



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:51 PM GMT

PDB ID : 1CT9
Title : CRYSTAL STRUCTURE OF ASPARAGINE SYNTHETASE B FROM ES-
CHERICHIA COLI
Authors : Larsen, T.M.; Boehlein, S.K.; Schuster, S.M.; Richards, N.G.J.; Thoden, J.B.;
Holden, H.M.; Rayment, I.
Deposited on : 1999-08-20
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

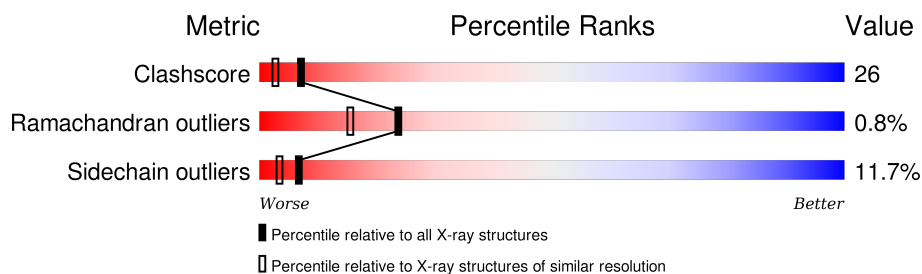
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	553	
1	B	553	
1	C	553	
1	D	553	

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
4	AMP	C	1114	-	-	X	-
4	AMP	D	1121	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16980 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.

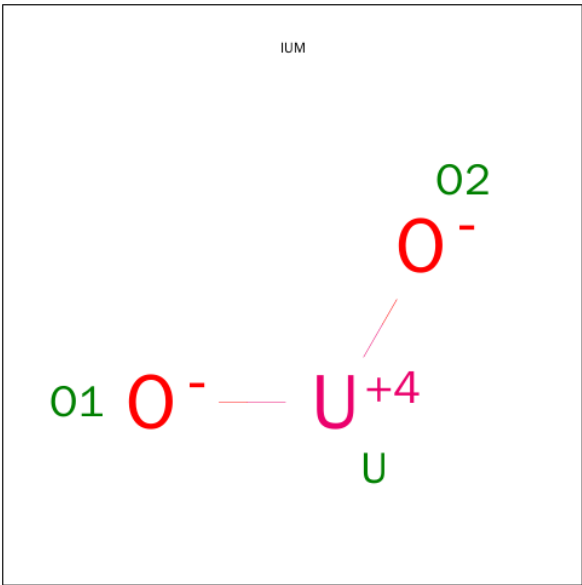
- Molecule 1 is a protein called ASPARAGINE SYNTHETASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	0
			3966	2530	671	745	20			
1	B	495	Total	C	N	O	S	0	0	0
			3942	2518	665	739	20			
1	C	495	Total	C	N	O	S	0	0	0
			3942	2518	665	739	20			
1	D	495	Total	C	N	O	S	0	0	0
			3930	2507	664	739	20			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	CYS	ENGINEERED	UNP P22106
B	1	ALA	CYS	ENGINEERED	UNP P22106
C	1	ALA	CYS	ENGINEERED	UNP P22106
D	1	ALA	CYS	ENGINEERED	UNP P22106

- Molecule 2 is URANYL (VI) ION (three-letter code: IUM) (formula: O₂U).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total U 1 1	0	0
2	A	1	Total O U 2 1 1	0	0
2	A	1	Total U 1 1	0	0
2	A	1	Total U 1 1	0	0
2	B	1	Total U 1 1	0	0
2	B	1	Total U 1 1	0	0
2	B	1	Total U 1 1	0	0
2	B	1	Total U 1 1	0	0
2	C	1	Total U 1 1	0	0
2	C	1	Total U 1 1	0	0
2	C	1	Total U 1 1	0	0
2	C	1	Total U 1 1	0	0
2	D	1	Total O U 2 1 1	0	0
2	D	1	Total U 1 1	0	0

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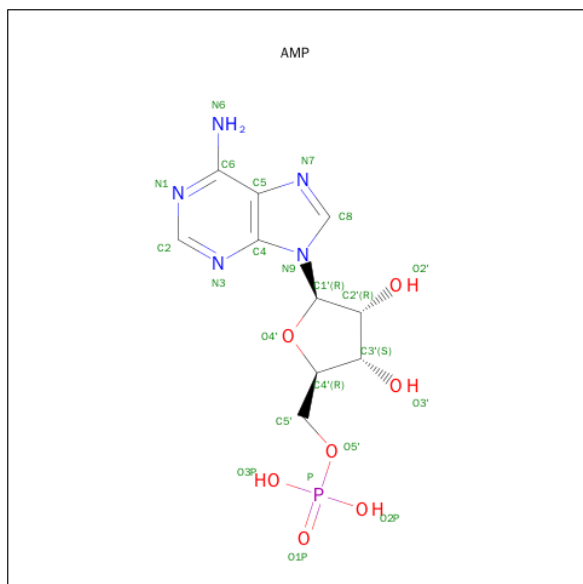
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	U	0	0
			1	1		
2	D	1	Total	U	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



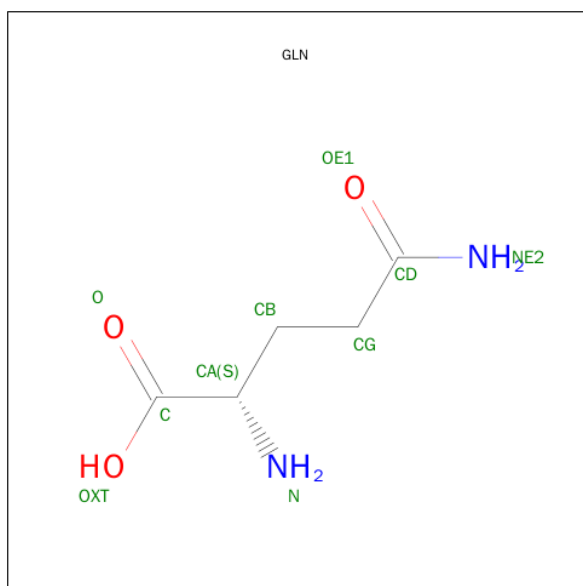
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 5 is GLUTAMINE (three-letter code: GLN) (formula: C₅H₁₀N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			10	5	2	3		
5	B	1	Total	C	N	O	0	0
			10	5	2	3		
5	C	1	Total	C	N	O	0	0
			10	5	2	3		
5	D	1	Total	C	N	O	0	0
			10	5	2	3		

- Molecule 6 is water.

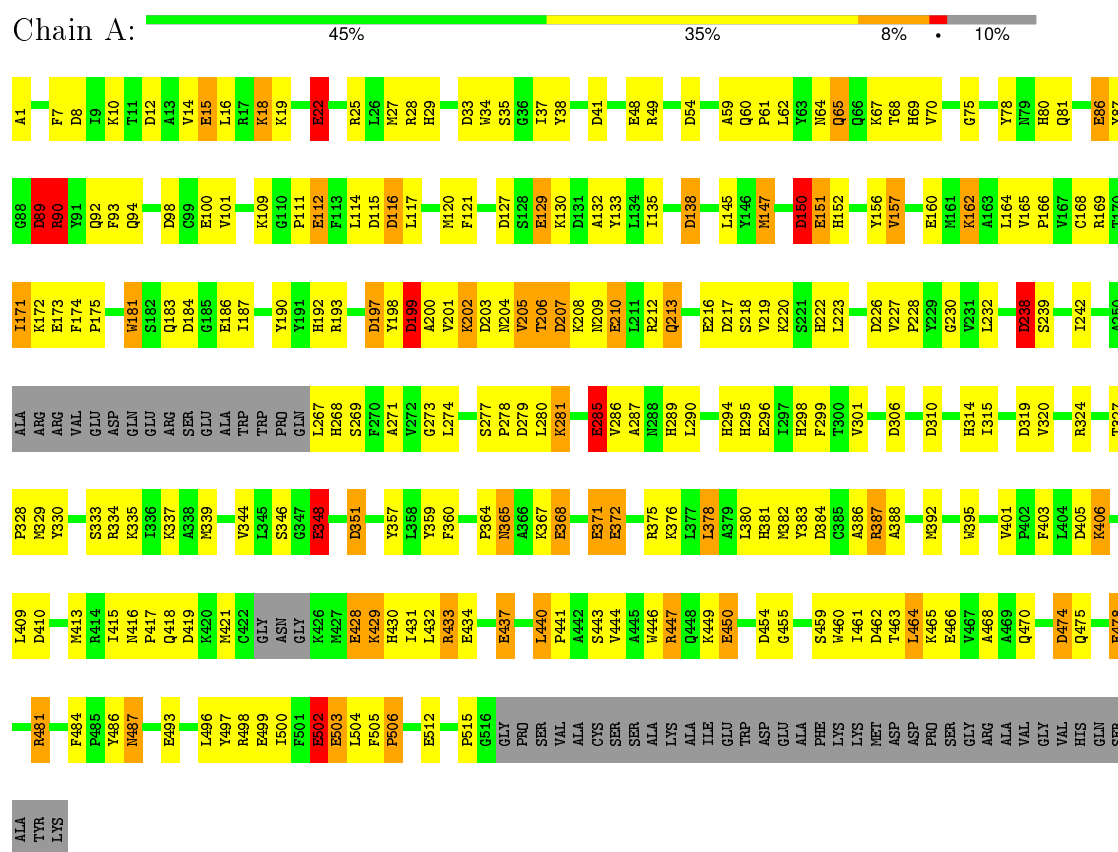
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	292	Total	O	0	0
			292	292		
6	B	235	Total	O	0	0
			235	235		
6	C	223	Total	O	0	0
			223	223		
6	D	296	Total	O	0	0
			296	296		

3 Residue-property plots

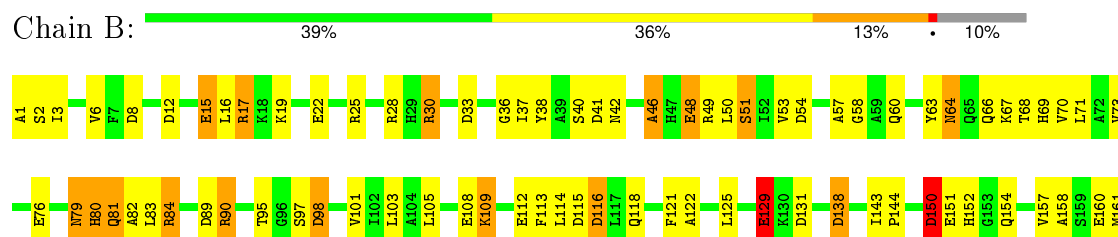
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

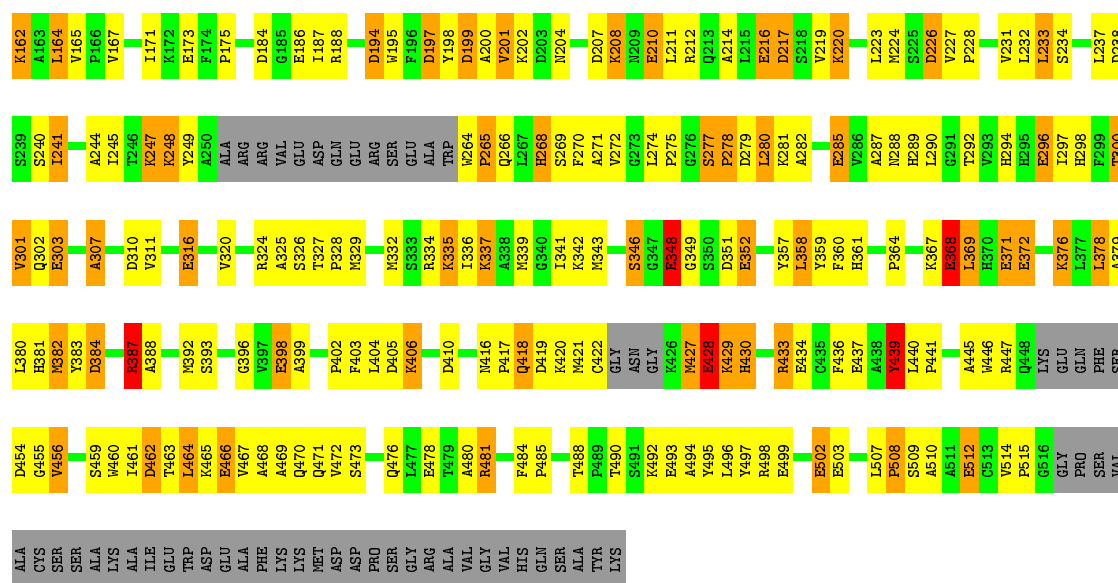
Note EDS was not executed.

• Molecule 1: ASPARAGINE SYNTHETASE B



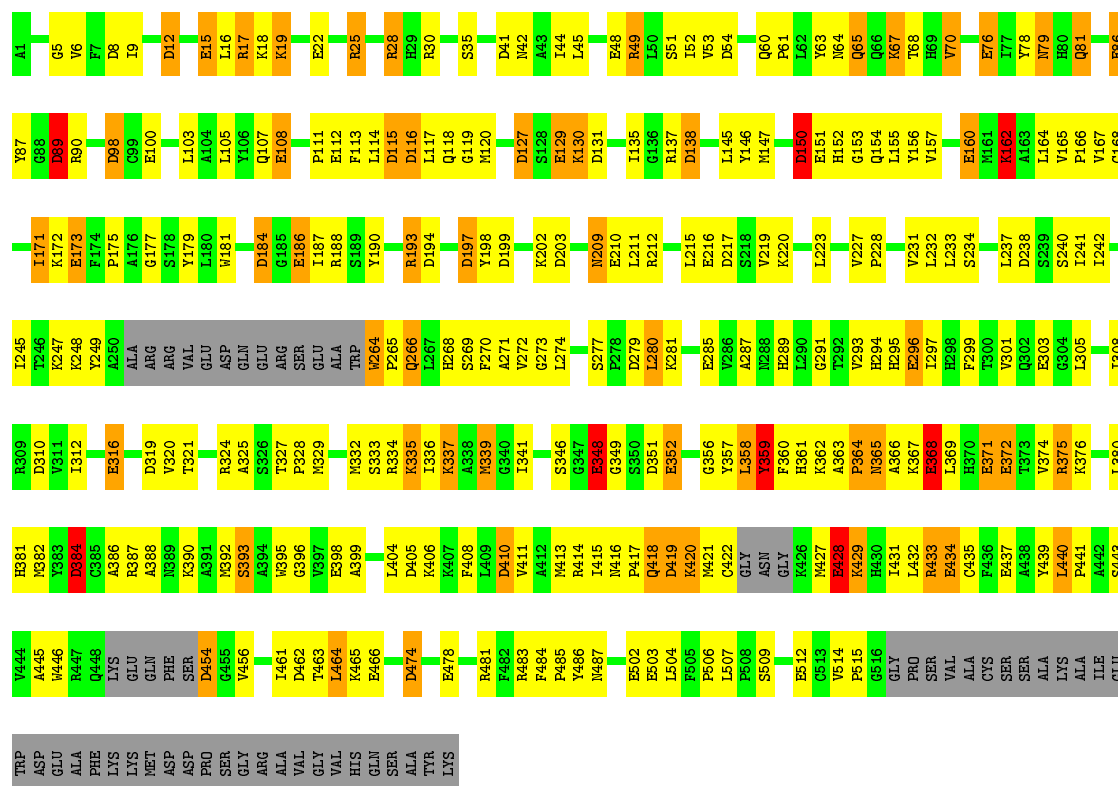
• Molecule 1: ASPARAGINE SYNTHETASE B





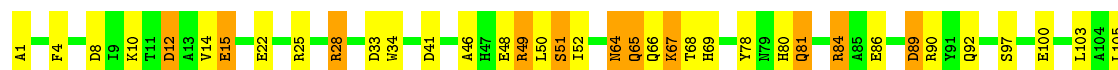
• Molecule 1: ASPARAGINE SYNTHETASE B

Chain C: 41% 37% 10% 10%



• Molecule 1: ASPARAGINE SYNTHETASE B

Chain D: 48% 31% 9% 10%



[illegible]

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.93 Å 127.10 Å 204.51 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00	Depositor
% Data completeness (in resolution range)	99.0 (30.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.197 , 0.297	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16980	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, IUM, CL

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	1.02	24/4060 (0.6%)	1.48	66/5493 (1.2%)
1	B	1.04	32/4037 (0.8%)	1.50	67/5466 (1.2%)
1	C	1.01	33/4037 (0.8%)	1.44	63/5466 (1.2%)
1	D	1.06	30/4022 (0.7%)	1.49	67/5443 (1.2%)
All	All	1.03	119/16156 (0.7%)	1.48	263/21868 (1.2%)

The worst 5 of 119 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	478	GLU	CD-OE2	9.23	1.35	1.25
1	D	398	GLU	CD-OE2	8.52	1.35	1.25
1	B	466	GLU	CD-OE2	7.96	1.34	1.25
1	D	48	GLU	CD-OE2	7.61	1.34	1.25
1	B	296	GLU	CD-OE2	7.58	1.33	1.25

The worst 5 of 263 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	150	ASP	CB-CG-OD2	-14.12	105.59	118.30
1	A	150	ASP	CB-CG-OD2	-13.62	106.05	118.30
1	C	150	ASP	CB-CG-OD2	-10.79	108.59	118.30
1	D	194	ASP	CB-CG-OD1	10.22	127.50	118.30
1	B	238	ASP	CB-CG-OD2	-10.11	109.20	118.30

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	3966	0	3862	192	0
1	B	3942	0	3828	247	0
1	C	3942	0	3827	204	0
1	D	3930	0	3818	186	0
2	A	5	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	5	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	23	0	11	5	0
4	B	23	0	12	3	0
4	C	23	0	11	7	0
4	D	23	0	12	8	0
5	A	10	0	7	2	0
5	B	10	0	7	4	0
5	C	10	0	7	1	0
5	D	10	0	7	2	0
6	A	292	0	0	8	0
6	B	235	0	0	13	0
6	C	223	0	0	7	0
6	D	296	0	0	19	0
All	All	16980	0	15409	822	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 26.

The worst 5 of 822 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:364:PRO:HG2	1:C:368:GLU:HG2	1.26	1.17
1:D:472:VAL:HB	1:D:492:LYS:HG2	1.22	1.12
1:D:364:PRO:HG2	1:D:368:GLU:HG2	1.40	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:THR:HG22	1:B:303:GLU:H	1.29	0.96
1:D:64:ASN:HB3	1:D:67:LYS:N	1.80	0.95

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	491/553 (89%)	465 (95%)	24 (5%)	2 (0%)	39	33
1	B	487/553 (88%)	449 (92%)	31 (6%)	7 (1%)	14	6
1	C	487/553 (88%)	450 (92%)	33 (7%)	4 (1%)	24	15
1	D	487/553 (88%)	467 (96%)	18 (4%)	2 (0%)	39	33
All	All	1952/2212 (88%)	1831 (94%)	106 (5%)	15 (1%)	24	15

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	428	GLU
1	C	266	GLN
1	A	138	ASP
1	B	265	PRO
1	B	460	TRP

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	418/462 (90%)	371 (89%)	47 (11%)	7	4
1	B	414/462 (90%)	358 (86%)	56 (14%)	5	2
1	C	414/462 (90%)	364 (88%)	50 (12%)	6	3
1	D	412/462 (89%)	371 (90%)	41 (10%)	9	5
All	All	1658/1848 (90%)	1464 (88%)	194 (12%)	7	3

5 of 194 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	406	LYS
1	C	65	GLN
1	D	341	ILE
1	B	429	LYS
1	B	473	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	288	ASN
1	C	42	ASN
1	D	288	ASN
1	B	302	GLN
1	B	361	HIS

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

Of 28 ligands modelled in this entry, 4 are monoatomic and 14 are modelled with single atom - leaving 10 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
4	AMP	A	1100	-	20,25,25	1.25	3 (15%)	22,38,38	1.90	5 (22%)
2	IUM	A	1102	-	0,1,2	0.00	-	0,0,1	0.00	-
5	GLN	A	1106	-	6,9,9	1.61	1 (16%)	5,11,11	0.30	0
4	AMP	B	1107	2	20,25,25	1.26	3 (15%)	22,38,38	1.29	3 (13%)
5	GLN	B	1113	-	6,9,9	1.29	1 (16%)	5,11,11	0.30	0
4	AMP	C	1114	-	20,25,25	1.23	3 (15%)	22,38,38	2.02	5 (22%)
5	GLN	C	1120	-	6,9,9	1.34	1 (16%)	5,11,11	0.51	0
4	AMP	D	1121	2	20,25,25	1.01	2 (10%)	22,38,38	2.31	7 (31%)
2	IUM	D	1122	4	0,1,2	0.00	-	0,0,1	0.00	-
5	GLN	D	1127	-	6,9,9	1.34	1 (16%)	5,11,11	0.45	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	AMP	A	1100	-	-	0/6/26/26	0/3/3/3
2	IUM	A	1102	-	-	0/0/0/0	0/0/0/0
5	GLN	A	1106	-	-	0/5/9/9	0/0/0/0
4	AMP	B	1107	2	-	0/6/26/26	0/3/3/3
5	GLN	B	1113	-	-	0/5/9/9	0/0/0/0
4	AMP	C	1114	-	-	0/6/26/26	0/3/3/3
5	GLN	C	1120	-	-	0/5/9/9	0/0/0/0
4	AMP	D	1121	2	-	0/6/26/26	0/3/3/3
2	IUM	D	1122	4	-	0/0/0/0	0/0/0/0
5	GLN	D	1127	-	-	0/5/9/9	0/0/0/0

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1106	GLN	CA-N	-3.81	1.33	1.48
5	B	1113	GLN	CA-N	-3.11	1.35	1.48
5	C	1120	GLN	CA-N	-3.10	1.35	1.48
5	D	1127	GLN	CA-N	-2.99	1.36	1.48
4	B	1107	AMP	C2-N1	2.31	1.38	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1121	AMP	O2P-P-O5'	-5.28	91.36	106.56
4	C	1114	AMP	C2'-C3'-C4'	-5.25	91.82	102.61
4	D	1121	AMP	C2'-C3'-C4'	-4.24	93.90	102.61
4	D	1121	AMP	N6-C6-N1	-4.00	110.63	119.20
4	D	1121	AMP	C4'-O4'-C1'	-3.76	105.59	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1100	AMP	5	0
5	A	1106	GLN	2	0
4	B	1107	AMP	3	0
5	B	1113	GLN	4	0
4	C	1114	AMP	7	0
5	C	1120	GLN	1	0
4	D	1121	AMP	8	0
5	D	1127	GLN	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.