



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:01 PM UTC

PDB ID : 8ONO / pdb_00008ono
Title : Modified oligopeptidase B from *S. proteamaculans* in intermediate conformation with 5 spermine molecule at 1.65 Å resolution
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Deposited on : 2023-04-03
Resolution : 1.65 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

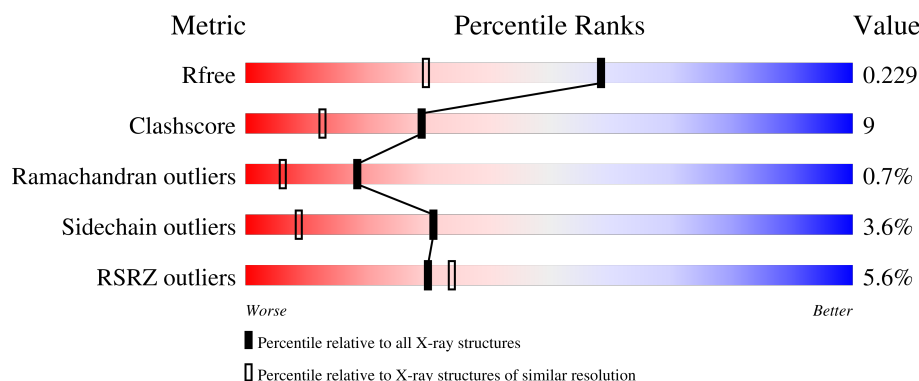
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	677	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SPM	A	702	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6158 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.

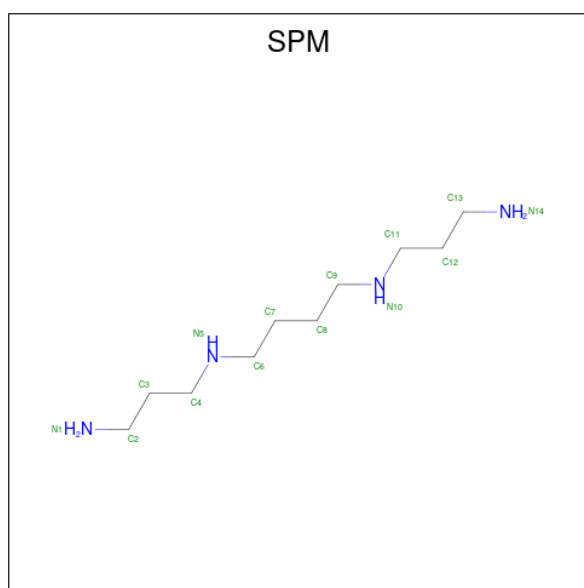
- Molecule 1 is a protein called Oligopeptidase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	677	5552	3526	933	1080	13	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	HIS	-	expression tag	UNP B3VI58
A	71	GLU	ILE	conflict	UNP B3VI58
A	72	ASN	PRO	conflict	UNP B3VI58
A	73	LEU	GLN	conflict	UNP B3VI58
A	74	TYR	GLN	conflict	UNP B3VI58
A	75	PHE	GLU	conflict	UNP B3VI58
A	76	GLN	HIS	conflict	UNP B3VI58

- Molecule 2 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			14	10	4		
2	A	1	Total	C	N	0	0
			14	10	4		
2	A	1	Total	C	N	0	0
			14	10	4		
2	A	1	Total	C	N	0	0
			14	10	4		
2	A	1	Total	C	N	0	0
			14	10	4		

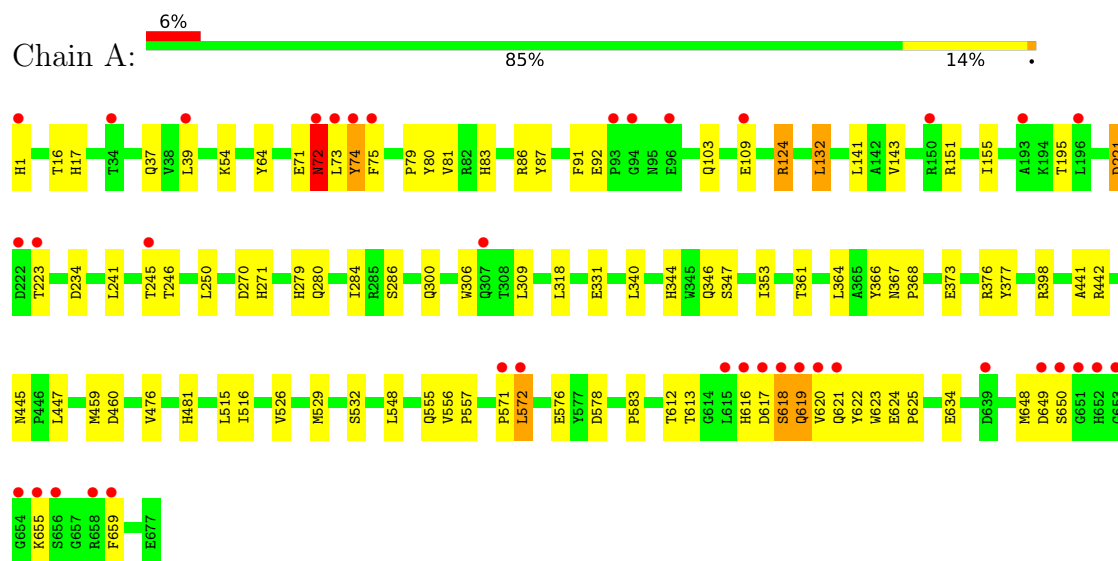
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	536	Total	O	0	0
			536	536		

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: Oligopeptidase B



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.09Å 100.62Å 108.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.59 – 1.65 29.59 – 1.65	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.59-1.65) 98.3 (29.59-1.65)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.186 , 0.220 (Not available) , 0.229	Depositor DCC
R_{free} test set	4673 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 32.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6158	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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: SPM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.07	1/5698 (0.0%)	1.22	2/7746 (0.0%)

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	A	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	481	HIS	CE1-NE2	5.32	1.37	1.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	234	ASP	CB-CA-C	-6.11	101.27	111.23
1	A	221	ASP	CA-CB-CG	5.91	118.51	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	619	GLN	Peptide
1	A	72	ASN	Peptide
1	A	73	LEU	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	5552	0	5263	89	0
2	A	70	0	130	27	0
3	A	536	0	0	17	0
All	All	6158	0	5393	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 9.

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)
1:A:132:LEU:CD2	1:A:141:LEU:HD11	1.90	1.02
1:A:132:LEU:HD22	1:A:141:LEU:HD11	1.43	0.98
1:A:376:ARG:HD2	2:A:702:SPM:H42	1.43	0.97
1:A:367:ASN:HD21	1:A:376:ARG:H	1.20	0.89
1:A:221:ASP:OD1	1:A:223:THR:HG22	1.74	0.86
1:A:376:ARG:HH11	2:A:702:SPM:HN11	1.25	0.84
1:A:223:THR:HG21	3:A:1256:HOH:O	1.79	0.82
1:A:80:TYR:CB	2:A:702:SPM:H31	2.11	0.80
2:A:702:SPM:H22	3:A:1005:HOH:O	1.82	0.78
1:A:81:VAL:H	2:A:702:SPM:H71	1.50	0.75
1:A:441:ALA:H	1:A:445:ASN:HD21	1.32	0.75
1:A:80:TYR:HB2	2:A:702:SPM:H31	1.70	0.73
1:A:71:GLU:O	1:A:72:ASN:HB2	1.90	0.72
2:A:704:SPM:H132	3:A:954:HOH:O	1.90	0.70
1:A:83:HIS:HD2	3:A:1028:HOH:O	1.74	0.70
1:A:81:VAL:H	2:A:702:SPM:C7	2.04	0.70
1:A:86:ARG:HH11	1:A:103:GLN:HE21	1.40	0.69
1:A:442:ARG:HH12	2:A:703:SPM:H121	1.56	0.69
1:A:621:GLN:HB3	1:A:623:TRP:CZ3	2.27	0.68
1:A:376:ARG:NH1	2:A:702:SPM:HN11	1.92	0.66
1:A:80:TYR:HB3	2:A:702:SPM:H31	1.76	0.66
1:A:245:THR:HG23	1:A:246:THR:OG1	1.97	0.65
1:A:271:HIS:HE1	1:A:286:SER:OG	1.81	0.64
1:A:331:GLU:HG2	1:A:364:LEU:HG	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:PRO:O	1:A:572:LEU:HB2	1.99	0.61
1:A:132:LEU:HD23	1:A:143:VAL:HG12	1.83	0.61
1:A:442:ARG:HG3	3:A:1194:HOH:O	2.02	0.60
1:A:572:LEU:HD21	1:A:619:GLN:OE1	2.02	0.60
1:A:621:GLN:HG3	1:A:623:TRP:CH2	2.38	0.58
1:A:86:ARG:HD2	1:A:103:GLN:HE21	1.67	0.57
1:A:376:ARG:CD	2:A:702:SPM:H42	2.29	0.57
1:A:634:GLU:HG3	3:A:1288:HOH:O	2.05	0.56
1:A:442:ARG:HH12	2:A:703:SPM:C12	2.17	0.56
1:A:442:ARG:HG2	3:A:1164:HOH:O	2.06	0.56
1:A:80:TYR:HB2	2:A:702:SPM:C3	2.36	0.55
1:A:279:HIS:HE1	3:A:885:HOH:O	1.90	0.55
1:A:83:HIS:HE1	3:A:1191:HOH:O	1.88	0.55
1:A:447:LEU:HD12	1:A:476:VAL:HB	1.88	0.55
1:A:71:GLU:O	1:A:72:ASN:CB	2.55	0.54
1:A:572:LEU:O	1:A:576:GLU:HG3	2.08	0.54
1:A:624:GLU:HB2	1:A:625:PRO:HD3	1.88	0.53
1:A:74:TYR:HB3	1:A:91:PHE:O	2.08	0.53
1:A:64:TYR:HH	1:A:659:PHE:HD1	1.54	0.53
1:A:617:ASP:CG	1:A:618:SER:H	2.17	0.52
1:A:279:HIS:HD2	3:A:898:HOH:O	1.91	0.52
1:A:151:ARG:NH1	1:A:617:ASP:OD1	2.43	0.52
1:A:613:THR:OG1	1:A:622:TYR:HA	2.09	0.51
1:A:377:TYR:OH	1:A:398:ARG:HD2	2.10	0.50
1:A:344:HIS:CD2	1:A:347:SER:H	2.28	0.50
1:A:271:HIS:HD2	3:A:1033:HOH:O	1.94	0.50
1:A:80:TYR:CB	2:A:702:SPM:C3	2.88	0.50
2:A:703:SPM:H92	3:A:1186:HOH:O	2.11	0.50
1:A:368:PRO:HD2	2:A:702:SPM:HN5	1.77	0.50
1:A:331:GLU:HG3	1:A:364:LEU:HD12	1.93	0.49
1:A:344:HIS:HE1	3:A:1014:HOH:O	1.96	0.48
1:A:366:TYR:O	2:A:702:SPM:H22	2.13	0.48
1:A:578:ASP:HB2	3:A:1018:HOH:O	2.12	0.48
2:A:702:SPM:C2	3:A:1005:HOH:O	2.51	0.48
1:A:344:HIS:HD2	1:A:347:SER:H	1.61	0.48
1:A:344:HIS:CD2	1:A:346:GLN:H	2.32	0.47
1:A:532:SER:OG	1:A:619:GLN:NE2	2.48	0.47
1:A:331:GLU:HG3	1:A:364:LEU:CD1	2.45	0.46
1:A:284:ILE:HG21	1:A:306:TRP:CH2	2.51	0.46
1:A:459:MET:HE1	2:A:704:SPM:H72	1.98	0.46
1:A:331:GLU:CG	1:A:364:LEU:HD12	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ARG:HH11	1:A:103:GLN:NE2	2.10	0.45
1:A:344:HIS:HD2	1:A:346:GLN:H	1.63	0.45
1:A:376:ARG:HD2	2:A:702:SPM:C4	2.31	0.44
1:A:516:ILE:HD11	1:A:526:VAL:HG21	1.99	0.44
1:A:221:ASP:CG	1:A:223:THR:HG22	2.43	0.44
1:A:271:HIS:CE1	1:A:286:SER:OG	2.64	0.44
1:A:132:LEU:CD2	1:A:143:VAL:HG12	2.46	0.44
1:A:557:PRO:O	1:A:620:VAL:HG11	2.17	0.43
1:A:622:TYR:CD1	1:A:622:TYR:C	2.97	0.43
1:A:620:VAL:HG23	3:A:883:HOH:O	2.18	0.43
1:A:80:TYR:HA	2:A:702:SPM:H71	2.01	0.43
1:A:17:HIS:HE1	1:A:583:PRO:O	2.02	0.43
1:A:72:ASN:ND2	1:A:74:TYR:HA	2.34	0.42
2:A:705:SPM:HN5	2:A:705:SPM:H82	1.80	0.42
1:A:143:VAL:O	1:A:155:ILE:HA	2.20	0.42
1:A:245:THR:OG1	1:A:270:ASP:HA	2.20	0.42
1:A:331:GLU:CG	1:A:364:LEU:CD1	2.97	0.42
1:A:340:LEU:HB2	1:A:353:ILE:HG12	2.02	0.42
1:A:74:TYR:O	1:A:75:PHE:HB2	2.19	0.42
1:A:124:ARG:HA	1:A:124:ARG:HE	1.85	0.42
2:A:702:SPM:H72	3:A:867:HOH:O	2.20	0.42
1:A:79:PRO:HA	1:A:87:TYR:O	2.19	0.42
2:A:705:SPM:H91	2:A:705:SPM:H122	1.74	0.42
1:A:376:ARG:CZ	2:A:702:SPM:H62	2.50	0.41
1:A:529:MET:HE3	1:A:529:MET:HB2	1.70	0.41
1:A:366:TYR:CZ	1:A:368:PRO:HB3	2.56	0.41
1:A:555:GLN:O	1:A:556:VAL:C	2.64	0.41
1:A:555:GLN:HA	1:A:612:THR:OG1	2.20	0.41
1:A:616:HIS:HD2	1:A:648:MET:O	2.03	0.41
1:A:81:VAL:N	2:A:702:SPM:H71	2.27	0.40
1:A:361:THR:OG1	1:A:460:ASP:HB3	2.21	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	676/677 (100%)	648 (96%)	23 (3%)	5 (1%)	18	6

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	618	SER
1	A	74	TYR
1	A	572	LEU
1	A	649	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	592/591 (100%)	571 (96%)	21 (4%)	32	10

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	HIS
1	A	16	THR
1	A	37	GLN
1	A	39	LEU
1	A	54	LYS
1	A	92	GLU
1	A	109	GLU
1	A	124	ARG
1	A	132	LEU
1	A	195	THR
1	A	241	LEU
1	A	250	LEU
1	A	280	GLN
1	A	300	GLN

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Mol	Chain	Res	Type
1	A	309	LEU
1	A	318	LEU
1	A	373	GLU
1	A	515	LEU
1	A	548	LEU
1	A	650	SER
1	A	655	LYS

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	1	HIS
1	A	17	HIS
1	A	37	GLN
1	A	72	ASN
1	A	83	HIS
1	A	103	GLN
1	A	172	ASN
1	A	181	ASN
1	A	262	GLN
1	A	271	HIS
1	A	279	HIS
1	A	280	GLN
1	A	339	GLN
1	A	344	HIS
1	A	367	ASN
1	A	445	ASN
1	A	502	GLN
1	A	518	GLN
1	A	544	GLN
1	A	585	GLN
1	A	616	HIS
1	A	619	GLN
1	A	621	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
2	SPM	A	705	-	13,13,13	0.39	0	12,12,12	0.82	1 (8%)
2	SPM	A	701	-	13,13,13	0.23	0	12,12,12	0.72	0
2	SPM	A	702	-	13,13,13	0.46	0	12,12,12	0.58	0
2	SPM	A	704	-	13,13,13	0.32	0	12,12,12	0.51	0
2	SPM	A	703	-	13,13,13	0.17	0	12,12,12	0.71	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
2	SPM	A	705	-	-	8/11/11/11	-
2	SPM	A	701	-	-	9/11/11/11	-
2	SPM	A	702	-	-	10/11/11/11	-
2	SPM	A	704	-	-	8/11/11/11	-
2	SPM	A	703	-	-	3/11/11/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	705	SPM	C11-N10-C9	2.18	123.70	113.40

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	705	SPM	C12-C11-N10-C9
2	A	701	SPM	C2-C3-C4-N5
2	A	704	SPM	N5-C6-C7-C8
2	A	704	SPM	C7-C8-C9-N10
2	A	703	SPM	C2-C3-C4-N5
2	A	702	SPM	C7-C8-C9-N10
2	A	702	SPM	N10-C11-C12-C13
2	A	701	SPM	C7-C8-C9-N10
2	A	705	SPM	N10-C11-C12-C13
2	A	701	SPM	C7-C6-N5-C4
2	A	701	SPM	C12-C11-N10-C9
2	A	702	SPM	C7-C6-N5-C4
2	A	704	SPM	C7-C6-N5-C4
2	A	705	SPM	N1-C2-C3-C4
2	A	705	SPM	C3-C4-N5-C6
2	A	701	SPM	C6-C7-C8-C9
2	A	704	SPM	C6-C7-C8-C9
2	A	705	SPM	C7-C6-N5-C4
2	A	705	SPM	N5-C6-C7-C8
2	A	704	SPM	N10-C11-C12-C13
2	A	705	SPM	C6-C7-C8-C9
2	A	701	SPM	C3-C4-N5-C6
2	A	702	SPM	N1-C2-C3-C4
2	A	702	SPM	C11-C12-C13-N14
2	A	703	SPM	N1-C2-C3-C4
2	A	702	SPM	C8-C9-N10-C11
2	A	702	SPM	N5-C6-C7-C8
2	A	701	SPM	N1-C2-C3-C4
2	A	701	SPM	C11-C12-C13-N14
2	A	703	SPM	C11-C12-C13-N14
2	A	704	SPM	N1-C2-C3-C4
2	A	704	SPM	C3-C4-N5-C6
2	A	704	SPM	C12-C11-N10-C9
2	A	705	SPM	C8-C9-N10-C11
2	A	702	SPM	C3-C4-N5-C6
2	A	702	SPM	C12-C11-N10-C9
2	A	701	SPM	C8-C9-N10-C11

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Mol	Chain	Res	Type	Atoms
2	A	702	SPM	C6-C7-C8-C9

There are no ring outliers.

4 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	705	SPM	2	0
2	A	702	SPM	20	0
2	A	704	SPM	2	0
2	A	703	SPM	3	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

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	677/677 (100%)	0.20	38 (5%)	30 34	10, 20, 46, 106	1 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	TYR	8.0
1	A	73	LEU	7.6
1	A	618	SER	5.6
1	A	652	HIS	5.5
1	A	651	GLY	4.3
1	A	653	GLY	4.2
1	A	615	LEU	4.2
1	A	619	GLN	4.1
1	A	616	HIS	4.0
1	A	620	VAL	3.9
1	A	654	GLY	3.8
1	A	94	GLY	3.7
1	A	72	ASN	3.7
1	A	659	PHE	3.7
1	A	93	PRO	3.5
1	A	193	ALA	3.5
1	A	1	HIS	3.5
1	A	617	ASP	3.3
1	A	571	PRO	3.2
1	A	150	ARG	3.2
1	A	34	THR	3.1
1	A	655	LYS	3.0
1	A	650	SER	3.0
1	A	658	ARG	2.8
1	A	656	SER	2.8
1	A	621	GLN	2.5
1	A	245	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	222	ASP	2.4
1	A	649	ASP	2.4
1	A	223	THR	2.4
1	A	572	LEU	2.2
1	A	75	PHE	2.2
1	A	196	LEU	2.1
1	A	39	LEU	2.1
1	A	96	GLU	2.1
1	A	639	ASP	2.1
1	A	109	GLU	2.0
1	A	307	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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
2	SPM	A	705	14/14	0.59	0.26	41,61,68,69	0
2	SPM	A	704	14/14	0.73	0.20	33,54,60,61	0
2	SPM	A	702	14/14	0.77	0.18	29,39,47,50	0
2	SPM	A	701	14/14	0.79	0.18	40,46,49,49	0
2	SPM	A	703	14/14	0.87	0.12	28,32,38,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.