



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:18 PM UTC

PDB ID : 8G9Z / pdb_00008g9z
Title : High-resolution crystal structure of the human selenomethionine-derived SepSecS-tRNA^{Sec} complex
Authors : Puppala, A.; Simonovic, M.; Castillo Suchkou, J.
Deposited on : 2023-02-22
Resolution : 2.07 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

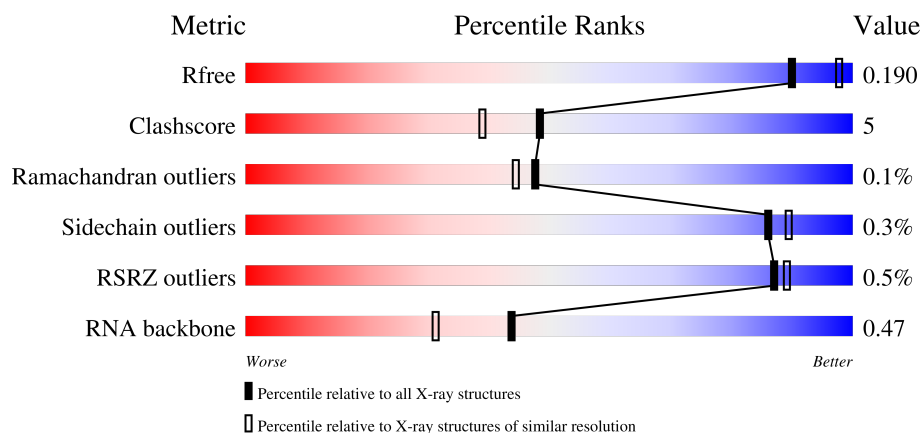
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)
RNA backbone	3983	1030 (2.40-1.72)

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	521	80% 9% 11%
1	B	521	79% 8% 12%
1	C	521	79% 10% 10%
1	D	521	78% 10% 12%

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Mol	Chain	Length	Quality of chain
2	E	90	2% 62% 34%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19942 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 O-phosphoseryl-tRNA(Sec) selenium transferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	466	Total	C	N	O	S	Se	0	24	0
			3725	2371	653	672	14	15			
1	B	456	Total	C	N	O	S	Se	0	27	0
			3672	2339	644	660	14	15			
1	C	468	Total	C	N	O	S	Se	0	31	0
			3788	2414	664	681	14	15			
1	D	457	Total	C	N	O	S	Se	0	30	0
			3694	2351	650	664	14	15			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	expression tag	UNP Q9HD40
A	-18	GLY	-	expression tag	UNP Q9HD40
A	-17	SER	-	expression tag	UNP Q9HD40
A	-16	SER	-	expression tag	UNP Q9HD40
A	-15	HIS	-	expression tag	UNP Q9HD40
A	-14	HIS	-	expression tag	UNP Q9HD40
A	-13	HIS	-	expression tag	UNP Q9HD40
A	-12	HIS	-	expression tag	UNP Q9HD40
A	-11	HIS	-	expression tag	UNP Q9HD40
A	-10	HIS	-	expression tag	UNP Q9HD40
A	-9	SER	-	expression tag	UNP Q9HD40
A	-8	SER	-	expression tag	UNP Q9HD40
A	-7	GLY	-	expression tag	UNP Q9HD40
A	-6	LEU	-	expression tag	UNP Q9HD40
A	-5	VAL	-	expression tag	UNP Q9HD40
A	-4	PRO	-	expression tag	UNP Q9HD40
A	-3	ARG	-	expression tag	UNP Q9HD40
A	-2	GLY	-	expression tag	UNP Q9HD40
A	-1	SER	-	expression tag	UNP Q9HD40
A	0	HIS	-	expression tag	UNP Q9HD40
A	491	ALA	VAL	engineered mutation	UNP Q9HD40

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MSE	-	expression tag	UNP Q9HD40
B	-18	GLY	-	expression tag	UNP Q9HD40
B	-17	SER	-	expression tag	UNP Q9HD40
B	-16	SER	-	expression tag	UNP Q9HD40
B	-15	HIS	-	expression tag	UNP Q9HD40
B	-14	HIS	-	expression tag	UNP Q9HD40
B	-13	HIS	-	expression tag	UNP Q9HD40
B	-12	HIS	-	expression tag	UNP Q9HD40
B	-11	HIS	-	expression tag	UNP Q9HD40
B	-10	HIS	-	expression tag	UNP Q9HD40
B	-9	SER	-	expression tag	UNP Q9HD40
B	-8	SER	-	expression tag	UNP Q9HD40
B	-7	GLY	-	expression tag	UNP Q9HD40
B	-6	LEU	-	expression tag	UNP Q9HD40
B	-5	VAL	-	expression tag	UNP Q9HD40
B	-4	PRO	-	expression tag	UNP Q9HD40
B	-3	ARG	-	expression tag	UNP Q9HD40
B	-2	GLY	-	expression tag	UNP Q9HD40
B	-1	SER	-	expression tag	UNP Q9HD40
B	0	HIS	-	expression tag	UNP Q9HD40
B	491	ALA	VAL	engineered mutation	UNP Q9HD40
C	-19	MSE	-	expression tag	UNP Q9HD40
C	-18	GLY	-	expression tag	UNP Q9HD40
C	-17	SER	-	expression tag	UNP Q9HD40
C	-16	SER	-	expression tag	UNP Q9HD40
C	-15	HIS	-	expression tag	UNP Q9HD40
C	-14	HIS	-	expression tag	UNP Q9HD40
C	-13	HIS	-	expression tag	UNP Q9HD40
C	-12	HIS	-	expression tag	UNP Q9HD40
C	-11	HIS	-	expression tag	UNP Q9HD40
C	-10	HIS	-	expression tag	UNP Q9HD40
C	-9	SER	-	expression tag	UNP Q9HD40
C	-8	SER	-	expression tag	UNP Q9HD40
C	-7	GLY	-	expression tag	UNP Q9HD40
C	-6	LEU	-	expression tag	UNP Q9HD40
C	-5	VAL	-	expression tag	UNP Q9HD40
C	-4	PRO	-	expression tag	UNP Q9HD40
C	-3	ARG	-	expression tag	UNP Q9HD40
C	-2	GLY	-	expression tag	UNP Q9HD40
C	-1	SER	-	expression tag	UNP Q9HD40
C	0	HIS	-	expression tag	UNP Q9HD40
C	491	ALA	VAL	engineered mutation	UNP Q9HD40

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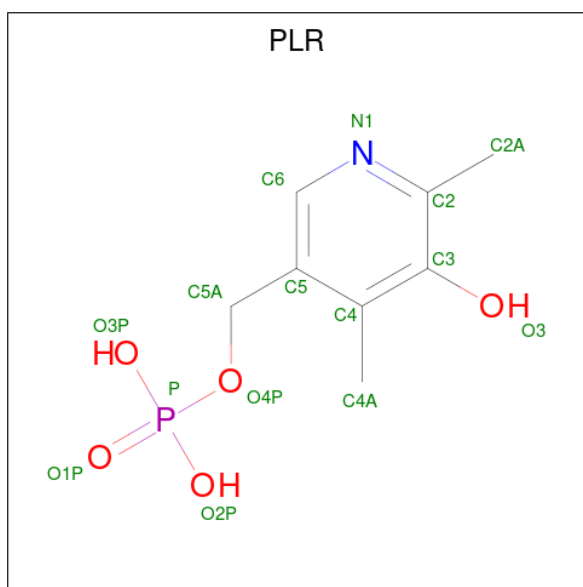
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MSE	-	expression tag	UNP Q9HD40
D	-18	GLY	-	expression tag	UNP Q9HD40
D	-17	SER	-	expression tag	UNP Q9HD40
D	-16	SER	-	expression tag	UNP Q9HD40
D	-15	HIS	-	expression tag	UNP Q9HD40
D	-14	HIS	-	expression tag	UNP Q9HD40
D	-13	HIS	-	expression tag	UNP Q9HD40
D	-12	HIS	-	expression tag	UNP Q9HD40
D	-11	HIS	-	expression tag	UNP Q9HD40
D	-10	HIS	-	expression tag	UNP Q9HD40
D	-9	SER	-	expression tag	UNP Q9HD40
D	-8	SER	-	expression tag	UNP Q9HD40
D	-7	GLY	-	expression tag	UNP Q9HD40
D	-6	LEU	-	expression tag	UNP Q9HD40
D	-5	VAL	-	expression tag	UNP Q9HD40
D	-4	PRO	-	expression tag	UNP Q9HD40
D	-3	ARG	-	expression tag	UNP Q9HD40
D	-2	GLY	-	expression tag	UNP Q9HD40
D	-1	SER	-	expression tag	UNP Q9HD40
D	0	HIS	-	expression tag	UNP Q9HD40
D	491	ALA	VAL	engineered mutation	UNP Q9HD40

- Molecule 2 is a RNA chain called RNA (90-MER).

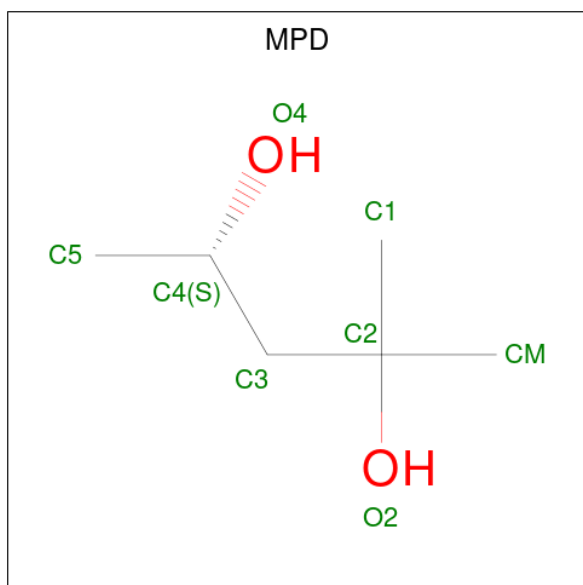
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	87	Total	C	N	O	P	0	87	0
			3640	1614	638	1214	174			

- Molecule 3 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (CCD ID: PLR) (formula: C₈H₁₂NO₅P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
3	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 8 6 2	0	0
4	B	1	Total C O 8 6 2	0	0
4	C	1	Total C O 8 6 2	0	0
4	D	1	Total C O 8 6 2	0	0

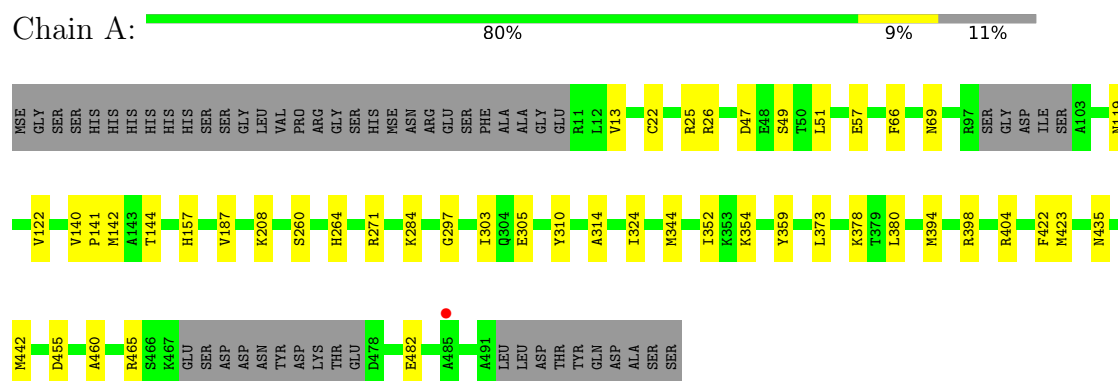
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	318	Total O 318 318	0	0
5	B	330	Total O 330 330	0	0
5	C	340	Total O 340 340	0	0
5	D	326	Total O 326 326	0	0
5	E	17	Total O 17 17	0	0

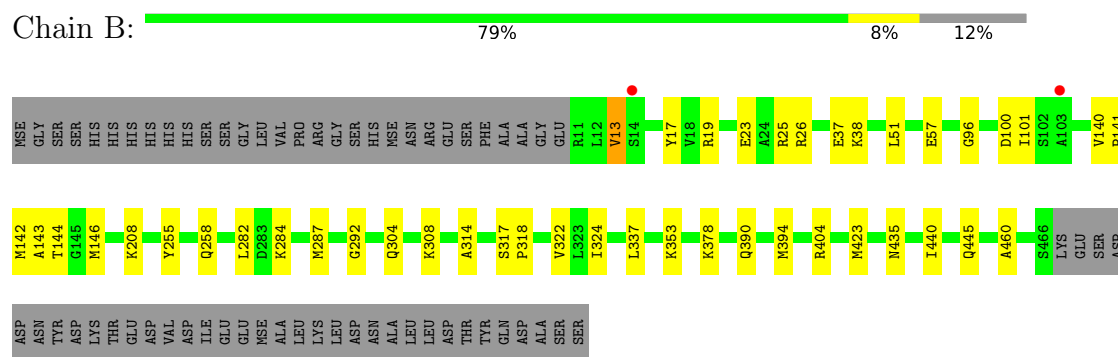
3 Residue-property plots

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.

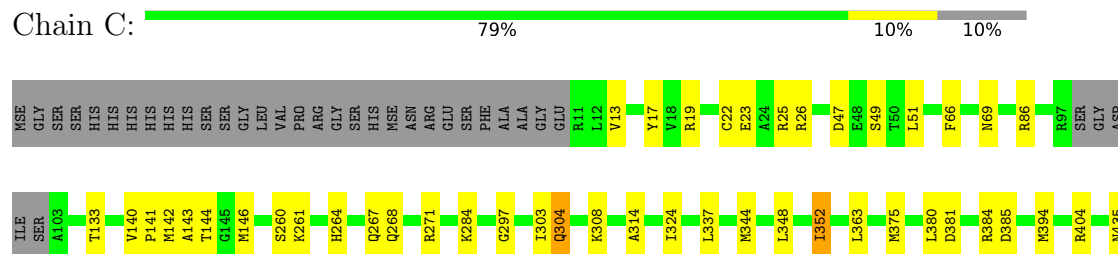
- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase

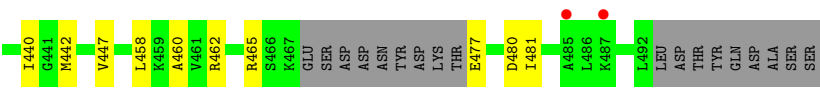


- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase

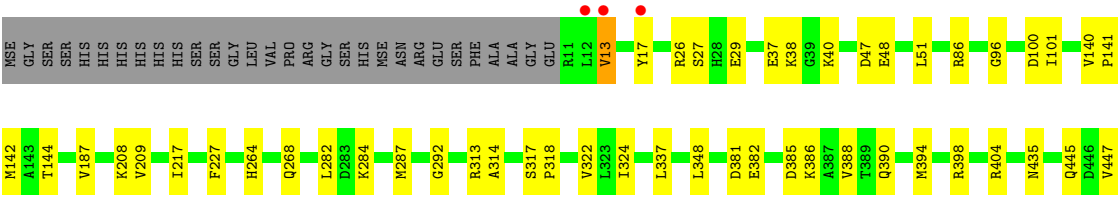
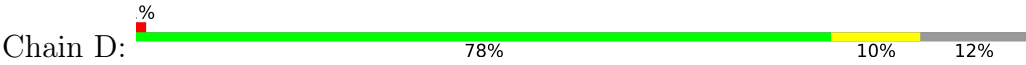


- Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase

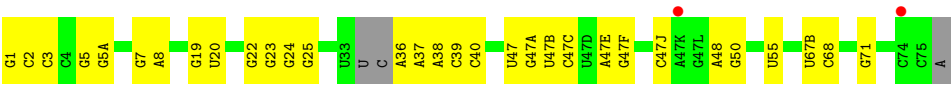




● Molecule 1: O-phosphoseryl-tRNA(Sec) selenium transferase



● Molecule 2: RNA (90-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α , β , γ	167.18Å 167.18Å 239.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.25 – 2.07 34.25 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.25-2.07) 91.0 (34.25-2.07)	Depositor EDS
R_{merge}	0.99	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.75 (at 2.06Å)	Xtriage
Refinement program	PHENIX DEV_3951	Depositor
R, R_{free}	0.177 , 0.190 0.178 , 0.190	Depositor DCC
R_{free} test set	2015 reflections (0.87%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.450 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19942	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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: PLR, MPD

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	0.11	0/3847	0.30	0/5168
1	B	0.11	0/3806	0.30	0/5116
1	C	0.18	0/3932	0.33	2/5282 (0.0%)
1	D	0.11	0/3838	0.30	0/5157
2	E	0.06	0/4060	0.20	0/6320
All	All	0.12	0/19483	0.28	2/27043 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	304[A]	GLN	CA-C-O	5.84	126.70	120.10
1	C	304[B]	GLN	CA-C-O	5.84	126.70	120.10

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	3725	0	3804	31	0
1	B	3672	0	3773	35	0
1	C	3788	0	3897	53	0
1	D	3694	0	3808	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	3640	0	1790	42	0
3	A	15	0	8	2	0
3	B	15	0	8	3	0
3	C	15	0	8	3	0
3	D	15	0	8	2	0
4	A	8	0	14	0	0
4	B	8	0	14	0	0
4	C	8	0	14	0	0
4	D	8	0	14	0	0
5	A	318	0	0	1	0
5	B	330	0	0	4	0
5	C	340	0	0	5	0
5	D	326	0	0	6	0
5	E	17	0	0	1	0
All	All	19942	0	17160	188	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 5.

All (188) 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:B:308:LYS:HD2	5:B:1132:HOH:O	1.79	0.81
1:B:287:MSE:HE1	1:B:337:LEU:HD13	1.63	0.81
1:A:380:LEU:HA	1:A:465:ARG:HH22	1.46	0.78
1:D:13:VAL:HG13	1:D:17:TYR:HB2	1.66	0.78
1:D:287:MSE:HE1	1:D:337:LEU:HD13	1.65	0.77
1:D:227:PHE:CD2	5:D:1325:HOH:O	2.39	0.75
1:D:96:GLY:O	1:D:313[A]:ARG:NH1	2.21	0.74
1:D:144:THR:HB	3:D:1001:PLR:H5A2	1.72	0.72
1:C:267[B]:GLN:NE2	5:C:1101:HOH:O	2.22	0.72
1:C:308:LYS:HD2	5:C:1197:HOH:O	1.91	0.71
1:A:26:ARG:NH2	2:E:3[A]:C:OP1	2.25	0.70
1:B:404:ARG:NH1	1:B:435:ASN:OD1	2.25	0.70
1:B:37[A]:GLU:HG3	1:B:38:LYS:HG3	1.74	0.70
1:B:353:LYS:HE2	5:B:1130:HOH:O	1.92	0.69
1:B:282:LEU:HD22	1:B:322[B]:VAL:HG11	1.73	0.69
1:D:37[B]:GLU:HG3	1:D:38:LYS:HG3	1.75	0.69
1:C:385:ASP:HB2	1:C:465:ARG:HH21	1.59	0.68
1:D:282:LEU:HD22	1:D:322[A]:VAL:HG11	1.73	0.68
1:D:404:ARG:NH1	1:D:435:ASN:OD1	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:SER:O	1:A:264[B]:HIS:ND1	2.27	0.67
1:B:404:ARG:HH21	1:B:423[B]:MSE:HE3	1.60	0.67
2:E:7[B]:G:HO2'	2:E:50[B]:G:H5'	1.60	0.67
2:E:48[A]:A:H4'	2:E:50[A]:G:H5''	1.76	0.66
1:C:465:ARG:HD3	5:C:1181:HOH:O	1.97	0.65
1:C:268:GLN:OE1	1:C:271[A]:ARG:NH1	2.30	0.65
1:D:404:ARG:HB2	1:D:435:ASN:HB2	1.78	0.64
1:C:404:ARG:HB3	1:C:435:ASN:HB2	1.80	0.64
1:D:268:GLN:NE2	5:D:1104:HOH:O	2.31	0.63
2:E:37[A]:A:H3'	2:E:38[A]:A:H8	1.64	0.62
1:D:96:GLY:HA3	1:D:101:ILE:HA	1.82	0.62
1:B:144:THR:HB	3:B:1001:PLR:H5A2	1.82	0.61
1:C:394:MSE:HE1	1:C:460:ALA:HB3	1.82	0.61
1:B:404:ARG:HB2	1:B:435:ASN:HB2	1.83	0.61
1:D:394:MSE:HG2	2:E:37[A]:A:H2	1.65	0.60
1:C:381:ASP:H	1:C:465:ARG:HH22	1.48	0.59
1:B:96:GLY:HA3	1:B:101:ILE:HA	1.85	0.59
1:C:66:PHE:HB2	1:C:69:ASN:HB2	1.85	0.58
1:D:398:ARG:NH1	2:E:38[A]:A:O2'	2.36	0.58
1:A:66:PHE:HB2	1:A:69:ASN:HB2	1.85	0.58
1:B:25[B]:ARG:NH2	1:B:57:GLU:OE2	2.31	0.58
1:C:271[B]:ARG:NH1	2:E:47(J)[B]:C:O3'	2.37	0.58
1:A:394:MSE:HE1	1:A:460:ALA:HB3	1.86	0.57
1:A:271[B]:ARG:NH2	2:E:55[B]:U:O3'	2.36	0.57
1:C:86[A]:ARG:HH21	1:D:86[A]:ARG:NH1	2.02	0.57
1:C:144:THR:HB	3:C:1001:PLR:H5A2	1.85	0.57
2:E:2[A]:C:H2'	2:E:3[A]:C:C6	2.40	0.56
1:B:353:LYS:CE	5:B:1130:HOH:O	2.50	0.56
1:C:404:ARG:NH1	1:C:435:ASN:OD1	2.38	0.56
1:C:261:LYS:HG3	2:E:47(C)[B]:C:H5''	1.86	0.56
1:C:381:ASP:H	1:C:465:ARG:HH12	1.52	0.56
2:E:8[A]:A:H1'	2:E:48[A]:A:N3	2.21	0.55
1:A:144:THR:HB	3:A:1001:PLR:H5A2	1.87	0.54
2:E:22[B]:G:H2'	2:E:23[B]:G:H8	1.72	0.54
1:A:22:CYS:O	1:A:26:ARG:HG3	2.06	0.54
1:B:282:LEU:HD12	1:B:292:GLY:HA3	1.88	0.54
2:E:19[B]:G:H4'	2:E:20[B]:U:O5'	2.07	0.54
1:A:404:ARG:HB3	1:A:435:ASN:HB2	1.90	0.54
1:B:23[A]:GLU:OE1	1:B:26:ARG:NH1	2.36	0.53
1:C:348:LEU:O	1:C:352[A]:ILE:HG23	2.08	0.53
1:D:382:GLU:HG3	1:D:388:VAL:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:465:ARG:CD	5:C:1181:HOH:O	2.56	0.53
1:D:187:VAL:HG11	1:D:208:LYS:HG2	1.91	0.53
1:D:100:ASP:HA	5:D:1119:HOH:O	2.08	0.53
1:C:51:LEU:HD21	1:C:324:ILE:HG23	1.91	0.52
1:D:40:LYS:NZ	5:D:1107:HOH:O	2.43	0.52
1:C:352[A]:ILE:HD13	1:C:375:MSE:HB2	1.91	0.52
1:C:47[B]:ASP:OD2	1:C:49:SER:OG	2.28	0.52
1:A:404:ARG:NH1	1:A:435:ASN:OD1	2.43	0.51
2:E:39[B]:C:H2'	2:E:40[B]:C:C6	2.45	0.51
1:B:100:ASP:HA	5:B:1193:HOH:O	2.10	0.51
1:C:348:LEU:HD13	1:C:447:VAL:HG22	1.91	0.51
1:A:47[B]:ASP:OD2	1:A:49:SER:OG	2.27	0.51
1:B:23[A]:GLU:CD	1:B:26:ARG:HH12	2.16	0.50
2:E:39[A]:C:H2'	2:E:40[A]:C:C6	2.47	0.50
2:E:47[A]:U:H2'	2:E:47(A)[A]:G:H8	1.77	0.50
1:C:260:SER:O	1:C:264[B]:HIS:ND1	2.27	0.50
1:B:13:VAL:HG23	1:B:17:TYR:HB2	1.94	0.50
1:D:390:GLN:O	1:D:394:MSE:HG3	2.12	0.50
1:B:304[A]:GLN:HG2	1:B:308:LYS:HE3	1.94	0.49
2:E:47[B]:U:H2'	2:E:47(A)[B]:G:C8	2.47	0.49
1:B:394:MSE:HG2	2:E:37[B]:A:H2	1.77	0.49
1:D:282:LEU:HD12	1:D:292:GLY:HA3	1.93	0.49
2:E:47[A]:U:H2'	2:E:47(A)[A]:G:C8	2.48	0.48
2:E:67(B)[A]:U:H2'	2:E:68[A]:C:C6	2.48	0.48
1:B:51:LEU:HD21	1:B:324:ILE:HG23	1.96	0.48
1:C:462:ARG:HA	1:C:465:ARG:HG3	1.95	0.48
1:C:142:MSE:SE	1:C:146:MSE:HG3	2.63	0.48
2:E:36[B]:A:H2'	2:E:37[B]:A:H8	1.79	0.48
1:B:404:ARG:NH2	1:B:423[B]:MSE:HE3	2.27	0.48
1:A:51:LEU:HD21	1:A:324:ILE:HG23	1.95	0.47
1:B:394:MSE:HE1	1:B:460:ALA:HB3	1.96	0.47
1:A:359:TYR:OH	1:A:455:ASP:OD1	2.27	0.47
1:D:394:MSE:HE1	1:D:460:ALA:HB3	1.96	0.47
1:D:456:ARG:NH1	2:E:25[A]:G:OP1	2.43	0.47
1:C:458:LEU:O	1:C:462:ARG:HG2	2.15	0.47
1:D:140:VAL:HG21	1:D:142:MSE:HE2	1.97	0.47
2:E:19[B]:G:N2	2:E:20[B]:U:O4	2.43	0.47
1:D:385:ASP:OD2	1:D:465:ARG:NE	2.48	0.47
2:E:2[A]:C:H2'	2:E:3[A]:C:H6	1.78	0.47
1:C:133:THR:OG1	1:C:267[B]:GLN:NE2	2.40	0.46
1:B:142:MSE:SE	1:B:146:MSE:HG3	2.65	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:ARG:HH22	2:E:3[B]:C:C5'	2.28	0.46
1:C:264[B]:HIS:CE1	2:E:47(B)[B]:U:H4'	2.51	0.46
1:C:86[A]:ARG:HH21	1:D:86[A]:ARG:CZ	2.28	0.46
1:C:22:CYS:O	1:C:26:ARG:HG3	2.14	0.46
1:B:140:VAL:HG21	1:B:142:MSE:HE2	1.96	0.46
1:D:51:LEU:HD21	1:D:324:ILE:HG23	1.97	0.46
2:E:7[B]:G:H3'	2:E:8[B]:A:H2'	1.97	0.46
1:C:352[A]:ILE:HD11	1:C:363:LEU:HB2	1.98	0.46
1:D:284:LYS:NZ	3:D:1001:PLR:O3	2.48	0.46
1:D:394:MSE:HG2	2:E:37[A]:A:C2	2.49	0.46
1:A:344:MSE:HB3	1:A:442:MSE:CE	2.45	0.45
1:A:422:PHE:CE2	1:A:423[A]:MSE:HE3	2.51	0.45
1:C:344:MSE:HB3	1:C:442:MSE:CE	2.47	0.45
1:C:381:ASP:N	1:C:465:ARG:HH22	2.13	0.45
1:A:140:VAL:HG21	1:A:142:MSE:HE2	1.96	0.45
1:B:390:GLN:O	1:B:394:MSE:HG3	2.16	0.45
1:C:352[A]:ILE:HD11	1:C:363:LEU:HD13	1.98	0.45
1:D:209:VAL:HA	1:D:217[A]:ILE:HD11	1.97	0.45
2:E:47[B]:U:H2'	2:E:47(A)[B]:G:H8	1.81	0.44
1:A:187:VAL:HG11	1:A:208:LYS:HG2	1.98	0.44
2:E:47(B)[B]:U:H2'	2:E:47(C)[B]:C:C6	2.52	0.44
1:B:284:LYS:NZ	3:B:1001:PLR:O3	2.50	0.44
1:C:86[A]:ARG:HH21	1:D:86[A]:ARG:HH12	1.66	0.44
1:C:141:PRO:CG	1:C:314:ALA:HB1	2.48	0.44
1:D:381:ASP:N	1:D:381:ASP:OD1	2.49	0.44
2:E:37[B]:A:H3'	2:E:38[B]:A:O4'	2.17	0.44
1:C:380:LEU:HA	1:C:465:ARG:HH12	1.82	0.44
1:D:348:LEU:HD13	1:D:447:VAL:HG22	2.00	0.44
2:E:8[B]:A:H1'	2:E:48[B]:A:N3	2.33	0.44
1:C:380:LEU:HA	1:C:465:ARG:NH1	2.32	0.44
1:C:19:ARG:O	1:C:23:GLU:HG2	2.18	0.44
1:D:141:PRO:CG	1:D:314:ALA:HB1	2.48	0.44
2:E:47(E)[B]:A:H2'	2:E:47(F)[B]:G:O4'	2.18	0.44
1:A:352:ILE:HD12	1:A:373[B]:LEU:HD13	2.00	0.43
1:B:394:MSE:HG2	2:E:37[B]:A:C2	2.52	0.43
1:C:13:VAL:HG13	1:C:17:TYR:HB2	2.01	0.43
1:D:445[B]:GLN:CD	1:D:445[B]:GLN:H	2.27	0.43
1:C:477:GLU:HA	1:C:480:ASP:HB3	2.00	0.43
1:B:141:PRO:CG	1:B:314:ALA:HB1	2.48	0.43
1:C:143:ALA:HB1	3:C:1001:PLR:O3P	2.19	0.43
1:A:284:LYS:NZ	3:A:1001:PLR:O3	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:ARG:NH2	1:A:482:GLU:OE2	2.50	0.43
1:A:404:ARG:HH21	1:A:423[A]:MSE:SE	2.52	0.43
2:E:2[A]:C:H42	2:E:71[A]:G:H1	1.67	0.43
1:A:25[A]:ARG:NH2	1:A:57:GLU:OE2	2.50	0.43
1:A:141:PRO:CG	1:A:314:ALA:HB1	2.49	0.42
2:E:38[A]:A:H2'	2:E:39[A]:C:O4'	2.19	0.42
1:B:143:ALA:HB1	3:B:1001:PLR:O3P	2.19	0.42
1:D:394:MSE:O	1:D:398:ARG:HD3	2.19	0.42
1:B:208:LYS:HD3	1:B:208:LYS:HA	1.90	0.42
2:E:48[B]:A:H4'	2:E:50[B]:G:H5''	2.00	0.42
2:E:23[B]:G:H2'	2:E:24[B]:G:C8	2.54	0.42
1:B:255:TYR:HB2	1:B:258:GLN:HE21	1.85	0.42
1:D:27[B]:SER:OG	5:D:1101:HOH:O	2.21	0.42
1:D:264[A]:HIS:HE1	5:D:1382:HOH:O	2.03	0.42
1:C:304[A]:GLN:HG2	1:C:308:LYS:HE3	2.02	0.42
1:D:382:GLU:HG2	1:D:386:LYS:HA	2.02	0.42
2:E:1[A]:G:OP3	5:E:101:HOH:O	2.22	0.42
1:C:297:GLY:HA3	1:C:303:ILE:HD11	2.01	0.41
1:A:157[B]:HIS:NE2	1:A:305[B]:GLU:OE2	2.52	0.41
1:C:140:VAL:HG21	1:C:142:MSE:HE2	2.02	0.41
1:D:26:ARG:O	1:D:29[B]:GLU:HG2	2.20	0.41
2:E:22[B]:G:H2'	2:E:23[B]:G:C8	2.54	0.41
1:B:317:SER:HB3	1:B:318:PRO:HD3	2.02	0.41
1:B:445[B]:GLN:CD	1:B:445[B]:GLN:H	2.26	0.41
1:C:25[A]:ARG:HG3	5:C:1158:HOH:O	2.20	0.41
1:C:337:LEU:HB3	1:C:440[A]:ILE:HG13	2.02	0.41
1:C:381:ASP:N	1:C:465:ARG:HH12	2.19	0.41
2:E:5[A]:G:H2'	2:E:5(A)[A]:G:O4'	2.21	0.41
1:D:141:PRO:HG3	1:D:314:ALA:HB1	2.02	0.41
1:C:284:LYS:NZ	3:C:1001:PLR:O3	2.54	0.41
1:C:384:ARG:NH1	1:C:385:ASP:OD1	2.53	0.41
1:A:297:GLY:HA3	1:A:303:ILE:HD11	2.02	0.41
1:A:378:LYS:HE3	1:A:378:LYS:HB2	1.89	0.41
1:C:141:PRO:HG3	1:C:314:ALA:HB1	2.02	0.41
1:A:310:TYR:OH	5:A:1101:HOH:O	2.22	0.40
1:A:422:PHE:O	1:A:423[A]:MSE:HB2	2.20	0.40
1:D:47[A]:ASP:OD1	1:D:48:GLU:N	2.54	0.40
1:A:119:ASN:HA	1:A:122[A]:VAL:HG22	2.02	0.40
1:B:19:ARG:O	1:B:23[A]:GLU:HG2	2.21	0.40
1:C:381:ASP:H	1:C:465:ARG:NH2	2.15	0.40
2:E:67(B)[B]:U:H2'	2:E:68[B]:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:LYS:HB2	1:B:378:LYS:HE3	1.77	0.40
1:D:317:SER:HB3	1:D:318:PRO:HD3	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	484/521 (93%)	472 (98%)	12 (2%)	0	100	100
1	B	481/521 (92%)	469 (98%)	11 (2%)	1 (0%)	43	38
1	C	493/521 (95%)	481 (98%)	12 (2%)	0	100	100
1	D	485/521 (93%)	473 (98%)	11 (2%)	1 (0%)	43	38
All	All	1943/2084 (93%)	1895 (98%)	46 (2%)	2 (0%)	48	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	13	VAL
1	D	13	VAL

5.3.2 Protein sidechains [i](#)

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	409/429 (95%)	407 (100%)	2 (0%)	81	85
1	B	407/429 (95%)	405 (100%)	2 (0%)	81	85
1	C	419/429 (98%)	416 (99%)	3 (1%)	76	79
1	D	412/429 (96%)	412 (100%)	0	100	100
All	All	1647/1716 (96%)	1640 (100%)	7 (0%)	86	87

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	VAL
1	A	354	LYS
1	B	440[A]	ILE
1	B	440[B]	ILE
1	C	352[A]	ILE
1	C	352[B]	ILE
1	C	481	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS
1	A	365	HIS
1	B	88	HIS
1	B	132	HIS
1	B	428	ASN
1	C	88	HIS
1	D	88	HIS
1	D	428	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	0/90	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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](#)

8 ligands are modelled in this entry.

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	MPD	B	1002	-	7,7,7	0.73	0	9,10,10	0.38	0
3	PLR	B	1001	1	15,15,15	1.07	1 (6%)	21,22,22	1.13	3 (14%)
4	MPD	D	1002	-	7,7,7	0.72	0	9,10,10	0.39	0
4	MPD	C	1002	-	7,7,7	0.73	0	9,10,10	0.38	0
3	PLR	A	1001	1	15,15,15	1.08	1 (6%)	21,22,22	1.15	3 (14%)
3	PLR	C	1001	1	15,15,15	1.09	1 (6%)	21,22,22	1.13	3 (14%)
3	PLR	D	1001	1	15,15,15	1.04	1 (6%)	21,22,22	1.10	2 (9%)
4	MPD	A	1002	-	7,7,7	0.73	0	9,10,10	0.38	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MPD	B	1002	-	-	3/5/5/5	-
3	PLR	B	1001	1	-	0/6/6/6	0/1/1/1
4	MPD	D	1002	-	-	3/5/5/5	-
4	MPD	C	1002	-	-	0/5/5/5	-
3	PLR	A	1001	1	-	0/6/6/6	0/1/1/1
3	PLR	C	1001	1	-	0/6/6/6	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLR	D	1001	1	-	0/6/6/6	0/1/1/1
4	MPD	A	1002	-	-	0/5/5/5	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1001	PLR	C2-N1	2.59	1.38	1.33
3	B	1001	PLR	C2-N1	2.55	1.38	1.33
3	A	1001	PLR	C2-N1	2.54	1.38	1.33
3	D	1001	PLR	C2-N1	2.47	1.38	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1001	PLR	O4P-C5A-C5	2.76	114.53	109.36
3	D	1001	PLR	O4P-C5A-C5	2.74	114.49	109.36
3	A	1001	PLR	O4P-C5A-C5	2.68	114.37	109.36
3	C	1001	PLR	O4P-C5A-C5	2.66	114.34	109.36
3	C	1001	PLR	C6-C5-C4	2.40	120.06	118.10
3	B	1001	PLR	C6-C5-C4	2.33	120.00	118.10
3	A	1001	PLR	C6-C5-C4	2.32	120.00	118.10
3	C	1001	PLR	C5-C6-N1	-2.20	120.26	123.83
3	A	1001	PLR	C5-C6-N1	-2.19	120.27	123.83
3	B	1001	PLR	C5-C6-N1	-2.18	120.28	123.83
3	D	1001	PLR	C5-C6-N1	-2.00	120.58	123.83

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1002	MPD	O2-C2-C3-C4
4	B	1002	MPD	C1-C2-C3-C4
4	B	1002	MPD	CM-C2-C3-C4
4	D	1002	MPD	CM-C2-C3-C4
4	D	1002	MPD	O2-C2-C3-C4
4	D	1002	MPD	C1-C2-C3-C4

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1001	PLR	3	0
3	A	1001	PLR	2	0
3	C	1001	PLR	3	0
3	D	1001	PLR	2	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	451/521 (86%)	-1.08	1 (0%) 91 93	20, 41, 115, 202	23 (5%)
1	B	442/521 (84%)	-1.00	2 (0%) 87 89	21, 42, 101, 168	27 (6%)
1	C	453/521 (86%)	-1.06	2 (0%) 88 90	21, 41, 121, 194	30 (6%)
1	D	443/521 (85%)	-1.03	3 (0%) 84 86	19, 42, 92, 169	37 (8%)
2	E	87/90 (96%)	0.15	2 (2%) 61 63	27, 46, 58, 76	87 (100%)
All	All	1876/2174 (86%)	-0.99	10 (0%) 87 89	19, 42, 110, 202	204 (10%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	ALA	3.8
1	D	13	VAL	3.4
1	D	12	LEU	2.5
1	C	487	LYS	2.5
1	B	14	SER	2.4
1	A	485	ALA	2.3
1	C	485	ALA	2.3
2	E	74[A]	C	2.1
2	E	47(K)[A]	A	2.0
1	D	17	TYR	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	MPD	C	1002	8/8	0.97	0.11	59,77,89,92	0
4	MPD	B	1002	8/8	0.98	0.09	59,82,103,112	0
4	MPD	D	1002	8/8	0.98	0.08	64,80,104,113	0
4	MPD	A	1002	8/8	0.99	0.07	69,87,92,102	0
3	PLR	A	1001	15/15	1.00	0.03	31,39,48,50	0
3	PLR	B	1001	15/15	1.00	0.04	29,37,45,47	0
3	PLR	C	1001	15/15	1.00	0.03	30,39,46,49	0
3	PLR	D	1001	15/15	1.00	0.03	28,39,46,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.