



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:16 PM EDT

PDB ID : 3OSJ / pdb_00003osj
Title : X-Ray Structure of Phycobilisome LCM core-membrane linker polypeptide (fragment 254-400) from *Synechocystis* sp. PCC 6803, Northeast Structural Genomics Consortium Target SgR209C
Authors : Kuzin, A.; Su, M.; Lew, S.; Seetharaman, J.; Sahdev, S.; Xiao, R.; Ciccosanti, C.; Lee, D.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2010-09-09
Resolution : 2.30 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)

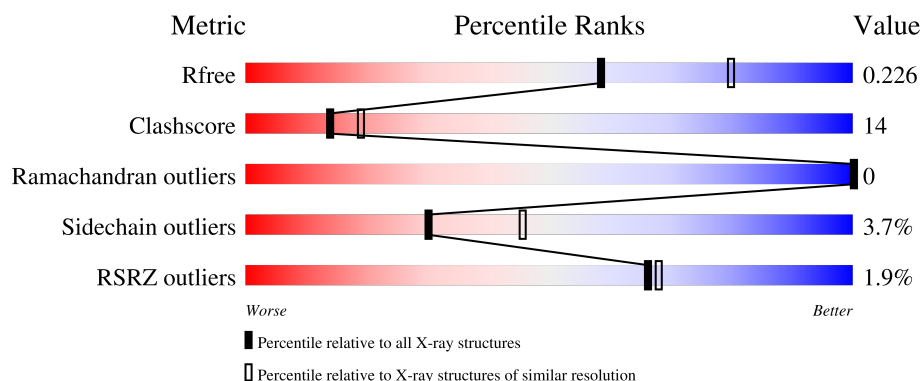
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	147	71% 19% • 8%
1	B	147	3% 65% 27% • 7%
1	C	147	2% 71% 17% • 10%
1	D	147	68% 22% • 8%

Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4871 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.

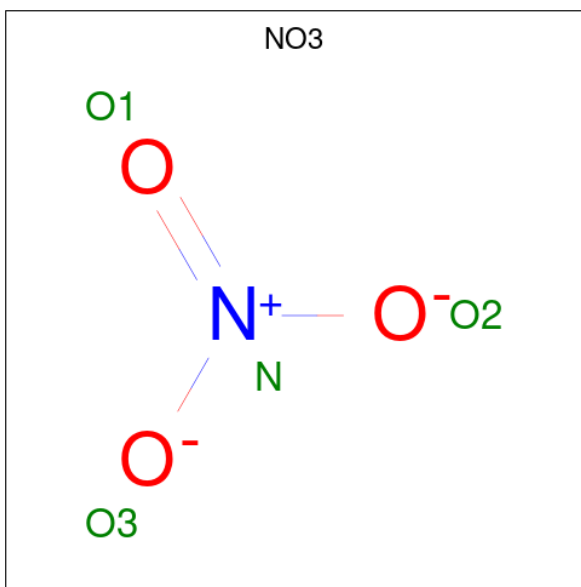
- Molecule 1 is a protein called Phycobilisome LCM core-membrane linker polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	135	Total	C	N	O	Se	0	1	0
			1105	707	193	203	2			
1	B	136	Total	C	N	O	Se	0	0	0
			1105	707	193	203	2			
1	C	132	Total	C	N	O	Se	0	1	0
			1079	693	186	198	2			
1	D	135	Total	C	N	O	Se	0	0	0
			1094	701	189	202	2			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Na	0	0
			3	3		
2	B	1	Total	Na	0	0
			1	1		
2	C	2	Total	Na	0	0
			2	2		
2	D	1	Total	Na	0	0
			1	1		

- Molecule 3 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	N	O	0	0
			4	1	3		

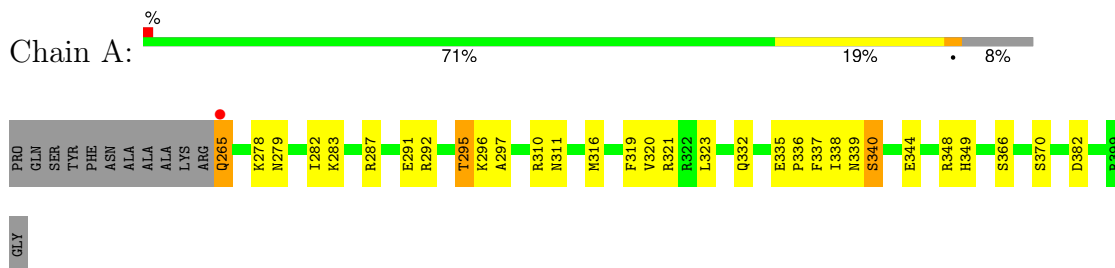
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	128	Total	O	0	0
			128	128		
4	C	132	Total	O	0	0
			132	132		
4	D	116	Total	O	0	0
			116	116		

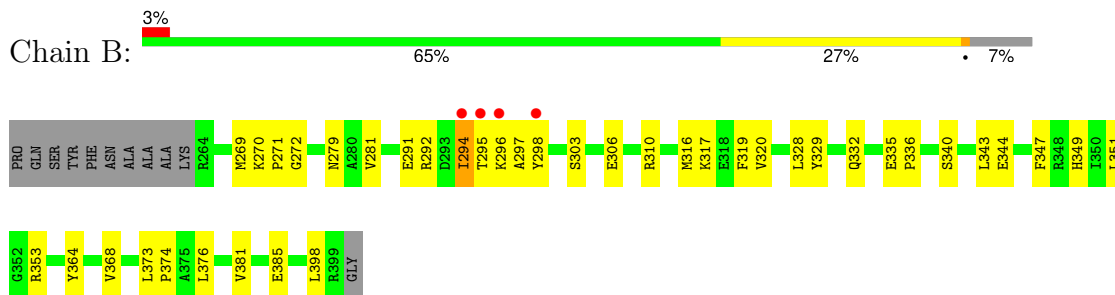
3 Residue-property plots

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.

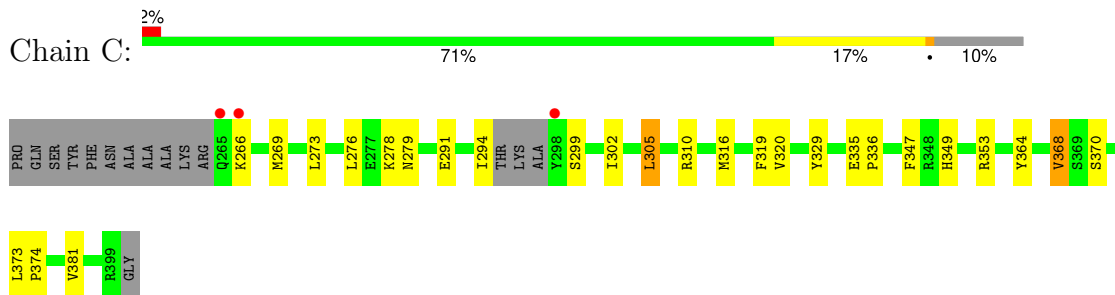
- Molecule 1: Phycobilisome LCM core-membrane linker polypeptide



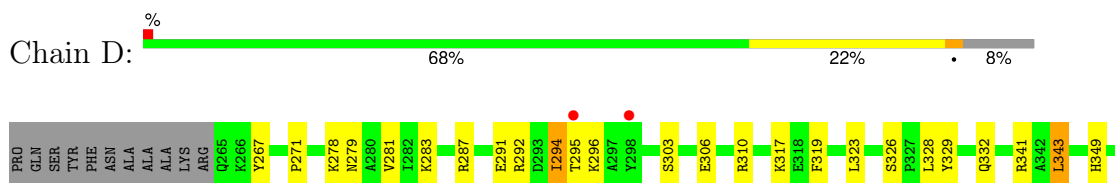
- Molecule 1: Phycobilisome LCM core-membrane linker polypeptide



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- Molecule 1: Phycobilisome LCM core-membrane linker polypeptide



S357	R358	E359	Y364	F365	S366	I367	V368	L373	L376	V377	Y386	E392	R399	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.57Å 79.61Å 73.70Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	41.29 – 2.30 41.29 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.3 (41.29-2.30) 98.3 (41.29-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.23 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.162 , 0.228 0.159 , 0.226	Depositor DCC
R_{free} test set	2000 reflections (7.40%)	wwPDB-VP
Wilson B-factor (Å ²)	15.8	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.2	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	4871	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, NO3

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	0.51	0/1126	0.84	2/1510 (0.1%)
1	B	0.49	0/1126	0.79	0/1510
1	C	0.51	0/1102	0.75	0/1476
1	D	0.49	0/1115	0.76	2/1496 (0.1%)
All	All	0.50	0/4469	0.79	4/5992 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	335	GLU	CA-C-N	-7.33	112.32	120.45
1	A	335	GLU	C-N-CA	-7.33	112.32	120.45
1	D	326	SER	CA-C-N	5.17	126.31	119.84
1	D	326	SER	C-N-CA	5.17	126.31	119.84

There are no chirality outliers.

There are no planarity outliers.

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	1105	0	1108	40	0
1	B	1105	0	1109	40	0
1	C	1079	0	1083	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1094	0	1096	26	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	D	4	0	0	1	0
4	A	101	0	0	2	0
4	B	128	0	0	0	0
4	C	132	0	0	1	0
4	D	116	0	0	1	0
All	All	4871	0	4396	127	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 14.

All (127) 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:C:316:MSE:HE2	1:C:320:VAL:HG23	1.25	1.19
1:D:295:THR:OG1	3:D:401:NO3:O3	1.64	1.16
1:B:316:MSE:HE2	1:B:320:VAL:HG23	1.12	1.07
1:A:316:MSE:HE2	1:A:320:VAL:HG23	1.13	1.06
1:A:295:THR:HG22	1:A:297:ALA:H	1.31	0.95
1:B:316:MSE:HE3	1:B:319:PHE:HB3	1.57	0.86
1:A:316:MSE:HE2	1:A:320:VAL:CG2	2.05	0.85
1:B:316:MSE:HE3	1:B:316:MSE:O	1.78	0.83
1:C:316:MSE:HE2	1:C:320:VAL:CG2	2.06	0.83
1:B:316:MSE:HE2	1:B:320:VAL:CG2	2.03	0.83
1:A:316:MSE:HE3	1:A:319:PHE:HB3	1.59	0.83
1:B:279:ASN:HD22	1:B:310:ARG:HH22	1.24	0.82
1:A:265:GLN:HE21	1:A:265:GLN:HA	1.44	0.81
1:C:316:MSE:O	1:C:316:MSE:HE3	1.81	0.80
1:C:316:MSE:HE3	1:C:319:PHE:HB3	1.63	0.80
1:B:279:ASN:ND2	1:B:310:ARG:HH22	1.81	0.79
1:A:316:MSE:CE	1:A:320:VAL:HG23	2.07	0.77
1:C:316:MSE:CE	1:C:320:VAL:HG23	2.13	0.75
1:B:292:ARG:HH12	1:B:332:GLN:HE22	1.34	0.74
1:D:291:GLU:OE1	1:D:349:HIS:HE1	1.71	0.74
1:A:316:MSE:HE3	1:A:316:MSE:O	1.89	0.73
1:C:279:ASN:ND2	1:C:310:ARG:HH12	1.87	0.72
1:B:269:MSE:HG2	1:B:281:VAL:HG11	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:329:TYR:OH	1:C:349:HIS:HD2	1.74	0.71
1:D:329:TYR:OH	1:D:349:HIS:HD2	1.76	0.69
1:B:351:LEU:HD22	1:B:385:GLU:HG2	1.76	0.67
1:D:279:ASN:ND2	1:D:310:ARG:HH22	1.93	0.67
1:C:364:TYR:O	1:C:368:VAL:HG23	1.94	0.67
1:A:283:LYS:HE2	1:A:287:ARG:HH12	1.62	0.64
1:A:291:GLU:OE2	1:A:349:HIS:HE1	1.80	0.64
1:D:368:VAL:HG22	1:D:376:LEU:HB2	1.81	0.63
1:B:316:MSE:CE	1:B:320:VAL:HG23	2.07	0.63
1:B:316:MSE:CE	1:B:319:PHE:HB3	2.28	0.63
1:B:364:TYR:O	1:B:368:VAL:HG23	1.98	0.63
1:B:329:TYR:OH	1:B:349:HIS:HD2	1.82	0.63
1:A:321:ARG:NH2	1:A:382:ASP:OD2	2.32	0.62
1:A:292[B]:ARG:NH1	1:A:332:GLN:HE22	1.98	0.62
1:A:340:SER:HB2	1:D:291:GLU:O	2.00	0.61
1:A:278:LYS:O	1:A:282:ILE:HG12	2.01	0.60
1:D:279:ASN:HD22	1:D:310:ARG:HH22	1.48	0.60
1:A:265:GLN:HA	1:A:265:GLN:NE2	2.17	0.60
1:B:298:TYR:CZ	1:B:328:LEU:HD13	2.36	0.60
1:B:279:ASN:HD22	1:B:310:ARG:NH2	1.98	0.59
1:B:269:MSE:HG2	1:B:281:VAL:CG1	2.32	0.59
1:A:316:MSE:HE1	1:A:319:PHE:CD2	2.42	0.55
1:C:291:GLU:OE2	1:C:349:HIS:HE1	1.88	0.55
1:C:373:LEU:HB3	1:C:374:PRO:HD3	1.89	0.55
1:B:292:ARG:NH2	1:B:294:ILE:HD11	2.21	0.55
1:A:291:GLU:OE2	1:A:349:HIS:CE1	2.59	0.55
1:A:321:ARG:HH22	1:A:382:ASP:CG	2.15	0.54
1:A:316:MSE:CE	1:A:319:PHE:HB3	2.33	0.54
1:B:316:MSE:O	1:B:316:MSE:CE	2.52	0.54
1:B:343:LEU:C	1:B:343:LEU:HD23	2.33	0.54
1:A:279:ASN:ND2	1:A:310:ARG:HH12	2.05	0.54
1:A:291:GLU:O	1:A:292[A]:ARG:HG3	2.07	0.54
1:B:291:GLU:OE2	1:B:349:HIS:HE1	1.92	0.53
1:D:292:ARG:HH21	1:D:332:GLN:NE2	2.06	0.53
1:C:316:MSE:HE1	1:C:319:PHE:CD2	2.44	0.52
1:A:292[B]:ARG:CZ	1:A:332:GLN:HE22	2.22	0.52
1:B:317:LYS:HG3	1:B:381:VAL:HG13	1.92	0.52
1:D:364:TYR:O	1:D:368:VAL:HG23	2.09	0.52
1:A:316:MSE:HE1	1:A:319:PHE:HD2	1.75	0.51
1:D:343:LEU:C	1:D:343:LEU:HD23	2.36	0.50
1:C:269:MSE:HE1	1:C:278:LYS:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:MSE:O	1:C:316:MSE:CE	2.56	0.50
1:B:295:THR:HG22	1:B:296:LYS:N	2.27	0.49
1:B:347:PHE:HB3	1:B:353:ARG:O	2.12	0.49
1:B:296:LYS:HB2	1:B:303:SER:HA	1.94	0.49
1:D:287:ARG:O	1:D:291:GLU:HA	2.11	0.49
1:C:347:PHE:HB3	1:C:353:ARG:O	2.13	0.49
1:B:295:THR:HG22	1:B:297:ALA:H	1.78	0.49
1:A:287:ARG:O	1:A:291:GLU:HA	2.12	0.48
1:A:292[B]:ARG:HH22	1:A:332:GLN:NE2	2.12	0.48
1:B:292:ARG:NH1	1:B:332:GLN:HE22	2.08	0.48
1:B:296:LYS:HB3	1:B:306:GLU:OE2	2.14	0.48
1:D:279:ASN:ND2	1:D:310:ARG:HH12	2.12	0.48
1:C:316:MSE:HE1	1:C:319:PHE:HD2	1.78	0.47
1:B:271:PRO:HA	1:B:272:GLY:HA2	1.60	0.47
1:A:336:PRO:HG2	1:A:337:PHE:CE1	2.50	0.47
1:C:269:MSE:HE3	1:C:273:LEU:HD12	1.97	0.47
1:D:271:PRO:HA	4:D:402:HOH:O	2.15	0.46
1:B:316:MSE:HE1	1:B:319:PHE:CD2	2.51	0.46
1:B:316:MSE:HE1	1:B:319:PHE:HD2	1.80	0.46
1:A:366:SER:O	1:A:370:SER:HB2	2.16	0.46
1:A:370:SER:HB3	4:A:177:HOH:O	2.15	0.46
1:B:340:SER:O	1:B:344:GLU:HG3	2.17	0.45
1:B:368:VAL:HG22	1:B:376:LEU:HB2	1.98	0.45
1:C:316:MSE:CE	1:C:319:PHE:HB3	2.41	0.45
1:B:279:ASN:ND2	1:B:310:ARG:NH2	2.56	0.45
1:D:294:ILE:HG12	1:D:328:LEU:HD21	1.99	0.45
1:A:292[B]:ARG:HH12	1:A:332:GLN:HE22	1.65	0.45
1:D:296:LYS:O	1:D:303:SER:HB2	2.17	0.44
1:A:279:ASN:ND2	1:A:310:ARG:HH22	2.15	0.44
1:A:311:ASN:HB2	4:A:54:HOH:O	2.18	0.44
1:A:344:GLU:O	1:A:348:ARG:HG3	2.17	0.44
1:C:299:SER:OG	1:C:302:ILE:HG12	2.17	0.44
1:A:278:LYS:HE2	1:A:310:ARG:O	2.18	0.44
1:A:319:PHE:CZ	1:A:323:LEU:HD11	2.52	0.44
1:D:283:LYS:HG2	1:D:287:ARG:HH11	1.83	0.44
1:A:292[B]:ARG:NH2	1:A:332:GLN:HE22	2.16	0.44
1:B:292:ARG:HH12	1:B:332:GLN:NE2	2.08	0.44
1:D:357:SER:OG	1:D:359:GLU:HG2	2.17	0.44
1:B:298:TYR:OH	1:B:328:LEU:HD13	2.18	0.43
1:C:266:LYS:HA	4:C:410:HOH:O	2.19	0.43
1:A:292[B]:ARG:NH2	1:A:332:GLN:NE2	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ASN:HD22	1:A:310:ARG:HH22	1.65	0.42
1:A:292[B]:ARG:HH12	1:A:332:GLN:NE2	2.17	0.42
1:D:329:TYR:CZ	1:D:349:HIS:HD2	2.38	0.42
1:B:373:LEU:HB3	1:B:374:PRO:HD3	2.01	0.42
1:D:386:TYR:C	1:D:386:TYR:CD1	2.98	0.42
1:A:316:MSE:CE	1:A:316:MSE:O	2.63	0.42
1:D:267:TYR:HB3	1:D:281:VAL:HG22	2.02	0.41
1:D:296:LYS:HB2	1:D:303:SER:HA	2.01	0.41
1:D:373:LEU:O	1:D:377:VAL:HG23	2.20	0.41
1:C:305:LEU:HD12	1:C:305:LEU:HA	1.92	0.41
1:B:296:LYS:HB2	1:B:296:LYS:HE3	1.70	0.41
1:A:338:ILE:O	1:A:339:ASN:C	2.62	0.41
1:B:306:GLU:O	1:B:310:ARG:HB2	2.20	0.41
1:C:335:GLU:HB3	1:C:336:PRO:HD3	2.03	0.41
1:D:319:PHE:CE2	1:D:323:LEU:HD11	2.55	0.41
1:C:276:LEU:H	1:C:276:LEU:HD12	1.85	0.41
1:A:295:THR:CG2	1:A:296:LYS:N	2.85	0.40
1:B:335:GLU:HB3	1:B:336:PRO:HD3	2.04	0.40
1:B:296:LYS:O	1:B:303:SER:HB2	2.22	0.40
1:D:291:GLU:OE1	1:D:349:HIS:CE1	2.60	0.40
1:D:296:LYS:HB3	1:D:306:GLU:OE2	2.21	0.40
1:D:317:LYS:HE2	1:D:392:GLU:OE2	2.21	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	134/147 (91%)	131 (98%)	3 (2%)	0	100	100
1	B	134/147 (91%)	131 (98%)	3 (2%)	0	100	100
1	C	129/147 (88%)	126 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	133/147 (90%)	127 (96%)	6 (4%)	0	100	100
All	All	530/588 (90%)	515 (97%)	15 (3%)	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	117/122 (96%)	114 (97%)	3 (3%)	40	59
1	B	117/122 (96%)	114 (97%)	3 (3%)	40	59
1	C	115/122 (94%)	110 (96%)	5 (4%)	26	39
1	D	116/122 (95%)	110 (95%)	6 (5%)	21	31
All	All	465/488 (95%)	448 (96%)	17 (4%)	30	45

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	GLN
1	A	295	THR
1	A	340	SER
1	B	270	LYS
1	B	294	ILE
1	B	398	LEU
1	C	294	ILE
1	C	305	LEU
1	C	368	VAL
1	C	370	SER
1	C	381	VAL
1	D	278	LYS
1	D	294	ILE
1	D	341	ARG
1	D	343	LEU
1	D	359	GLU

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Mol	Chain	Res	Type
1	D	366	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	265	GLN
1	A	279	ASN
1	A	288	GLN
1	A	300	GLN
1	A	308	GLN
1	A	332	GLN
1	A	349	HIS
1	B	279	ASN
1	B	288	GLN
1	B	308	GLN
1	B	332	GLN
1	B	349	HIS
1	B	362	GLN
1	C	279	ASN
1	C	288	GLN
1	C	311	ASN
1	C	349	HIS
1	D	279	ASN
1	D	288	GLN
1	D	300	GLN
1	D	308	GLN
1	D	332	GLN
1	D	349	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 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	$\# Z > 2$
3	NO3	D	401	-	1,3,3	1.27	0	0,3,3	-	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	NO3	1	0

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	A	133/147 (90%)	-0.50	1 (0%) 82 83	6, 17, 40, 64	1 (0%)
1	B	134/147 (91%)	-0.39	4 (2%) 52 54	6, 17, 56, 74	0
1	C	130/147 (88%)	-0.48	3 (2%) 61 63	7, 15, 44, 77	1 (0%)
1	D	133/147 (90%)	-0.42	2 (1%) 72 73	7, 17, 47, 64	0
All	All	530/588 (90%)	-0.45	10 (1%) 66 68	6, 17, 45, 77	2 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	298	TYR	4.8
1	B	296	LYS	3.7
1	D	295	THR	3.4
1	B	295	THR	3.1
1	A	265	GLN	2.8
1	B	298	TYR	2.6
1	C	265	GLN	2.5
1	C	266	LYS	2.3
1	D	298	TYR	2.3
1	B	294	ILE	2.2

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
3	NO3	D	401	4/4	0.71	0.15	51,55,56,57	0
2	NA	C	5	1/1	0.95	0.10	23,23,23,23	0
2	NA	B	6	1/1	0.97	0.11	26,26,26,26	0
2	NA	C	3	1/1	0.97	0.05	19,19,19,19	0
2	NA	A	4	1/1	0.98	0.12	22,22,22,22	0
2	NA	D	1	1/1	0.98	0.06	10,10,10,10	0
2	NA	A	7	1/1	0.98	0.10	11,11,11,11	0
2	NA	A	2	1/1	0.99	0.07	7,7,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.