:HG3	2.00	0.43
1:A:214:ILE:HG22	1:A:216:THR:HG23	1.99	0.43
1:C:3:HIS:NE2	5:C:1:HOH:O	2.36	0.43
1:A:216:THR:OG1	1:A:260:HIS:HB2	2.17	0.43
1:C:103:LEU:HA	1:C:103:LEU:HD12	1.68	0.43
1:A:103:LEU:N	1:A:103:LEU:HD12	2.34	0.43
1:A:121:LYS:CG	2:B:1:ILE:HG12	2.48	0.43
1:C:76:MET:CE	5:C:962:HOH:O	2.65	0.42
1:A:88:SER:O	5:A:982:HOH:O	2.20	0.42
1:C:232:GLU:OE1	2:D:28:SER:OG	2.28	0.42
1:A:210:PRO:O	1:A:263:HIS:HE1	2.02	0.42
1:A:271:MET:SD	1:A:271:MET:C	2.98	0.42
1:C:76:MET:HG2	5:C:394:HOH:O	2.20	0.42
1:C:105:SER:CA	1:C:106:ASP:OD1	2.66	0.42
2:D:6:LYS:HE3	2:D:28:SER:OG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ASP:C	1:A:110:ILE:CG2	2.87	0.41
1:A:91:SER:OG	5:A:982:HOH:O	2.20	0.41
1:A:218:GLN:HG3	1:A:260:HIS:CD2	2.56	0.41
1:C:19:GLU:OE2	1:C:75:ARG:NH1	2.52	0.41
1:A:195:PHE:O	1:A:196:ASP:CB	2.67	0.41
2:B:0:MET:HA	5:B:899:HOH:O	2.20	0.41
2:D:83:ASN:HD22	2:D:84:HIS:N	2.15	0.41
1:A:103:LEU:HA	1:A:110:ILE:HG22	2.03	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	271/273 (99%)	265 (98%)	6 (2%)	0	100	100
1	C	272/273 (100%)	264 (97%)	7 (3%)	1 (0%)	34	18
2	B	99/100 (99%)	98 (99%)	1 (1%)	0	100	100
2	D	99/100 (99%)	99 (100%)	0	0	100	100
3	P	7/9 (78%)	7 (100%)	0	0	100	100
3	Q	7/9 (78%)	7 (100%)	0	0	100	100
All	All	755/764 (99%)	740 (98%)	14 (2%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	196	ASP

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	230/230 (100%)	224 (97%)	6 (3%)	46	28
1	C	231/230 (100%)	225 (97%)	6 (3%)	46	28
2	B	96/95 (101%)	95 (99%)	1 (1%)	76	67
2	D	96/95 (101%)	94 (98%)	2 (2%)	53	36
3	P	8/8 (100%)	8 (100%)	0	100	100
3	Q	8/8 (100%)	8 (100%)	0	100	100
All	All	669/666 (100%)	654 (98%)	15 (2%)	50	34

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	MET
1	A	35	ARG
1	A	106	ASP
1	A	181	ARG
1	A	255	GLN
1	A	268	GLU
2	B	70	PHE
1	C	25	MET
1	C	35	ARG
1	C	66	ASN
1	C	103	LEU
1	C	110	ILE
1	C	197	TYR
2	D	70	PHE
2	D	83	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	70	HIS

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Mol	Chain	Res	Type
1	A	127	ASN
1	A	191	HIS
1	A	192	HIS
1	A	255	GLN
1	A	263	HIS
1	C	32	GLN
1	C	66	ASN
1	C	127	ASN
1	C	180	GLN
1	C	191	HIS
1	C	263	HIS
2	D	83	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

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, 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	273/273 (100%)	0.20	15 (5%) 25 27	19, 29, 48, 73	0
1	C	273/273 (100%)	0.45	23 (8%) 11 12	20, 31, 52, 72	0
2	B	100/100 (100%)	0.06	6 (6%) 21 24	20, 28, 45, 59	0
2	D	100/100 (100%)	0.10	5 (5%) 28 32	21, 28, 45, 67	0
3	P	9/9 (100%)	0.22	0 100 100	24, 31, 35, 36	0
3	Q	9/9 (100%)	0.55	0 100 100	23, 24, 28, 32	0
All	All	764/764 (100%)	0.26	49 (6%) 19 21	19, 29, 49, 73	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	195	PHE	10.4
1	C	105	SER	8.3
1	C	226	GLN	7.1
1	A	105	SER	7.0
2	D	0	MET	6.6
1	A	195	PHE	5.8
1	C	197	TYR	5.5
1	C	196	ASP	4.8
1	C	106	ASP	4.3
2	D	98	ASP	4.3
2	D	1	ILE	4.2
1	A	106	ASP	4.2
1	A	42	SER	4.0
2	B	99	MET	3.8
1	C	57	PRO	3.8
1	C	194	VAL	3.8
1	C	225	THR	3.6
2	B	75	LYS	3.6
1	C	16	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	192	HIS	3.6
1	A	103	LEU	3.6
1	A	267	PRO	3.5
1	A	104	GLY	3.5
1	A	268	GLU	3.2
1	A	225	THR	3.1
1	A	41	ALA	3.1
1	C	17	ARG	3.0
1	C	268	GLU	2.9
1	C	98	MET	2.7
1	C	104	GLY	2.7
1	C	2	SER	2.7
1	C	227	ASP	2.3
2	B	98	ASP	2.3
1	A	196	ASP	2.3
1	C	42	SER	2.3
1	A	212	GLU	2.3
1	C	97	TRP	2.2
1	A	108	ARG	2.1
1	C	193	PRO	2.1
2	B	1	ILE	2.1
2	B	0	MET	2.1
1	C	56	GLY	2.1
2	D	88	SER	2.1
1	C	267	PRO	2.1
2	B	16	GLU	2.1
1	C	54	GLN	2.1
1	A	17	ARG	2.0
2	D	75	LYS	2.0
1	A	226	GLN	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(\AA^2)	Q<0.9
4	CO	B	100	1/1	0.77	0.07	86,86,86,86	0
4	CO	D	100	1/1	0.82	0.07	82,82,82,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.