Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 11:08 AM GMT

PDB ID : 3O82

Title : Structure of BasE N-terminal domain from Acinetobacter baumannii bound to 5'-O-[N-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine

Authors : Drake, E.J.; Duckworth, B.P.; Neres, J.; Aldrich, C.C.; Gulick, A.M.

Deposited on : 2010-08-02

Resolution : 2.70 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.70 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	Percentile Ranks	Value
Rfree		0.249
Clashscore		7
Ramachandran outliers		0.5%
Sidechain outliers		3.7%
RSRZ outliers		2.0%

Worse .... *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
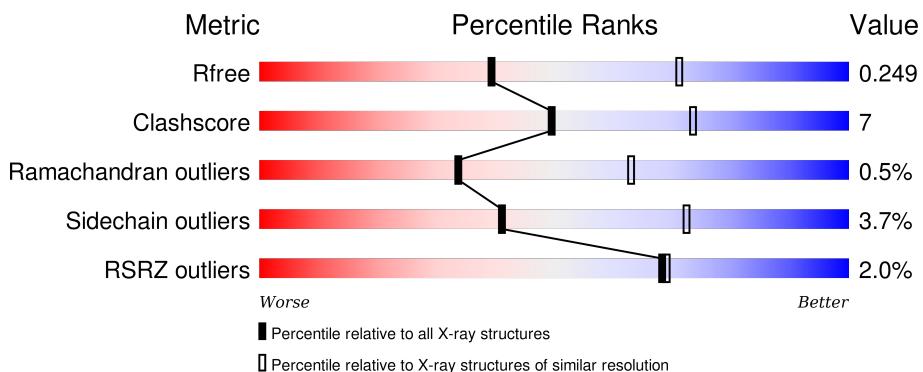
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	544	2% — 68% · 11% · 20%
1	B	544	% — 63% · 16% · 20%
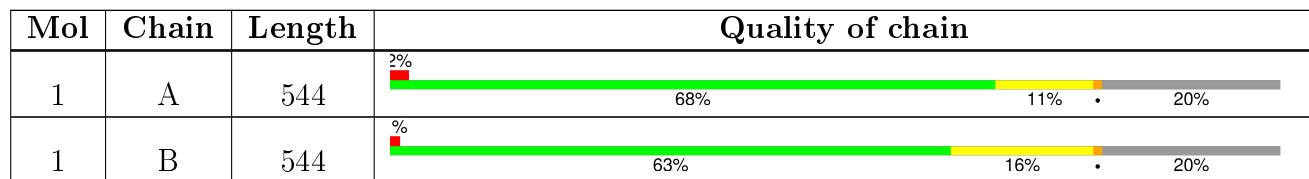
2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6881 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 Peptide arylation enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	0	0
			3378	2153	578	633	14			
1	B	435	Total	C	N	O	S	0	0	0
			3384	2155	579	636	14			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP B2HVG8
A	0	HIS	-	EXPRESSION TAG	UNP B2HVG8
A	45	LEU	PRO	ENGINEERED MUTATION	UNP B2HVG8
A	68	THR	SER	SEE REMARK 999	UNP B2HVG8
A	149	ASP	GLU	SEE REMARK 999	UNP B2HVG8
A	180	PHE	LEU	SEE REMARK 999	UNP B2HVG8
A	226	GLY	ASP	SEE REMARK 999	UNP B2HVG8
A	329	LEU	ILE	SEE REMARK 999	UNP B2HVG8
A	378	ARG	LYS	SEE REMARK 999	UNP B2HVG8
B	-1	GLY	-	EXPRESSION TAG	UNP B2HVG8
B	0	HIS	-	EXPRESSION TAG	UNP B2HVG8
B	45	LEU	PRO	ENGINEERED MUTATION	UNP B2HVG8
B	68	THR	SER	SEE REMARK 999	UNP B2HVG8
B	149	ASP	GLU	SEE REMARK 999	UNP B2HVG8
B	180	PHE	LEU	SEE REMARK 999	UNP B2HVG8
B	226	GLY	ASP	SEE REMARK 999	UNP B2HVG8
B	329	LEU	ILE	SEE REMARK 999	UNP B2HVG8
B	378	ARG	LYS	SEE REMARK 999	UNP B2HVG8

- Molecule 2 is 5'-O-{[(2,3-DIHYDROXYPHENYL)CARBONYL]SULFAMOYL}ADENOSINE (three-letter code: HP8) (formula: $C_{17}H_{18}N_6O_9S$).
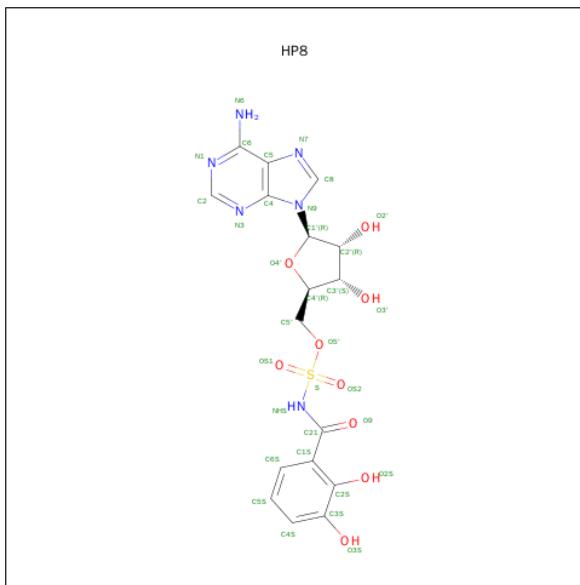
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 33	C 17	N 6	O 9	S 1	0	0
2	B	1	Total 33	C 17	N 6	O 9	S 1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Ca 2	0	0
3	A	2	Total 2	Ca 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	25	Total 25	O 25	0	0
4	B	24	Total 24	O 24	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Peptide arylation enzyme
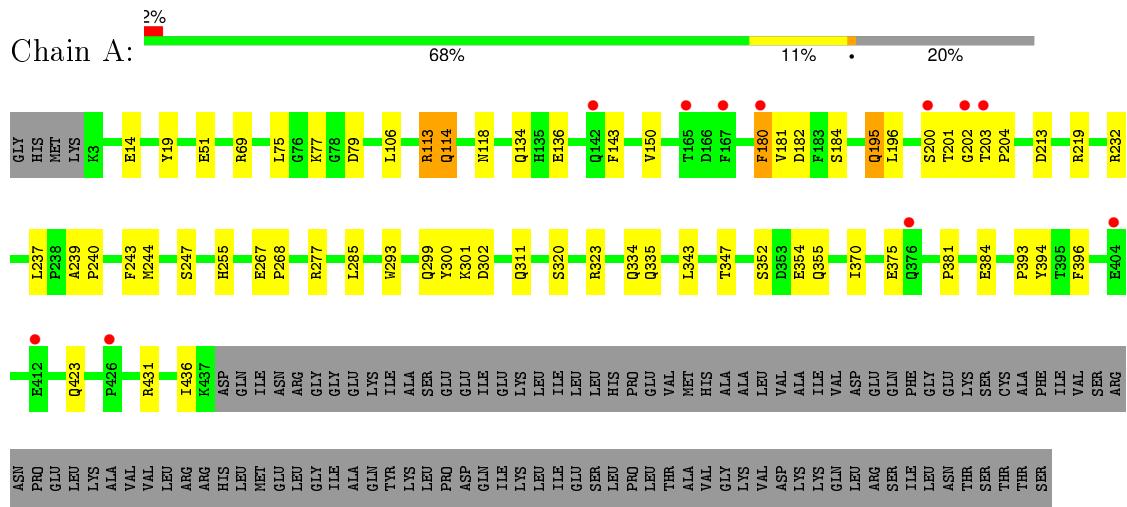
• Molecule 1: Peptide arylation enzyme
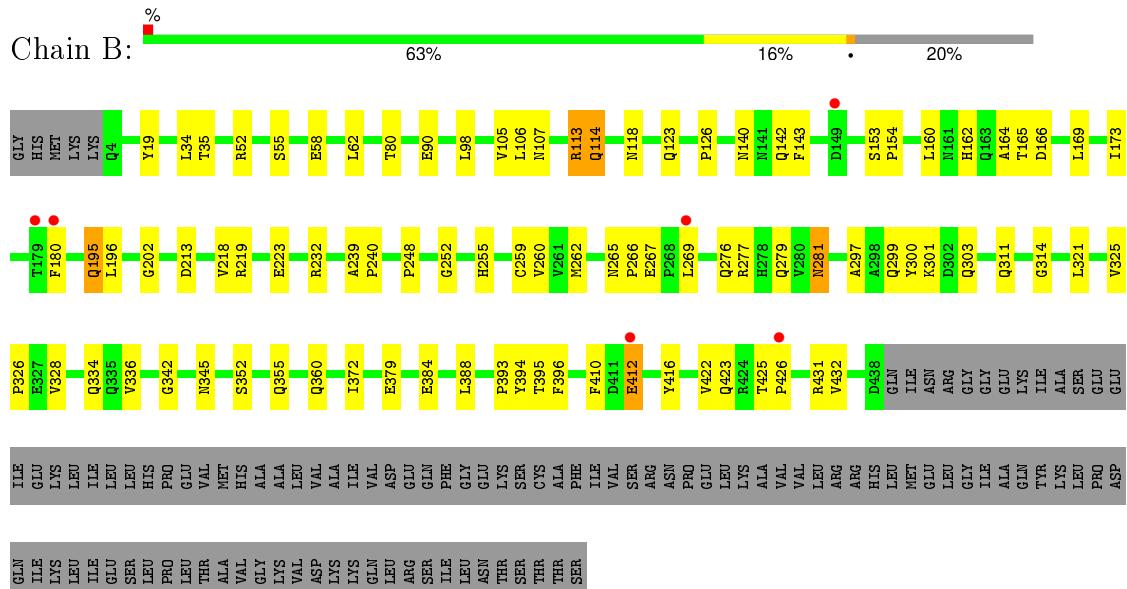
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.45Å 145.26Å 149.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.70 39.57 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.5 (40.00-2.70) 97.5 (39.57-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.200 , 0.251 0.202 , 0.249	Depositor DCC
R_{free} test set	1967 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	44.1	Xtriage
Anisotropy	0.547	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 30.8	EDS
Estimated twinning fraction	0.009 for -h,l,k	Xtriage
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Outliers	0 of 38918 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	6881	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, HP8

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	0.85	2/3457 (0.1%)	0.84	2/4710 (0.0%)
1	B	0.85	0/3462	0.85	0/4715
All	All	0.85	2/6919 (0.0%)	0.84	2/9425 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	GLU	CG-CD	5.67	1.60	1.51
1	A	375	GLU	CG-CD	5.11	1.59	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	302	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	232	ARG	NE-CZ-NH1	5.20	122.90	120.30

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	3378	0	3284	35	0
1	B	3384	0	3297	60	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	33	0	17	0	0
2	B	33	0	17	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	25	0	0	0	1
4	B	24	0	0	2	0
All	All	6881	0	6615	95	1

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 7.

All (95) 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:360:GLN:HE21	1:B:432:VAL:H	1.11	0.93
1:B:232:ARG:H	1:B:281:ASN:HD21	1.20	0.88
1:B:106:LEU:HD11	1:B:196:LEU:HD21	1.63	0.81
1:B:360:GLN:NE2	1:B:432:VAL:H	1.81	0.79
1:A:352:SER:H	1:A:355:GLN:HE21	1.29	0.78
1:A:423:GLN:HE21	1:A:431:ARG:HH11	1.35	0.74
1:A:106:LEU:HD11	1:A:196:LEU:HD21	1.69	0.74
1:B:52:ARG:NH2	1:B:90:GLU:OE2	2.22	0.73
1:B:352:SER:H	1:B:355:GLN:HE21	1.38	0.72
1:B:213:ASP:HB2	1:B:394:TYR:HA	1.71	0.71
1:A:381:PRO:HG2	1:A:384:GLU:HG3	1.74	0.69
1:B:232:ARG:H	1:B:281:ASN:ND2	1.89	0.69
1:A:114:GLN:H	1:A:114:GLN:HE21	1.41	0.67
1:A:213:ASP:HB2	1:A:394:TYR:HA	1.78	0.66
1:A:118:ASN:HD22	1:A:143:PHE:HE1	1.42	0.65
1:A:195:GLN:HE21	1:A:196:LEU:H	1.46	0.63
1:B:260:VAL:HG12	1:B:262:MET:HE3	1.81	0.63
1:A:77:LYS:NZ	1:A:184:SER:OG	2.31	0.62
1:B:352:SER:H	1:B:355:GLN:NE2	2.01	0.57
1:B:423:GLN:HE21	1:B:431:ARG:HH11	1.52	0.57
1:A:75:LEU:HA	1:A:79:ASP:OD2	2.04	0.57
1:B:55:SER:OG	1:B:58:GLU:HG2	2.04	0.57
1:B:52:ARG:HH22	1:B:90:GLU:CD	2.09	0.56
1:A:113:ARG:NH2	1:A:136:GLU:CB	2.69	0.55
1:B:202:GLY:HA2	4:B:561:HOH:O	2.06	0.54
1:A:114:GLN:H	1:A:114:GLN:NE2	2.05	0.54
1:B:412:GLU:CD	1:B:412:GLU:H	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:VAL:HG12	1:B:262:MET:CE	2.39	0.52
1:B:372:ILE:HD13	1:B:422:VAL:HG23	1.92	0.52
1:A:195:GLN:NE2	1:A:196:LEU:H	2.08	0.52
1:A:352:SER:H	1:A:355:GLN:NE2	2.03	0.51
1:A:180:PHE:O	1:A:180:PHE:CD2	2.64	0.51
1:B:195:GLN:HE21	1:B:196:LEU:H	1.59	0.51
1:B:248:PRO:HD3	1:B:311:GLN:HE22	1.74	0.51
1:A:150:VAL:O	1:A:150:VAL:HG12	2.11	0.51
1:B:118:ASN:ND2	1:B:143:PHE:HE1	2.09	0.51
1:B:113:ARG:HB3	1:B:114:GLN:HE21	1.76	0.50
1:A:237:LEU:HB2	1:A:244:MET:SD	2.51	0.50
1:B:342:GLY:HA3	1:B:395:THR:HA	1.94	0.50
1:B:239:ALA:N	1:B:240:PRO:HD2	2.27	0.50
1:B:260:VAL:CG1	1:B:262:MET:CE	2.90	0.49
1:B:219:ARG:HG2	1:B:255:HIS:CE1	2.47	0.49
1:B:160:LEU:HD13	1:B:169:LEU:HD23	1.95	0.49
1:B:297:ALA:HB3	1:B:328:VAL:HG12	1.95	0.48
1:A:195:GLN:HE21	1:A:196:LEU:N	2.11	0.48
1:B:410:PHE:CE2	1:B:416:TYR:HB2	2.49	0.47
1:B:166:ASP:OD1	4:B:554:HOH:O	2.20	0.47
1:B:314:GLY:HA2	2:B:602:HP8:H6S	1.96	0.47
1:B:98:LEU:HD13	1:B:105:VAL:HB	1.97	0.46
1:B:321:LEU:HD23	1:B:321:LEU:HA	1.74	0.46
1:B:232:ARG:N	1:B:281:ASN:HD21	2.01	0.45
1:A:311:GLN:HA	1:A:334:GLN:O	2.17	0.45
1:B:336:VAL:HA	1:B:345:ASN:O	2.17	0.45
1:B:162:HIS:HB2	1:B:166:ASP:HB2	1.99	0.44
1:B:80:THR:OG1	1:B:126:PRO:HA	2.17	0.44
1:A:335:GLN:HB2	1:A:347:THR:HG23	1.99	0.44
1:A:181:VAL:CG1	1:A:182:ASP:N	2.81	0.44
1:B:62:LEU:HD22	1:B:173:ILE:HG22	2.00	0.44
1:A:285:LEU:HD11	1:A:293:TRP:CE2	2.53	0.44
1:B:34:LEU:HA	1:B:34:LEU:HD12	1.50	0.44
1:B:55:SER:H	1:B:58:GLU:HG3	1.83	0.43
1:B:140:ASN:CG	1:B:142:GLN:HE21	2.21	0.43
1:B:218:VAL:HG13	1:B:252:GLY:HA2	2.00	0.43
1:B:388:LEU:HD13	1:B:422:VAL:HG21	2.00	0.43
1:B:352:SER:N	1:B:355:GLN:HE21	2.11	0.43
1:B:113:ARG:NH1	1:B:113:ARG:HG3	2.32	0.43
1:B:360:GLN:NE2	1:B:432:VAL:N	2.58	0.43
1:A:114:GLN:N	1:A:114:GLN:HE21	2.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:GLU:CD	1:A:277:ARG:HH12	2.22	0.42
1:A:113:ARG:HH22	1:A:136:GLU:CB	2.32	0.42
1:A:219:ARG:HG2	1:A:255:HIS:CE1	2.54	0.42
1:B:34:LEU:O	1:B:35:THR:C	2.58	0.42
1:B:265:ASN:HB2	1:B:266:PRO:CD	2.50	0.42
1:B:232:ARG:HA	1:B:259:CYS:O	2.20	0.42
1:A:239:ALA:N	1:A:240:PRO:HD2	2.34	0.42
1:A:243:PHE:HA	1:A:247:SER:HB2	2.01	0.42
1:A:300:TYR:O	1:A:301:LYS:C	2.58	0.42
1:B:266:PRO:O	1:B:267:GLU:C	2.56	0.42
1:A:181:VAL:HG12	1:A:182:ASP:N	2.35	0.42
1:B:311:GLN:HA	1:B:334:GLN:O	2.20	0.41
1:A:19:TYR:CE1	1:A:393:PRO:HA	2.55	0.41
1:B:260:VAL:CG1	1:B:262:MET:HE1	2.50	0.41
1:B:425:THR:HB	1:B:426:PRO:HD2	2.02	0.41
1:B:153:SER:HA	1:B:154:PRO:HD2	1.92	0.41
1:A:203:THR:HA	1:A:204:PRO:HD3	1.98	0.41
1:B:106:LEU:HD12	1:B:107:ASN:N	2.36	0.41
1:B:262:MET:HE2	1:B:262:MET:HA	2.03	0.41
1:A:180:PHE:HD2	1:A:180:PHE:O	2.02	0.41
1:B:19:TYR:CE1	1:B:393:PRO:HA	2.55	0.41
1:A:323:ARG:NH2	1:A:354:GLU:OE2	2.53	0.41
1:B:300:TYR:O	1:B:301:LYS:C	2.60	0.41
1:A:267:GLU:HA	1:A:268:PRO:HD3	1.92	0.40
1:B:276:GLN:HB2	1:B:303:GLN:O	2.21	0.40
1:B:325:VAL:HB	1:B:326:PRO:HD3	2.02	0.40
1:B:423:GLN:NE2	1:B:431:ARG:HH11	2.16	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:GLN:OE1	4:A:554:HOH:O[1_655]	1.97	0.23

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	433/544 (80%)	406 (94%)	25 (6%)	2 (0%)	34	63
1	B	433/544 (80%)	411 (95%)	20 (5%)	2 (0%)	34	63
All	All	866/1088 (80%)	817 (94%)	45 (5%)	4 (0%)	34	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	164	ALA
1	B	165	THR
1	A	343	LEU
1	A	202	GLY

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	363/472 (77%)	350 (96%)	13 (4%)	42	73
1	B	365/472 (77%)	351 (96%)	14 (4%)	40	71
All	All	728/944 (77%)	701 (96%)	27 (4%)	41	72

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ARG
1	A	113	ARG
1	A	114	GLN
1	A	134	GLN
1	A	180	PHE
1	A	195	GLN
1	A	200	SER
1	A	201	THR

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Mol	Chain	Res	Type
1	A	299	GLN
1	A	320	SER
1	A	370	ILE
1	A	396	PHE
1	A	436	ILE
1	B	113	ARG
1	B	114	GLN
1	B	123	GLN
1	B	180	PHE
1	B	195	GLN
1	B	223	GLU
1	B	269	LEU
1	B	277	ARG
1	B	281	ASN
1	B	299	GLN
1	B	379	GLU
1	B	384	GLU
1	B	396	PHE
1	B	412	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	GLN
1	A	195	GLN
1	A	270	ASN
1	A	303	GLN
1	A	355	GLN
1	A	423	GLN
1	B	41	HIS
1	B	53	GLN
1	B	114	GLN
1	B	118	ASN
1	B	134	GLN
1	B	162	HIS
1	B	195	GLN
1	B	270	ASN
1	B	281	ASN
1	B	303	GLN
1	B	335	GLN
1	B	355	GLN
1	B	360	GLN

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Mol	Chain	Res	Type
1	B	423	GLN

5.3.3   RNA (i)

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 carbohydrates in this entry.

5.6   Ligand geometry (i)

Of 6 ligands modelled in this entry, 4 are 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	#$|Z| > 2$
2	HP8	A	601	-	29,36,36	1.54	2 (6%)	38,54,54	2.40	12 (31%)
2	HP8	B	602	-	29,36,36	1.56	3 (10%)	38,54,54	2.43	9 (23%)

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	HP8	A	601	-	-	0/14/35/35	0/4/4/4
2	HP8	B	602	-	-	0/14/35/35	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	HP8	C21-NHS	-6.26	1.32	1.39
2	B	602	HP8	C21-NHS	-5.64	1.33	1.39
2	A	601	HP8	C3S-C2S	-2.56	1.37	1.39
2	B	602	HP8	C3S-C2S	-2.05	1.37	1.39
2	B	602	HP8	OS1-S	4.47	1.46	1.42

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	HP8	N3-C2-N1	-8.75	122.19	128.89
2	A	601	HP8	N3-C2-N1	-8.54	122.36	128.89
2	B	602	HP8	C1S-C2S-C3S	-5.41	116.61	120.14
2	B	602	HP8	C21-NHS-S	-5.33	117.19	123.35
2	A	601	HP8	C2'-C1'-N9	-5.25	106.27	114.29
2	A	601	HP8	C4-C5-N7	-4.41	105.43	109.48
2	B	602	HP8	OS2-S-NHS	-3.52	103.80	108.50
2	A	601	HP8	C21-NHS-S	-3.18	119.67	123.35
2	B	602	HP8	C2'-C1'-N9	-3.02	109.67	114.29
2	A	601	HP8	C1S-C2S-C3S	-2.89	118.25	120.14
2	A	601	HP8	OS2-S-OS1	-2.74	117.48	120.77
2	A	601	HP8	OS1-S-NHS	-2.67	104.93	108.50
2	A	601	HP8	C5S-C4S-C3S	-2.64	116.64	120.04
2	B	602	HP8	OS2-S-OS1	-2.42	117.87	120.77
2	A	601	HP8	C1S-C21-NHS	2.17	118.52	115.83
2	A	601	HP8	O5'-S-OS2	2.20	112.47	105.66
2	B	602	HP8	C6S-C1S-C2S	2.48	121.34	118.70
2	B	602	HP8	O9-C21-NHS	3.26	123.81	120.80
2	A	601	HP8	C4'-O4'-C1'	3.26	113.31	109.72
2	B	602	HP8	C4S-C3S-C2S	4.57	124.13	120.09
2	A	601	HP8	C4S-C3S-C2S	5.12	124.62	120.09

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
2	B	602	HP8	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	435/544 (79%)	-0.08	11 (2%)	61	61	41, 55, 81, 96	0
1	B	435/544 (79%)	-0.12	6 (1%)	78	77	41, 56, 80, 93	0
All	All	870/1088 (79%)	-0.10	17 (1%)	68	69	41, 55, 80, 96	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	GLY	5.0
1	B	180	PHE	4.1
1	A	412	GLU	3.5
1	A	376	GLN	3.5
1	A	426	PRO	3.5
1	B	426	PRO	3.4
1	A	142	GLN	2.9
1	A	180	PHE	2.6
1	B	269	LEU	2.5
1	B	412	GLU	2.5
1	A	200	SER	2.5
1	A	203	THR	2.3
1	B	179	THR	2.3
1	A	167	PHE	2.2
1	A	404	GLU	2.2
1	A	165	THR	2.2
1	B	149	ASP	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
3	CA	B	544	1/1	0.95	0.15	0.05	62,62,62,62	0
2	HP8	B	602	33/33	0.98	0.15	-0.20	44,48,51,55	0
2	HP8	A	601	33/33	0.98	0.15	-0.36	36,40,49,55	0
3	CA	A	543	1/1	0.97	0.12	-0.48	53,53,53,53	0
3	CA	A	544	1/1	0.96	0.14	-0.60	56,56,56,56	0
3	CA	B	543	1/1	0.95	0.12	-	89,89,89,89	0

6.5 Other polymers (i)

There are no such residues in this entry.