Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2024 – 10:53 AM JST

PDB ID	:	5XNH
Title	:	Crystal structure of the branched-chain polyamine synthase (BpsA) in complex with spermidine
Authors	:	Mizohata, E.; Tse, K.M.; Fujita, J.; Inoue, T.
Deposited on	:	2017-05-22
Resolution	:	1.95 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:

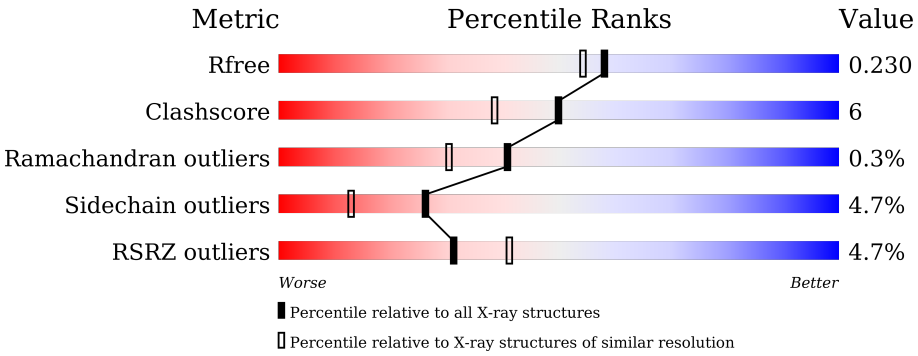
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 <=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	371	5% 77% 11% • • 8%
1	H	371	3% 77% 12% • 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5669 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 N(4)-bis(aminopropyl)spermidine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	1	0
			2756	1759	462	528	7			
1	H	338	Total	C	N	O	S	0	0	0
			2728	1743	461	517	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q5JIZ3
A	-18	GLY	-	expression tag	UNP Q5JIZ3
A	-17	SER	-	expression tag	UNP Q5JIZ3
A	-16	SER	-	expression tag	UNP Q5JIZ3
A	-15	HIS	-	expression tag	UNP Q5JIZ3
A	-14	HIS	-	expression tag	UNP Q5JIZ3
A	-13	HIS	-	expression tag	UNP Q5JIZ3
A	-12	HIS	-	expression tag	UNP Q5JIZ3
A	-11	HIS	-	expression tag	UNP Q5JIZ3
A	-10	HIS	-	expression tag	UNP Q5JIZ3
A	-9	SER	-	expression tag	UNP Q5JIZ3
A	-8	SER	-	expression tag	UNP Q5JIZ3
A	-7	GLY	-	expression tag	UNP Q5JIZ3
A	-6	LEU	-	expression tag	UNP Q5JIZ3
A	-5	VAL	-	expression tag	UNP Q5JIZ3
A	-4	PRO	-	expression tag	UNP Q5JIZ3
A	-3	ARG	-	expression tag	UNP Q5JIZ3
A	-2	GLY	-	expression tag	UNP Q5JIZ3
A	-1	SER	-	expression tag	UNP Q5JIZ3
A	0	HIS	-	expression tag	UNP Q5JIZ3
H	-19	MET	-	expression tag	UNP Q5JIZ3
H	-18	GLY	-	expression tag	UNP Q5JIZ3
H	-17	SER	-	expression tag	UNP Q5JIZ3
H	-16	SER	-	expression tag	UNP Q5JIZ3
H	-15	HIS	-	expression tag	UNP Q5JIZ3

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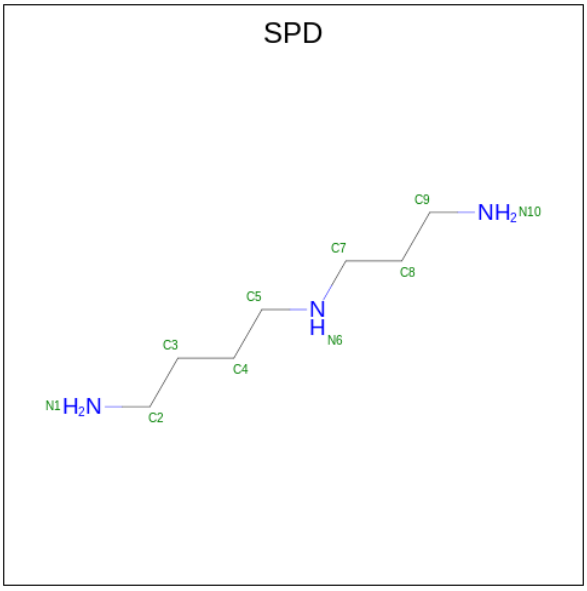
Chain	Residue	Modelled	Actual	Comment	Reference
H	-14	HIS	-	expression tag	UNP Q5JIZ3
H	-13	HIS	-	expression tag	UNP Q5JIZ3
H	-12	HIS	-	expression tag	UNP Q5JIZ3
H	-11	HIS	-	expression tag	UNP Q5JIZ3
H	-10	HIS	-	expression tag	UNP Q5JIZ3
H	-9	SER	-	expression tag	UNP Q5JIZ3
H	-8	SER	-	expression tag	UNP Q5JIZ3
H	-7	GLY	-	expression tag	UNP Q5JIZ3
H	-6	LEU	-	expression tag	UNP Q5JIZ3
H	-5	VAL	-	expression tag	UNP Q5JIZ3
H	-4	PRO	-	expression tag	UNP Q5JIZ3
H	-3	ARG	-	expression tag	UNP Q5JIZ3
H	-2	GLY	-	expression tag	UNP Q5JIZ3
H	-1	SER	-	expression tag	UNP Q5JIZ3
H	0	HIS	-	expression tag	UNP Q5JIZ3

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0

- Molecule 3 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 10 7 3	0	0
3	H	1	Total C N 10 7 3	0	0

- Molecule 4 is water.

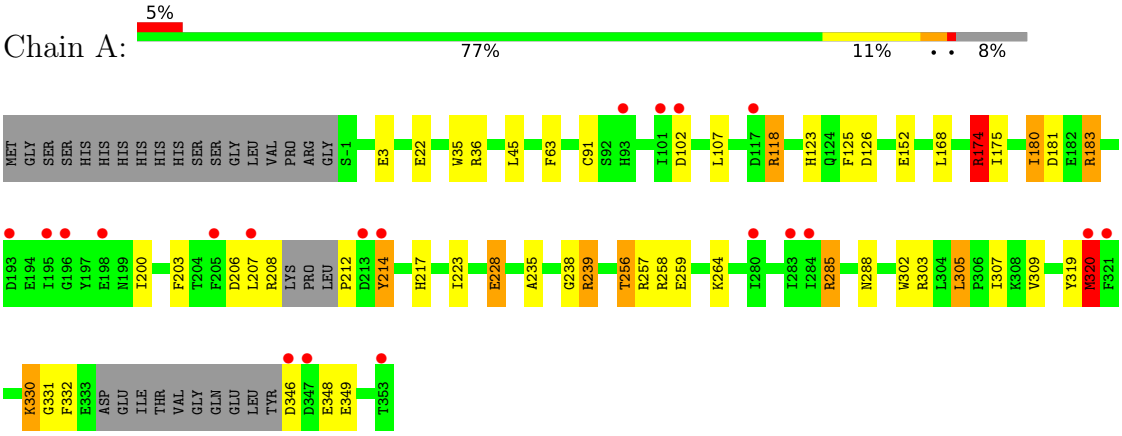
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	88	Total O 88 88	0	0
4	H	76	Total O 76 76	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

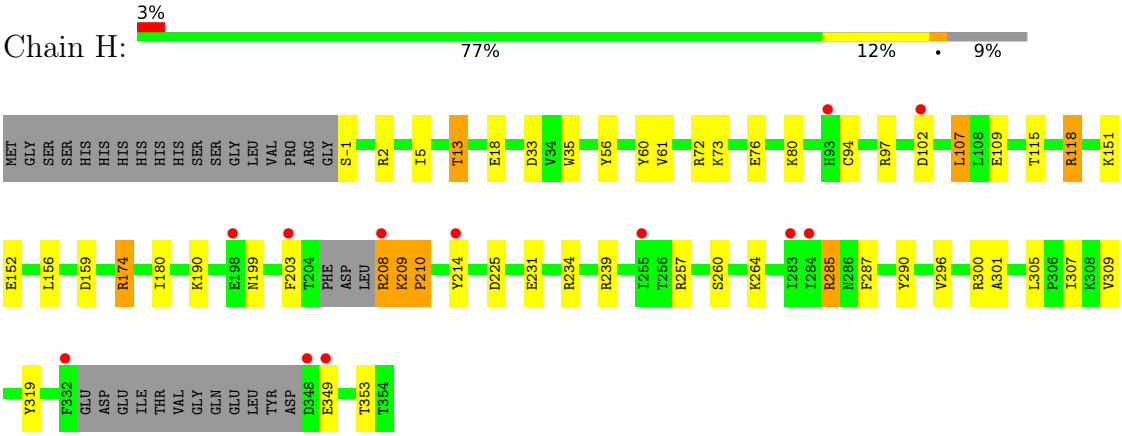
• Molecule 1: N(4)-bis(aminopropyl)spermidine synthase

Chain A:



• Molecule 1: N(4)-bis(aminopropyl)spermidine synthase

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.87Å 78.78Å 79.41Å 90.00° 90.16° 90.00°	Depositor
Resolution (Å)	50.01 – 1.95 35.46 – 1.95	Depositor EDS
% Data completeness (in resolution range)	84.8 (50.01-1.95) 84.8 (35.46-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.70 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.171 , 0.225 0.181 , 0.230	Depositor DCC
R_{free} test set	1964 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	19.9	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 50.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.010 for -h,l,k 0.021 for -h,-l,-k 0.136 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5669	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SPD, FE

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	0.88	1/2815 (0.0%)	0.98	10/3813 (0.3%)
1	H	0.86	0/2784	0.98	13/3772 (0.3%)
All	All	0.87	1/5599 (0.0%)	0.98	23/7585 (0.3%)

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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	THR	CB-CG2	-6.95	1.29	1.52

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	320	MET	CG-SD-CE	9.31	115.09	100.20
1	H	174	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	H	285	ARG	NE-CZ-NH2	-7.57	116.51	120.30
1	A	174	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	H	174	ARG	NE-CZ-NH2	-7.34	116.63	120.30
1	A	285	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	H	118	ARG	NE-CZ-NH1	-6.94	116.83	120.30
1	H	300	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	H	72	ARG	NE-CZ-NH1	6.54	123.57	120.30
1	H	285	ARG	NE-CZ-NH1	6.53	123.57	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	183	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	A	180	ILE	CB-CA-C	-6.27	99.06	111.60
1	H	257	ARG	NE-CZ-NH1	6.01	123.30	120.30
1	H	208	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	174	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	228	GLU	CA-CB-CG	-5.30	101.74	113.40
1	A	257	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	H	107	LEU	CA-CB-CG	5.25	127.38	115.30
1	H	33	ASP	CB-CG-OD1	5.13	122.92	118.30
1	H	234	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	H	118	ARG	CG-CD-NE	-5.03	101.24	111.80
1	A	239	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	A	36	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	126	ASP	Peptide

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	2756	0	2725	35	0
1	H	2728	0	2710	31	0
2	A	1	0	0	0	0
3	A	10	0	19	0	0
3	H	10	0	19	2	0
4	A	88	0	0	2	0
4	H	76	0	0	3	0
All	All	5669	0	5473	64	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 6.

All (64) 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:H:209:LYS:HB3	1:H:210:PRO:HD2	1.55	0.86
1:A:118:ARG:NH2	4:A:501:HOH:O	2.12	0.82
1:A:228:GLU:OE2	1:A:256:THR:HB	1.84	0.76
1:A:256:THR:HG23	1:A:258:ARG:H	1.49	0.75
1:H:307:ILE:HG22	1:H:309:VAL:HG23	1.68	0.75
1:H:209:LYS:HB3	1:H:210:PRO:CD	2.17	0.74
1:A:320:MET:HE2	1:A:320:MET:HA	1.69	0.73
1:H:209:LYS:HA	1:H:239:ARG:HH21	1.54	0.73
1:A:264:LYS:NZ	4:A:503:HOH:O	2.22	0.73
1:H:296:VAL:HG21	4:H:522:HOH:O	1.91	0.70
1:A:118:ARG:HG3	1:A:118:ARG:HH21	1.58	0.69
1:H:296:VAL:HB	4:H:572:HOH:O	1.94	0.66
1:H:231:GLU:H	1:H:231:GLU:CD	2.00	0.64
1:A:256:THR:HG23	1:A:258:ARG:N	2.13	0.62
1:A:63:PHE:CD1	1:A:307:ILE:HD11	2.33	0.62
1:A:288:ASN:HD21	1:A:320:MET:HE3	1.64	0.62
1:H:209:LYS:CB	1:H:210:PRO:CD	2.76	0.61
1:H:115:THR:O	1:H:118:ARG:HG2	2.01	0.61
1:A:228:GLU:CD	1:A:256:THR:HB	2.22	0.59
1:A:256:THR:HG22	1:A:259:GLU:H	1.69	0.57
1:H:35:TRP:CZ2	1:H:305:LEU:HD11	2.40	0.57
1:A:181:ASP:OD1	1:A:183:ARG:HD3	2.04	0.57
1:A:152:GLU:OE2	1:A:174:ARG:HD3	2.04	0.57
1:H:209:LYS:HD2	1:H:210:PRO:HD3	1.87	0.56
1:A:330:LYS:HD2	1:A:331:GLY:O	2.06	0.56
1:A:288:ASN:HD21	1:A:320:MET:CE	2.20	0.55
1:H:97:ARG:HD3	1:H:287:PHE:O	2.06	0.55
1:H:152:GLU:OE2	1:H:174:ARG:HD3	2.06	0.54
1:A:264:LYS:HE3	1:A:349:GLU:OE1	2.08	0.54
1:A:35:TRP:CZ2	1:A:305:LEU:HD21	2.44	0.52
1:A:256:THR:CG2	1:A:259:GLU:H	2.22	0.52
1:H:260:SER:CB	1:H:264:LYS:HE2	2.38	0.52
1:H:35:TRP:CH2	1:H:305:LEU:HD11	2.45	0.52
1:H:260:SER:OG	1:H:264:LYS:HE2	2.12	0.49
1:H:225:ASP:OD1	1:H:290:TYR:OH	2.29	0.48
1:A:45:LEU:HD23	1:A:45:LEU:C	2.35	0.47
1:A:302:TRP:HA	1:A:305:LEU:HD22	1.97	0.47
1:A:118:ARG:NH2	1:A:118:ARG:HG3	2.26	0.46
1:A:123:HIS:O	1:A:125:PHE:O	2.33	0.46
1:H:152:GLU:HG2	1:H:174:ARG:HG2	1.98	0.46
1:H:296:VAL:CG2	4:H:522:HOH:O	2.57	0.46
1:H:60:TYR:CE1	1:H:73:LYS:HE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:285:ARG:HA	1:H:319:TYR:CD2	2.52	0.44
1:A:307:ILE:HG22	1:A:309:VAL:HG23	2.00	0.44
1:H:76:GLU:O	1:H:80:LYS:HB2	2.18	0.44
1:H:301:ALA:O	1:H:305:LEU:HG	2.18	0.44
1:A:285:ARG:HA	1:A:319:TYR:CD2	2.52	0.43
1:A:22:GLU:OE1	1:H:151:LYS:NZ	2.40	0.43
1:H:13:THR:OG1	1:H:349:GLU:OE2	2.15	0.43
1:A:181:ASP:OD2	1:A:183:ARG:NH1	2.50	0.43
1:H:56:TYR:HB2	1:H:61:VAL:HG23	2.00	0.42
1:A:107:LEU:CD1	1:A:168:LEU:HB2	2.50	0.42
1:A:175:ILE:O	1:A:200:ILE:HA	2.19	0.42
1:A:208:ARG:HH21	1:A:212:PRO:N	2.18	0.42
1:H:203:PHE:CE2	1:H:214:TYR:CE1	3.08	0.41
1:H:225:ASP:OD2	3:H:401:SPD:H92	2.20	0.41
1:A:208:ARG:NH2	1:A:212:PRO:N	2.69	0.41
1:A:238:GLY:HA3	1:A:332:PHE:HB2	2.03	0.41
1:H:5:ILE:HD11	1:H:18:GLU:HA	2.02	0.41
1:H:353:THR:OG1	3:H:401:SPD:H21	2.21	0.41
1:A:91:CYS:SG	1:H:94:CYS:HB3	2.61	0.40
1:A:63:PHE:HD1	1:A:307:ILE:HD11	1.84	0.40
1:A:203:PHE:HZ	1:A:214:TYR:CD2	2.39	0.40
1:A:235:ALA:O	1:A:239:ARG:CG	2.69	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	335/371 (90%)	329 (98%)	5 (2%)	1 (0%)	41	30
1	H	332/371 (90%)	324 (98%)	7 (2%)	1 (0%)	41	30
All	All	667/742 (90%)	653 (98%)	12 (2%)	2 (0%)	41	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	ASP
1	H	210	PRO

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	300/326 (92%)	284 (95%)	16 (5%)	22 10
1	H	296/326 (91%)	283 (96%)	13 (4%)	28 15
All	All	596/652 (91%)	567 (95%)	29 (5%)	26 12

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3[A]	GLU
1	A	3[B]	GLU
1	A	102	ASP
1	A	118	ARG
1	A	174	ARG
1	A	180	ILE
1	A	207	LEU
1	A	214	TYR
1	A	217	HIS
1	A	223	ILE
1	A	303	ARG
1	A	305	LEU
1	A	320	MET
1	A	330	LYS
1	A	346	ASP
1	A	348	GLU
1	H	-1	SER
1	H	2	ARG
1	H	13	THR
1	H	102	ASP
1	H	107	LEU

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Mol	Chain	Res	Type
1	H	109	GLU
1	H	156	LEU
1	H	159	ASP
1	H	180	ILE
1	H	190	LYS
1	H	199	ASN
1	H	208	ARG
1	H	209	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	65	ASN
1	A	110	GLN
1	A	150	ASN
1	A	288	ASN
1	A	292	ASN
1	H	0	HIS
1	H	29	GLN
1	H	65	ASN
1	H	123	HIS
1	H	292	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	SPD	H	401	-	9,9,9	0.56	0	8,8,8	1.07	0
3	SPD	A	402	-	9,9,9	0.40	0	8,8,8	1.16	1 (12%)

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
3	SPD	H	401	-	-	2/7/7/7	-
3	SPD	A	402	-	-	7/7/7/7	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	402	SPD	C7-N6-C5	2.49	125.18	113.45

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	SPD	C3-C4-C5-N6
3	A	402	SPD	N6-C7-C8-C9
3	A	402	SPD	C4-C5-N6-C7
3	A	402	SPD	C7-C8-C9-N10
3	A	402	SPD	C2-C3-C4-C5
3	A	402	SPD	N1-C2-C3-C4
3	H	401	SPD	C2-C3-C4-C5
3	H	401	SPD	C3-C4-C5-N6
3	A	402	SPD	C8-C7-N6-C5

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	401	SPD	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

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, 95^{th} 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	340/371 (91%)	0.21	20 (5%)	22	30	9, 22, 48, 66	0
1	H	338/371 (91%)	0.16	12 (3%)	42	52	10, 24, 45, 74	0
All	All	678/742 (91%)	0.18	32 (4%)	31	41	9, 23, 46, 74	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	TYR	7.5
1	H	214	TYR	4.7
1	A	93	HIS	4.2
1	A	283	ILE	3.9
1	A	284	ILE	3.7
1	A	102	ASP	3.6
1	A	346	ASP	3.5
1	H	198	GLU	3.3
1	H	284	ILE	3.3
1	A	347	ASP	3.0
1	H	93	HIS	2.8
1	A	196	GLY	2.7
1	H	348	ASP	2.7
1	H	349	GLU	2.7
1	A	193	ASP	2.7
1	A	207	LEU	2.5
1	A	280	ILE	2.5
1	H	283	ILE	2.4
1	A	213	ASP	2.4
1	H	208	ARG	2.3
1	H	332	PHE	2.3
1	H	255	ILE	2.3
1	A	353	THR	2.3
1	A	321	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	102	ASP	2.2
1	A	320	MET	2.2
1	A	198	GLU	2.1
1	A	195	ILE	2.1
1	A	101	ILE	2.1
1	A	117	ASP	2.0
1	H	203	PHE	2.0
1	A	205	PHE	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 monosaccharides 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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SPD	H	401	10/10	0.91	0.23	26,36,40,42	0
3	SPD	A	402	10/10	0.92	0.19	25,31,34,34	0
2	FE	A	401	1/1	0.99	0.04	25,25,25,25	1

6.5 Other polymers (i)

There are no such residues in this entry.