



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:45 AM UTC

PDB ID : 7P0A / pdb_00007p0a
Title : CRYSTAL STRUCTURE OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH LCMV-DERIVED GP33 PEPTIDE with D-AMINOACID (p3P6f)
Authors : Brogini, L.; Ricagno, S.
Deposited on : 2021-06-29
Resolution : 2.43 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

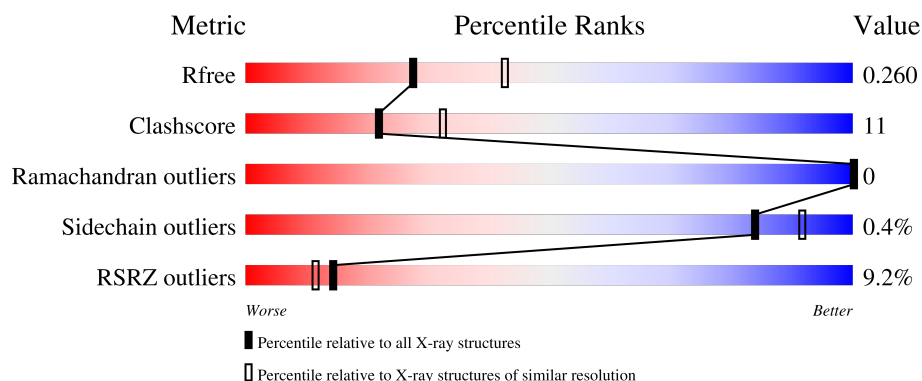
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	276	8% 69% 21% 9%
1	D	276	12% 73% 18% 8%
2	B	101	4% 65% 33% .
2	E	101	4% 83% 14% ..
3	C	9	11% 67% 33%

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Mol	Chain	Length	Quality of chain
3	F	9	33% 67% 33%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5723 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 H-2 class I histocompatibility antigen, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			1977	1254	352	363	8			
1	D	255	Total	C	N	O	S	0	0	0
			1900	1206	338	349	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			764	491	127	140	6			
2	E	99	Total	C	N	O	S	0	0	0
			786	503	134	142	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	MET	-	initiating methionine	UNP P01887
B	0	GLY	-	expression tag	UNP P01887
B	85	ASP	ALA	conflict	UNP P01887
E	-1	MET	-	initiating methionine	UNP P01887
E	0	GLY	-	expression tag	UNP P01887
E	85	ASP	ALA	conflict	UNP P01887

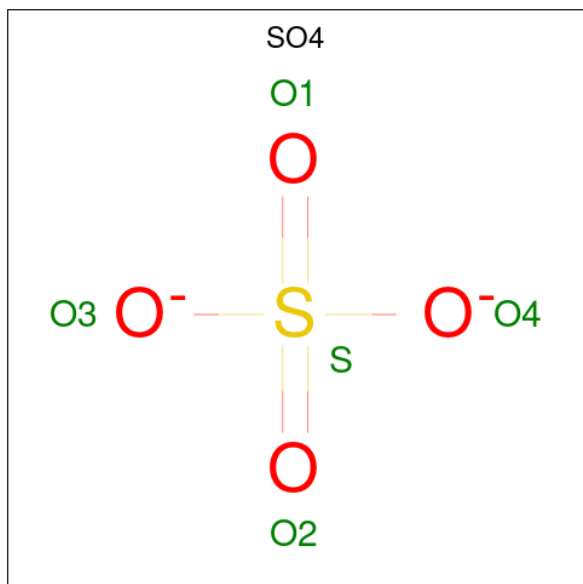
- Molecule 3 is a protein called Stable signal peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			73	48	11	13	1			
3	F	9	Total	C	N	O	S	0	0	0
			73	48	11	13	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3	PRO	VAL	conflict	UNP P09991
C	6	DPN	PHE	engineered mutation	UNP P09991
C	9	MET	CYS	conflict	UNP P09991
F	3	PRO	VAL	conflict	UNP P09991
F	6	DPN	PHE	engineered mutation	UNP P09991
F	9	MET	CYS	conflict	UNP P09991

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	2	Total Cl 2 2	0	0

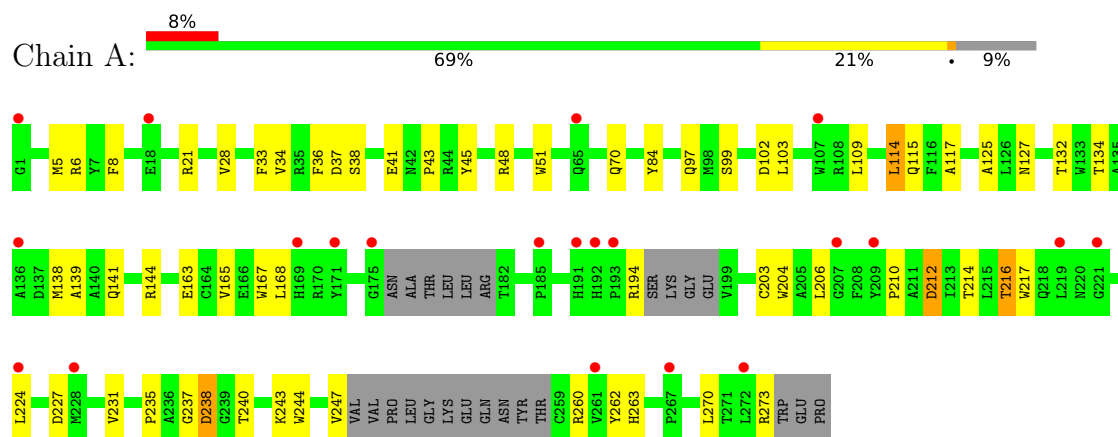
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	48	Total O 48 48	0	0
6	B	21	Total O 21 21	0	0
6	C	3	Total O 3 3	0	0
6	D	26	Total O 26 26	0	0
6	E	19	Total O 19 19	0	0
6	F	1	Total O 1 1	0	0

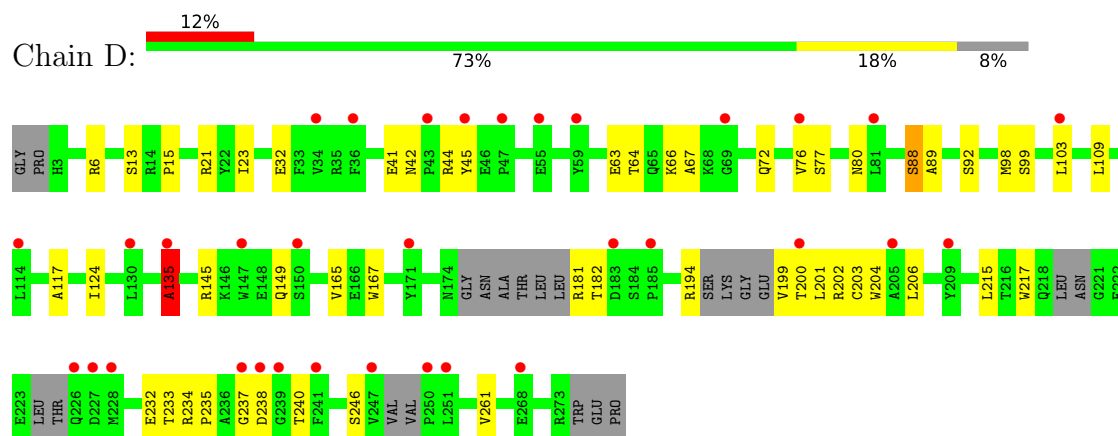
3 Residue-property plots [i](#)

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.

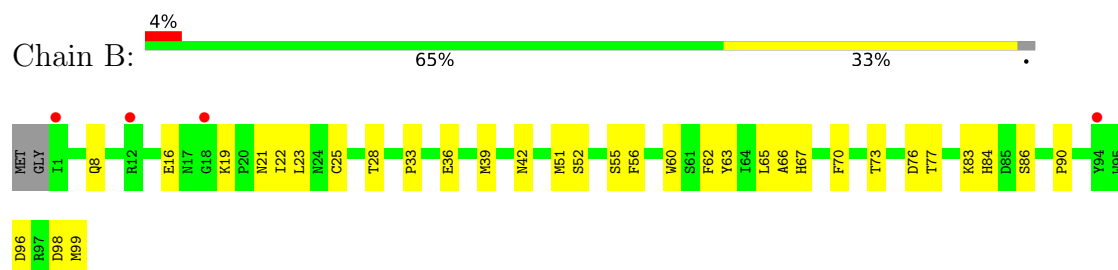
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



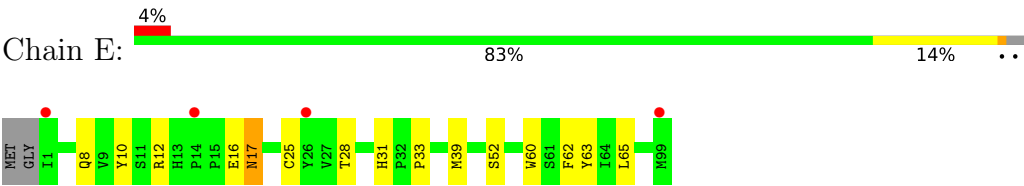
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



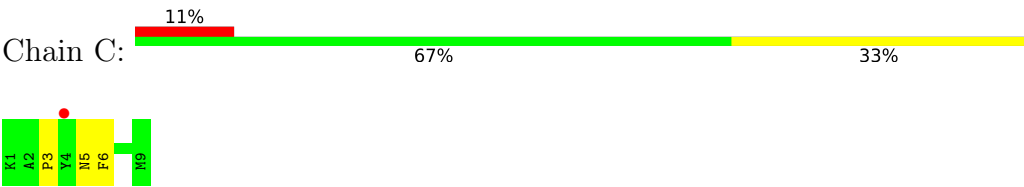
- Molecule 2: Beta-2-microglobulin



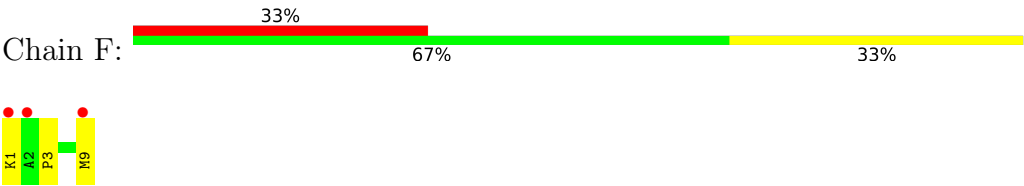
• Molecule 2: Beta-2-microglobulin



• Molecule 3: Stable signal peptide



• Molecule 3: Stable signal peptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	120.65Å 125.96Å 92.93Å 90.00° 126.63° 90.00°	Depositor
Resolution (Å)	48.41 – 2.43 48.41 – 2.43	Depositor EDS
% Data completeness (in resolution range)	72.1 (48.41-2.43) 72.1 (48.41-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.42Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.210 , 0.256 0.216 , 0.260	Depositor DCC
R_{free} test set	1990 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 94.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5723	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.00% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, DPN

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	0/2035	0.55	7/2771 (0.3%)
1	D	0.15	0/1955	0.68	8/2672 (0.3%)
2	B	0.18	0/789	0.46	0/1081
2	E	0.15	0/812	0.58	3/1108 (0.3%)
3	C	0.13	0/62	0.43	0/80
3	F	0.24	0/62	0.54	0/80
All	All	0.19	0/5715	0.59	18/7792 (0.2%)

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	D	0	1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	135	ALA	N-CA-C	18.42	136.81	111.39
2	E	17	ASN	CB-CA-C	9.55	124.17	109.84
2	E	17	ASN	N-CA-C	-8.89	97.18	110.24
1	D	135	ALA	CB-CA-C	-8.66	99.59	111.89
1	D	135	ALA	CA-C-N	8.33	131.78	120.54
1	D	135	ALA	C-N-CA	8.33	131.78	120.54
1	A	238	ASP	CB-CA-C	-7.60	93.86	111.95
1	A	114	LEU	N-CA-C	-6.42	97.08	108.13
1	D	233	THR	N-CA-C	-6.37	100.47	109.96
1	A	273	ARG	NE-CZ-NH2	6.17	124.75	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	ASP	N-CA-C	-5.92	100.57	108.74
1	A	114	LEU	CB-CA-C	5.69	118.55	110.24
2	E	31	HIS	CB-CA-C	5.37	120.75	110.17
1	D	88	SER	CB-CA-C	-5.25	100.66	113.15
1	D	32	GLU	CB-CA-C	-5.17	101.62	109.89
1	A	212	ASP	N-CA-C	-5.08	101.83	109.15
1	A	227	ASP	N-CA-C	-5.03	99.59	108.08
1	D	233	THR	CB-CA-C	5.02	117.39	110.16

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	135	ALA	Peptide

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	1977	0	1791	45	0
1	D	1900	0	1620	38	0
2	B	764	0	687	24	0
2	E	786	0	734	14	0
3	C	73	0	71	5	0
3	F	73	0	71	5	0
4	A	15	0	0	0	0
4	D	10	0	0	0	0
4	E	5	0	0	0	0
5	E	2	0	0	1	0
6	A	48	0	0	2	0
6	B	21	0	0	0	0
6	C	3	0	0	0	0
6	D	26	0	0	0	0
6	E	19	0	0	2	0
6	F	1	0	0	0	0
All	All	5723	0	4974	113	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 (113) 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:D:41:GLU:HB3	1:D:44:ARG:HH12	1.37	0.89
1:A:97:GLN:HE22	3:C:5:ASN:HD21	1.28	0.80
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.65	0.78
1:A:238:ASP:OD1	1:A:238:ASP:C	2.31	0.74
1:A:204:TRP:HZ2	2:B:99:MET:HA	1.55	0.70
1:A:212:ASP:O	1:A:263:HIS:ND1	2.25	0.70
1:D:237:GLY:HA3	2:E:12:ARG:HE	1.59	0.67
5:E:103:CL:CL	6:E:216:HOH:O	2.51	0.65
2:B:36:GLU:HB2	2:B:83:LYS:HB2	1.79	0.64
1:A:70:GLN:HE22	3:C:5:ASN:H	1.45	0.64
2:B:16:GLU:HB2	2:B:19:LYS:HD3	1.80	0.63
1:A:238:ASP:OD1	1:A:238:ASP:O	2.18	0.62
1:D:80:ASN:ND2	3:F:9:MET:OXT	2.30	0.60
1:D:15:PRO:HD3	1:D:92:SER:HB2	1.83	0.60
1:D:194:ARG:HB2	1:D:200:THR:HG23	1.84	0.59
1:A:48:ARG:NH1	6:A:402:HOH:O	2.34	0.59
1:D:42:ASN:O	1:D:44:ARG:HD3	2.03	0.59
2:E:16:GLU:O	2:E:17:ASN:C	2.44	0.59
1:A:127:ASN:ND2	1:A:132:THR:OG1	2.30	0.58
1:A:235:PRO:HG2	2:B:65:LEU:HD13	1.86	0.57
1:D:194:ARG:H	1:D:199:VAL:HA	1.67	0.57
1:D:13:SER:O	1:D:92:SER:OG	2.21	0.57
2:B:51:MET:HG3	2:B:66:ALA:HA	1.87	0.57
2:B:28:THR:HG22	2:B:63:TYR:HB2	1.87	0.56
1:D:72:GLN:O	1:D:76:VAL:HG22	2.06	0.56
1:A:216:THR:CG2	1:A:262:TYR:HE1	2.20	0.55
1:D:202:ARG:HA	1:D:246:SER:HB2	1.89	0.55
1:D:88:SER:OG	1:D:89:ALA:N	2.37	0.54
1:D:77:SER:HB3	3:F:9:MET:HB2	1.88	0.54
1:A:41:GLU:H	1:A:41:GLU:CD	2.16	0.54
2:B:84:HIS:HD1	2:B:86:SER:HG	1.55	0.54
1:D:201:LEU:O	1:D:246:SER:OG	2.21	0.54
2:E:52:SER:HB2	2:E:65:LEU:HB3	1.90	0.53
2:B:96:ASP:HB2	2:B:98:ASP:OD2	2.08	0.53
1:A:216:THR:HG21	1:A:262:TYR:HE1	1.73	0.53
1:A:38:SER:HA	1:A:43:PRO:HB3	1.91	0.53
1:D:215:LEU:HD22	1:D:261:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:MET:HA	1:A:141:GLN:HG2	1.91	0.52
2:E:12:ARG:NH1	6:E:202:HOH:O	2.42	0.52
1:A:21:ARG:NH2	1:A:37:ASP:OD2	2.41	0.51
1:D:6:ARG:HD2	1:D:98:MET:HE2	1.92	0.51
1:D:21:ARG:HH11	1:D:23:ILE:HD11	1.75	0.51
2:B:25:CYS:HB3	2:B:66:ALA:HB3	1.92	0.51
1:D:217:TRP:HE1	1:D:246:SER:HA	1.76	0.51
2:E:52:SER:HB3	2:E:65:LEU:H	1.75	0.51
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.46	0.51
1:D:217:TRP:NE1	1:D:246:SER:HA	2.26	0.50
1:A:216:THR:HG22	1:A:260:ARG:O	2.12	0.50
2:B:25:CYS:HB2	2:B:39:MET:HE3	1.92	0.50
1:A:115:GLN:HG2	1:A:125:ALA:HB1	1.94	0.49
1:D:204:TRP:HB3	1:D:206:LEU:HD11	1.93	0.48
1:D:99:SER:OG	3:F:3:PRO:HG3	2.14	0.48
1:A:231:VAL:O	1:A:243:LYS:NZ	2.35	0.48
1:A:84:TYR:HB3	1:A:139:ALA:HB1	1.96	0.48
1:A:34:VAL:HG22	1:A:45:TYR:HD1	1.78	0.48
1:A:8:PHE:HD2	2:B:56:PHE:CE1	2.32	0.47
1:D:238:ASP:OD1	1:D:240:THR:HG22	2.13	0.47
1:D:63:GLU:OE1	1:D:66:LYS:NZ	2.48	0.47
1:A:260:ARG:HA	1:A:270:LEU:O	2.14	0.47
2:B:42:ASN:ND2	2:B:77:THR:H	2.13	0.47
2:B:33:PRO:HG3	2:B:62:PHE:CE1	2.50	0.47
2:B:33:PRO:HG3	2:B:62:PHE:CZ	2.50	0.46
1:D:103:LEU:HD21	1:D:165:VAL:HG12	1.96	0.46
1:D:167:TRP:CE3	3:F:1:LYS:HG2	2.50	0.46
2:E:33:PRO:HG3	2:E:62:PHE:CZ	2.50	0.46
1:D:232:GLU:HB2	2:E:8:GLN:NE2	2.30	0.46
2:B:8:GLN:HE21	2:B:8:GLN:HB3	1.61	0.46
2:E:25:CYS:HB2	2:E:39:MET:HE3	1.98	0.46
1:D:232:GLU:HB2	2:E:8:GLN:HE22	1.80	0.45
1:A:109:LEU:HB2	1:A:165:VAL:HG11	1.98	0.45
1:A:127:ASN:OD1	1:A:134:THR:OG1	2.30	0.45
2:B:52:SER:HB3	2:B:65:LEU:H	1.81	0.45
2:B:83:LYS:HG2	2:B:90:PRO:HG3	1.98	0.45
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.52	0.45
2:B:55:SER:OG	2:B:56:PHE:N	2.49	0.45
1:D:124:ILE:HG13	1:D:135:ALA:HB2	1.98	0.45
1:D:42:ASN:H	1:D:44:ARG:NH1	2.15	0.44
1:D:181:ARG:HB3	1:D:182:THR:H	1.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:CYS:HB2	1:D:217:TRP:CZ2	2.52	0.44
1:A:6:ARG:HH22	1:A:102:ASP:CG	2.26	0.44
1:A:194:ARG:NH2	6:A:401:HOH:O	2.31	0.44
1:A:103:LEU:HD21	1:A:168:LEU:HD23	2.00	0.44
1:D:234:ARG:HD2	2:E:10:TYR:CE1	2.53	0.44
1:A:114:LEU:HD22	1:A:114:LEU:HA	1.88	0.44
1:A:36:PHE:CZ	1:A:43:PRO:HB2	2.53	0.43
1:A:204:TRP:HB3	1:A:206:LEU:CD1	2.48	0.43
1:A:141:GLN:OE1	1:A:144:ARG:NH2	2.50	0.43
1:A:99:SER:OG	3:C:3:PRO:HG3	2.18	0.43
1:A:238:ASP:C	1:A:240:THR:H	2.27	0.43
2:B:73:THR:OG1	2:B:76:ASP:OD1	2.36	0.42
2:E:33:PRO:HG3	2:E:62:PHE:CE2	2.54	0.42
3:F:1:LYS:HD3	3:F:1:LYS:HA	1.91	0.42
1:D:44:ARG:HA	1:D:64:THR:HG23	2.00	0.42
1:A:70:GLN:NE2	3:C:5:ASN:H	2.14	0.42
1:D:145:ARG:O	1:D:149:GLN:HB2	2.19	0.42
1:A:217:TRP:CE2	1:A:247:VAL:HG12	2.54	0.42
1:A:210:PRO:O	1:A:263:HIS:HE1	2.02	0.42
2:B:23:LEU:O	2:B:67:HIS:HA	2.20	0.42
1:A:51:TRP:CD1	1:A:51:TRP:H	2.38	0.41
1:A:237:GLY:HA3	2:B:22:ILE:HG21	2.02	0.41
2:B:42:ASN:HD21	2:B:77:THR:H	1.66	0.41
1:A:28:VAL:HG23	1:A:33:PHE:CE1	2.56	0.41
1:D:235:PRO:HG2	2:E:65:LEU:HD22	2.02	0.41
1:A:203:CYS:O	1:A:244:TRP:HA	2.21	0.41
3:C:5:ASN:O	3:C:6:DPN:HB2	2.19	0.41
1:D:103:LEU:HD23	1:D:109:LEU:HA	2.03	0.41
1:A:163:GLU:HG3	1:A:167:TRP:CD1	2.56	0.41
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.56	0.40
1:A:214:THR:HB	1:A:262:TYR:HB2	2.04	0.40
1:A:138:MET:HB2	1:A:138:MET:HE2	1.68	0.40
1:D:238:ASP:OD1	1:D:238:ASP:N	2.54	0.40
1:D:45:TYR:HE2	1:D:67:ALA:HB2	1.86	0.40
2:E:28:THR:HG22	2:E:63:TYR:HB2	2.04	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	244/276 (88%)	229 (94%)	15 (6%)	0	100	100
1	D	243/276 (88%)	227 (93%)	16 (7%)	0	100	100
2	B	97/101 (96%)	92 (95%)	5 (5%)	0	100	100
2	E	97/101 (96%)	95 (98%)	2 (2%)	0	100	100
3	C	6/9 (67%)	4 (67%)	2 (33%)	0	100	100
3	F	6/9 (67%)	6 (100%)	0	0	100	100
All	All	693/772 (90%)	653 (94%)	40 (6%)	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	189/234 (81%)	187 (99%)	2 (1%)	65	81
1	D	165/234 (70%)	165 (100%)	0	100	100
2	B	79/95 (83%)	79 (100%)	0	100	100
2	E	85/95 (90%)	85 (100%)	0	100	100
3	C	6/6 (100%)	6 (100%)	0	100	100
3	F	6/6 (100%)	6 (100%)	0	100	100
All	All	530/670 (79%)	528 (100%)	2 (0%)	84	92

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	THR
1	A	224	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	29	GLN
2	B	42	ASN
3	C	5	ASN
1	D	30	ASN
1	D	127	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	302	-	4,4,4	0.25	0	6,6,6	0.07	0
4	SO4	D	302	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	E	101	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	301	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	301	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	303	-	4,4,4	0.24	0	6,6,6	0.06	0

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 ⓘ

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	252/276 (91%)	0.65	21 (8%) 17 14	22, 77, 150, 195	0
1	D	255/276 (92%)	1.03	33 (12%) 7 5	48, 96, 148, 180	0
2	B	99/101 (98%)	0.50	4 (4%) 42 38	38, 71, 128, 198	0
2	E	99/101 (98%)	0.38	4 (4%) 42 38	39, 69, 108, 118	0
3	C	8/9 (88%)	0.50	1 (12%) 8 6	44, 56, 74, 82	0
3	F	8/9 (88%)	1.90	3 (37%) 1 0	90, 105, 120, 135	0
All	All	721/772 (93%)	0.74	66 (9%) 14 11	22, 82, 143, 198	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	135	ALA	4.6
1	D	59	TYR	4.2
1	D	239	GLY	3.6
1	D	130	LEU	3.6
3	F	1	LYS	3.5
1	D	227	ASP	3.4
1	A	1	GLY	3.2
2	E	14	PRO	3.2
1	D	171	TYR	3.1
1	D	55	GLU	3.1
1	A	193	PRO	3.1
1	A	192	HIS	3.0
1	A	261	VAL	3.0
1	D	45	TYR	3.0
1	A	136	ALA	2.9
1	D	69	GLY	2.9
1	A	191	HIS	2.9
3	C	4	TYR	2.9
1	D	237	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	247	VAL	2.7
1	D	103	LEU	2.7
2	B	94	TYR	2.6
1	A	221	GLY	2.6
1	D	238	ASP	2.6
1	D	36	PHE	2.6
3	F	2	ALA	2.6
1	A	228	MET	2.5
2	E	99	MET	2.5
2	B	18	GLY	2.5
1	D	268	GLU	2.5
1	D	200	THR	2.5
1	A	18	GLU	2.5
1	A	65	GLN	2.4
1	D	76	VAL	2.4
1	A	169	HIS	2.3
1	A	272	LEU	2.3
1	D	81	LEU	2.3
1	D	114	LEU	2.3
1	D	251	LEU	2.3
1	D	47	PRO	2.3
2	E	1	ILE	2.3
1	D	209	TYR	2.3
1	D	250	PRO	2.3
1	A	224	LEU	2.2
2	B	1	ILE	2.2
1	A	185	PRO	2.2
1	D	34	VAL	2.2
1	D	226	GLN	2.2
3	F	9	MET	2.2
1	D	150	SER	2.2
1	D	43	PRO	2.2
1	D	228	MET	2.2
1	D	185	PRO	2.2
1	D	241	PHE	2.2
1	D	147	TRP	2.2
1	A	267	PRO	2.1
1	A	107	TRP	2.1
1	A	175	GLY	2.1
1	A	171	TYR	2.1
1	D	205	ALA	2.1
2	E	26	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	12	ARG	2.0
1	A	219	LEU	2.0
1	A	207	GLY	2.0
1	D	183	ASP	2.0
1	A	209	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	DPN	F	6	11/12	0.87	0.15	98,110,134,138	0
3	DPN	C	6	11/12	0.95	0.11	56,63,90,94	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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	SO4	D	301	5/5	0.40	0.11	166,166,167,168	0
4	SO4	E	101	5/5	0.51	0.09	172,174,174,176	0
4	SO4	D	302	5/5	0.60	0.11	153,155,157,158	0
4	SO4	A	303	5/5	0.75	0.12	126,134,136,139	0
4	SO4	A	301	5/5	0.85	0.09	104,104,117,121	0
4	SO4	A	302	5/5	0.92	0.11	107,108,121,123	0
5	CL	E	102	1/1	0.94	0.12	76,76,76,76	0
5	CL	E	103	1/1	0.95	0.15	86,86,86,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.