



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:43 PM UTC

PDB ID : 8H9D / pdb_00008h9d
Title : Crystal structure of Cas12a protein
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Deposited on : 2022-10-25
Resolution : 3.10 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

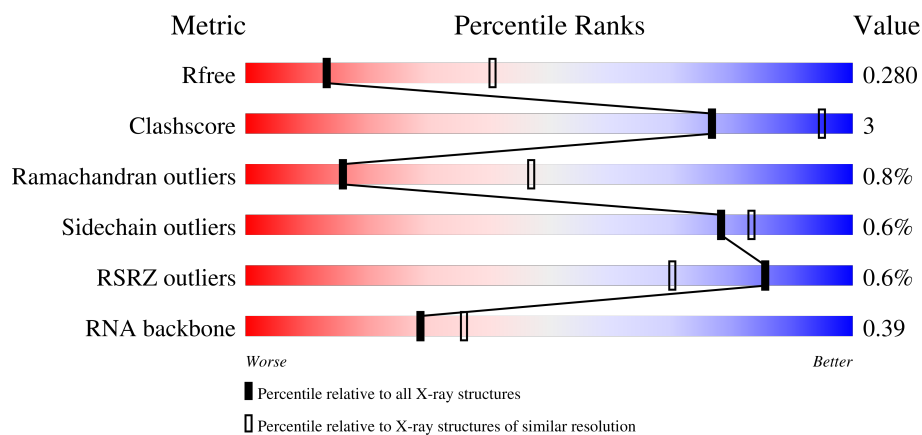
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

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	B	1206	 74% 22%
2	A	1207	 85% 7% 8%
3	G	21	 67% 19% 14%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16986 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 Cas12A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	946	7557	4835	1262	1439	21	0	0	0

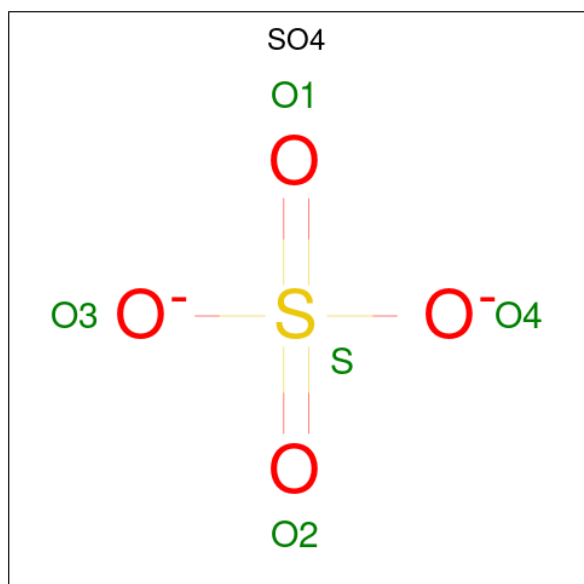
- Molecule 2 is a protein called Cas12A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	1114	8973	5713	1512	1726	22	0	0	0

- Molecule 3 is a RNA chain called RNA (5'-R(P*AP*AP*UP*UP*UP*CP*UP*AP*CP*UP*AP*AP*GP*UP*GP*UP*AP*GP*AP*UP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	G	21	443	199	75	148	21	0	0	0

- 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		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	G	1	Total	Mg	0	0
			1	1		

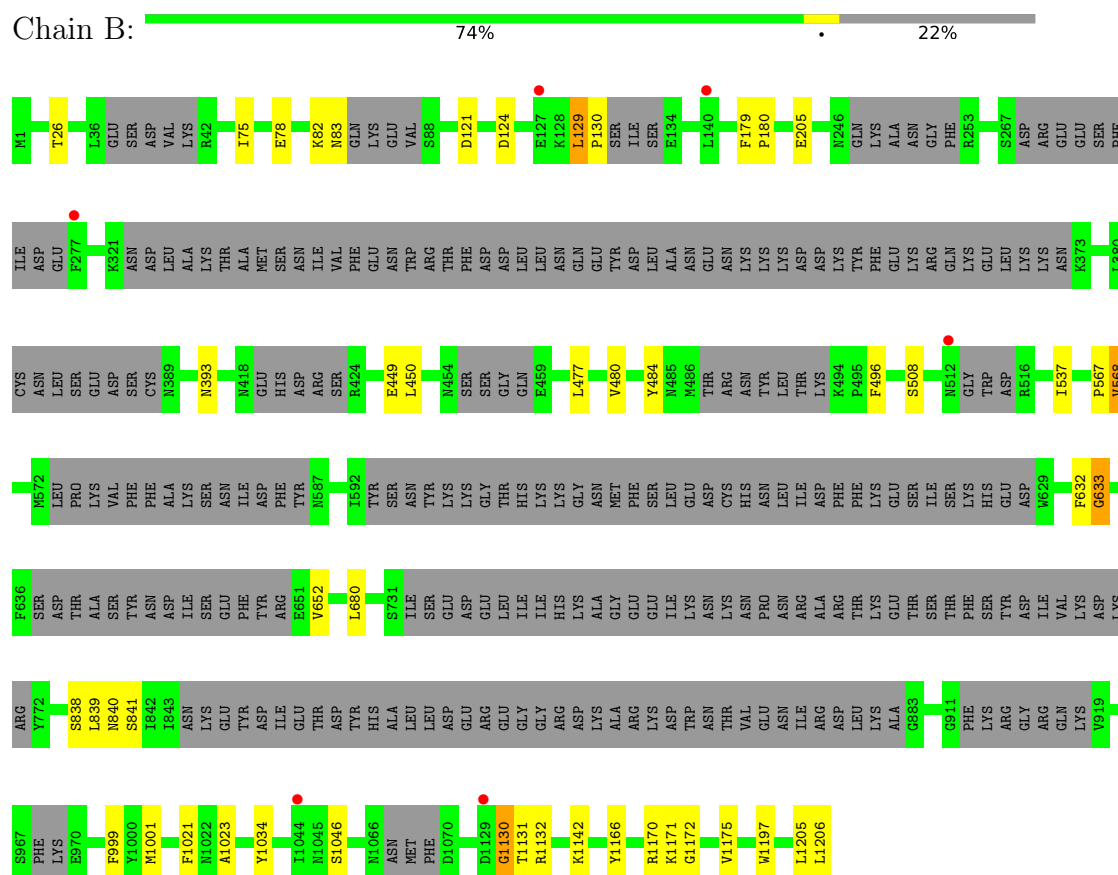
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	6	Total	O	0	0
			6	6		

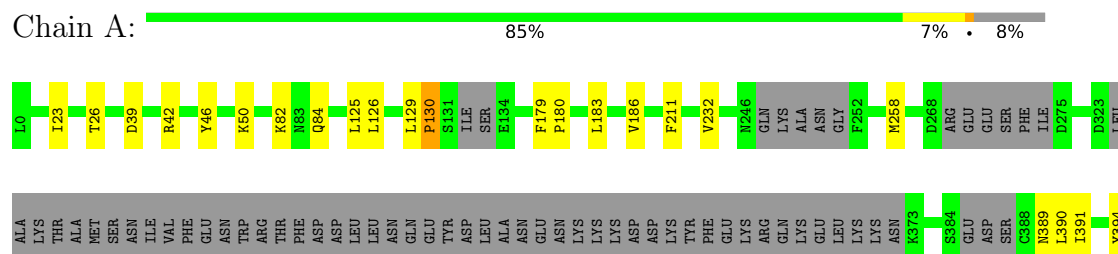
3 Residue-property plots [i](#)

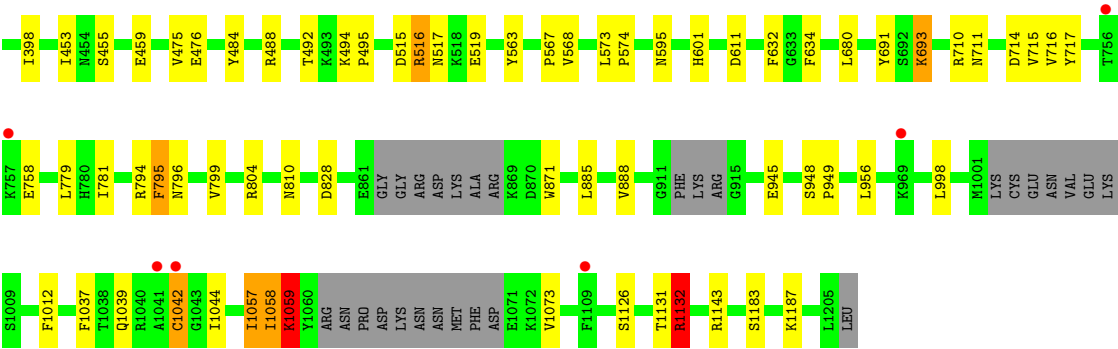
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Cas12A

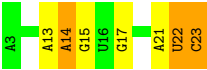


• Molecule 2: Cas12A





● Molecule 3: RNA (5'-R(P*AP*AP*UP*UP*UP*CP*UP*AP*CP*UP*AP*AP*GP*UP*GP*U
P*AP*GP*AP*UP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	235.70Å 85.63Å 139.30Å 90.00° 110.15° 90.00°	Depositor
Resolution (Å)	29.98 – 3.10 29.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.98-3.10) 99.7 (29.98-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 3.11Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.232 , 0.252 (Not available) , 0.280	Depositor DCC
R_{free} test set	2000 reflections (3.88%)	wwPDB-VP
Wilson B-factor (Å ²)	93.7	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	16986	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: SO4, MG

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	B	0.22	0/7671	0.47	0/10328
2	A	0.29	0/9126	0.57	7/12290 (0.1%)
3	G	0.38	0/494	0.78	2/766 (0.3%)
All	All	0.26	0/17291	0.53	9/23384 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	14	A	C2'-C3'-O3'	9.47	123.70	109.50
3	G	22	U	P-O3'-C3'	8.78	133.37	120.20
2	A	1057	ILE	O-C-N	6.80	129.10	122.30
2	A	1057	ILE	CA-C-N	6.31	133.32	121.97
2	A	1057	ILE	C-N-CA	6.31	133.32	121.97
2	A	795	PHE	CA-C-O	-5.23	114.87	120.42
2	A	1132	ARG	N-CA-C	5.17	121.81	110.80
2	A	794	ARG	N-CA-C	-5.10	103.59	110.68
2	A	1187	LYS	CA-C-O	-5.10	115.58	121.19

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	B	7557	0	7410	30	0
2	A	8973	0	8794	62	0
3	G	443	0	224	4	0
4	A	5	0	0	0	0
5	A	1	0	0	0	0
5	G	1	0	0	0	0
6	G	6	0	0	0	0
All	All	16986	0	16428	96	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 3.

All (96) 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:A:1059:LYS:CE	2:A:1126:SER:HB2	1.36	1.54
2:A:1059:LYS:CE	2:A:1126:SER:CB	2.30	1.10
2:A:1059:LYS:HE2	2:A:1126:SER:HB2	1.41	0.97
2:A:1059:LYS:HE3	2:A:1126:SER:HB2	0.97	0.96
2:A:1059:LYS:HE3	2:A:1126:SER:CB	1.90	0.96
2:A:716:VAL:HG12	2:A:717:TYR:H	1.40	0.86
2:A:998:LEU:HD13	2:A:1042:CYS:SG	2.19	0.82
2:A:998:LEU:CD1	2:A:1042:CYS:SG	2.72	0.77
2:A:1059:LYS:HE2	2:A:1126:SER:CB	2.09	0.74
3:G:23:C:OP2	3:G:23:C:H3'	1.89	0.71
2:A:711:ASN:HA	2:A:716:VAL:HG21	1.72	0.71
1:B:26:THR:HG21	1:B:680:LEU:H	1.58	0.69
2:A:1059:LYS:NZ	2:A:1126:SER:HB2	2.10	0.66
1:B:393:ASN:O	1:B:393:ASN:ND2	2.23	0.64
1:B:393:ASN:HD22	1:B:393:ASN:C	2.03	0.62
2:A:488:ARG:O	2:A:492:THR:HG22	1.99	0.62
2:A:516:ARG:N	2:A:563:TYR:O	2.31	0.62
2:A:26:THR:HG21	2:A:680:LEU:H	1.65	0.61
3:G:23:C:H2'	3:G:23:C:O2	2.02	0.59
1:B:450:LEU:HD12	1:B:477:LEU:CD1	2.31	0.59
1:B:1172:GLY:O	1:B:1175:VAL:HG22	2.02	0.59
2:A:179:PHE:HB3	2:A:180:PRO:HD3	1.86	0.57
2:A:716:VAL:HG12	2:A:717:TYR:N	2.17	0.56
2:A:885:LEU:HA	2:A:888:VAL:HG22	1.88	0.56
2:A:716:VAL:CG1	2:A:717:TYR:H	2.14	0.55
2:A:475:VAL:O	2:A:476:GLU:HB2	2.06	0.54
2:A:795:PHE:C	2:A:795:PHE:CD1	2.86	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:948:SER:N	2:A:949:PRO:HD3	2.22	0.54
1:B:496:PHE:CE2	1:B:537:ILE:HD11	2.43	0.54
1:B:1142:LYS:HG3	1:B:1206:LEU:HD11	1.91	0.53
3:G:21:A:H2'	3:G:22:U:O4'	2.08	0.53
2:A:716:VAL:HG22	2:A:956:LEU:HD22	1.90	0.52
2:A:394:TYR:CZ	2:A:398:ILE:HD11	2.45	0.52
2:A:183:LEU:O	2:A:186:VAL:HG22	2.10	0.52
1:B:838:SER:O	1:B:841:SER:HB2	2.10	0.51
2:A:515:ASP:OD1	2:A:563:TYR:CB	2.58	0.51
2:A:573:LEU:HB2	2:A:574:PRO:HD3	1.92	0.51
2:A:129:LEU:HB2	2:A:130:PRO:HD3	1.94	0.50
2:A:1057:ILE:HG12	2:A:1073:VAL:HG22	1.93	0.50
2:A:389:ASN:O	2:A:391:ILE:N	2.40	0.50
2:A:710:ARG:O	2:A:716:VAL:HG21	2.12	0.50
1:B:839:LEU:C	1:B:841:SER:H	2.19	0.50
1:B:75:ILE:HA	1:B:78:GLU:OE2	2.12	0.49
1:B:1171:LYS:HE2	1:B:1197:TRP:CD2	2.47	0.49
2:A:82:LYS:HB2	2:A:84:GLN:OE1	2.13	0.48
2:A:455:SER:HB2	2:A:459:GLU:OE1	2.14	0.48
2:A:1132:ARG:NH1	2:A:1132:ARG:HB3	2.29	0.48
1:B:567:PRO:O	1:B:568:VAL:C	2.56	0.47
2:A:632:PHE:HB2	2:A:634:PHE:CE2	2.49	0.47
2:A:714:ASP:C	2:A:716:VAL:N	2.73	0.47
2:A:26:THR:CG2	2:A:680:LEU:H	2.28	0.46
1:B:450:LEU:CD1	1:B:477:LEU:CD1	2.92	0.46
2:A:23:ILE:O	2:A:26:THR:HG23	2.15	0.46
2:A:515:ASP:HA	2:A:563:TYR:CB	2.46	0.46
1:B:839:LEU:O	1:B:840:ASN:HB2	2.16	0.46
2:A:691:TYR:O	2:A:693:LYS:HE3	2.16	0.46
2:A:595:ASN:ND2	2:A:611:ASP:OD1	2.48	0.46
1:B:450:LEU:CD1	1:B:477:LEU:HD12	2.46	0.45
2:A:810:ASN:OD1	2:A:828:ASP:HA	2.17	0.45
2:A:517:ASN:C	2:A:519:GLU:H	2.24	0.45
2:A:795:PHE:CD1	2:A:795:PHE:O	2.70	0.45
2:A:1058:ILE:HG22	2:A:1058:ILE:O	2.18	0.44
2:A:232:VAL:HG13	2:A:258:MET:HB2	1.98	0.44
2:A:1143:ARG:HD2	2:A:1143:ARG:H	1.82	0.44
2:A:779:LEU:HD21	2:A:781:ILE:HD11	2.00	0.44
2:A:186:VAL:HG12	2:A:211:PHE:HA	2.00	0.43
1:B:82:LYS:O	1:B:83:ASN:C	2.61	0.43
2:A:484:TYR:HH	2:A:871:TRP:HZ3	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:796:ASN:O	2:A:799:VAL:N	2.46	0.43
1:B:999:PHE:HB3	1:B:1001:MET:HG3	2.01	0.43
2:A:601:HIS:CD2	2:A:601:HIS:H	2.36	0.43
1:B:1166:TYR:CE2	1:B:1170:ARG:HD2	2.53	0.42
2:A:125:LEU:O	2:A:126:LEU:C	2.62	0.42
2:A:567:PRO:O	2:A:568:VAL:C	2.62	0.42
2:A:1012:PHE:CE1	2:A:1037:PHE:HE2	2.37	0.42
1:B:632:PHE:O	1:B:633:GLY:C	2.62	0.42
1:B:179:PHE:HB3	1:B:180:PRO:HD3	2.01	0.42
1:B:1034:TYR:HB2	1:B:1046:SER:HB2	2.01	0.42
2:A:475:VAL:HG12	2:A:476:GLU:N	2.35	0.42
2:A:494:LYS:HB3	2:A:495:PRO:HD2	2.02	0.42
2:A:1058:ILE:HD12	2:A:1058:ILE:H	1.85	0.42
2:A:389:ASN:O	2:A:390:LEU:HB2	2.20	0.42
2:A:717:TYR:N	2:A:717:TYR:CD1	2.88	0.42
1:B:496:PHE:CZ	1:B:537:ILE:HD11	2.54	0.41
2:A:453:ILE:O	2:A:453:ILE:HG22	2.20	0.41
1:B:121:ASP:OD1	1:B:121:ASP:N	2.52	0.41
1:B:1130:GLY:O	1:B:1131:THR:C	2.62	0.41
1:B:1205:LEU:O	1:B:1206:LEU:HB2	2.20	0.41
2:A:39:ASP:OD1	2:A:42:ARG:NH1	2.53	0.41
2:A:46:TYR:CZ	2:A:50:LYS:HD2	2.56	0.41
1:B:652:VAL:HG12	1:B:652:VAL:O	2.19	0.40
1:B:1021:PHE:CE2	1:B:1023:ALA:HA	2.56	0.40
3:G:23:C:O2	3:G:23:C:C2'	2.67	0.40
1:B:480:VAL:HG22	1:B:480:VAL:O	2.21	0.40
1:B:484:TYR:CD1	1:B:484:TYR:C	3.00	0.40
1:B:129:LEU:H	1:B:130:PRO:CD	2.33	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	B	906/1206 (75%)	843 (93%)	56 (6%)	7 (1%)	16	47
2	A	1094/1207 (91%)	1034 (94%)	52 (5%)	8 (1%)	18	49
All	All	2000/2413 (83%)	1877 (94%)	108 (5%)	15 (1%)	16	47

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	516	ARG
2	A	945	GLU
1	B	124	ASP
2	A	715	VAL
2	A	1042	CYS
2	A	1059	LYS
1	B	129	LEU
1	B	205	GLU
2	A	1058	ILE
2	A	1131	THR
1	B	508	SER
1	B	633	GLY
1	B	1130	GLY
1	B	568	VAL
2	A	130	PRO

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	B	812/1110 (73%)	810 (100%)	2 (0%)	87	89
2	A	975/1111 (88%)	967 (99%)	8 (1%)	73	81
All	All	1787/2221 (80%)	1777 (99%)	10 (1%)	78	83

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	449	GLU

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Mol	Chain	Res	Type
1	B	1132	ARG
2	A	693	LYS
2	A	758	GLU
2	A	804	ARG
2	A	1039	GLN
2	A	1044	ILE
2	A	1059	LYS
2	A	1132	ARG
2	A	1183	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	97	GLN
1	B	113	ASN
1	B	470	HIS
1	B	479	GLN
1	B	504	ASN
1	B	539	ASN
1	B	780	HIS
1	B	1053	ASN
1	B	1204	HIS
2	A	9	GLN
2	A	48	HIS
2	A	522	ASN
2	A	780	HIS
2	A	844	ASN
2	A	1163	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	G	20/21 (95%)	5 (25%)	1 (5%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	G	13	A
3	G	14	A
3	G	15	G

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Mol	Chain	Res	Type
3	G	17	G
3	G	23	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	G	14	A

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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	1301	-	4,4,4	0.26	0	6,6,6	0.10	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 [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	B	946/1206 (78%)	-0.11	6 (0%) 85 70	30, 100, 139, 168	0
2	A	1114/1207 (92%)	-0.13	6 (0%) 87 73	30, 95, 137, 169	0
3	G	21/21 (100%)	-0.16	0 100 100	60, 66, 95, 125	0
All	All	2081/2434 (85%)	-0.12	12 (0%) 85 70	30, 97, 139, 169	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	969	LYS	3.4
1	B	512	ASN	3.3
1	B	127	GLU	3.2
2	A	1042	CYS	3.1
1	B	1129	ASP	2.7
2	A	1109	PHE	2.5
2	A	757	LYS	2.4
2	A	1041	ALA	2.3
1	B	1044	ILE	2.3
1	B	277	PHE	2.1
2	A	756	THR	2.1
1	B	140	LEU	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](#)

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($\text{\AA}^2$)	Q<0.9
4	SO4	A	1301	5/5	0.75	0.12	111,113,140,145	0
5	MG	A	1302	1/1	0.92	0.28	66,66,66,66	0
5	MG	G	101	1/1	0.99	0.03	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.