



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 03:47 PM GMT

PDB ID : 1C3O
Title : CRYSTAL STRUCTURE OF THE CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT MUTANT C269S WITH BOUND GLUTAMINE
Authors : Thoden, J.B.; Huang, X.; Raushel, F.M.; Holden, H.M.
Deposited on : 1999-07-28
Resolution : 2.10 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

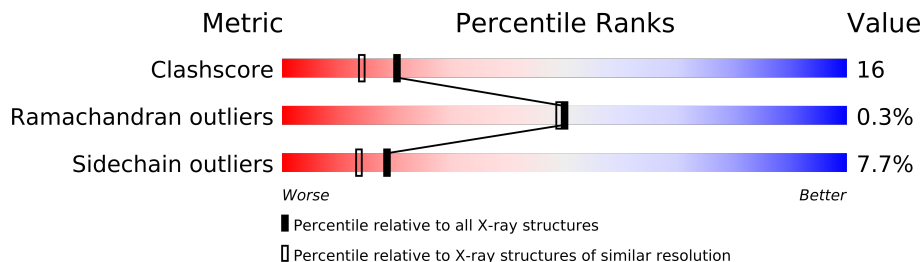
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1073	
1	C	1073	
1	E	1073	
1	G	1073	
2	B	382	
2	D	382	
2	F	382	
2	H	382	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 48477 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CARBAMOYL PHOSPHATE SYNTHETASE: LARGE SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1058	Total	C	N	O	S	0	6	0
			8195	5146	1433	1570	46			
1	C	1058	Total	C	N	O	S	0	7	0
			8192	5144	1428	1575	45			
1	E	1058	Total	C	N	O	S	0	10	0
			8211	5155	1431	1580	45			
1	G	1058	Total	C	N	O	S	0	4	0
			8180	5135	1425	1574	46			

- Molecule 2 is a protein called CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	379	Total	C	N	O	S	0	0	0
			2895	1825	508	553	9			
2	D	379	Total	C	N	O	S	0	0	0
			2895	1825	508	553	9			
2	F	379	Total	C	N	O	S	0	0	0
			2895	1825	508	553	9			
2	H	379	Total	C	N	O	S	0	0	0
			2895	1825	508	553	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	269	SER	CYS	MUTATION	UNP P00907
D	269	SER	CYS	MUTATION	UNP P00907
F	269	SER	CYS	MUTATION	UNP P00907
H	269	SER	CYS	MUTATION	UNP P00907

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	3	Total Mn 3 3	0	0
3	A	3	Total Mn 3 3	0	0
3	C	3	Total Mn 3 3	0	0
3	E	3	Total Mn 3 3	0	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	7	Total K 7 7	0	0
4	D	1	Total K 1 1	0	0
4	E	7	Total K 7 7	0	0
4	H	1	Total K 1 1	0	0
4	B	1	Total K 1 1	0	0
4	C	7	Total K 7 7	0	0
4	A	7	Total K 7 7	0	0
4	F	1	Total K 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

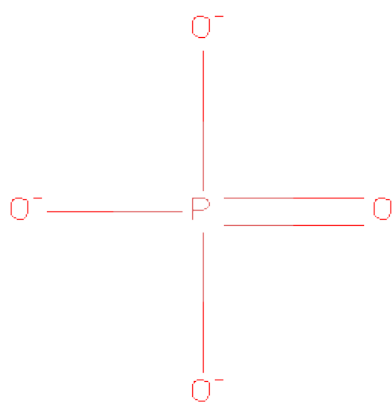
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	3	Total Cl 3 3	0	0
5	D	1	Total Cl 1 1	0	0
5	E	3	Total Cl 3 3	0	0
5	H	1	Total Cl 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	3	Total Cl 3 3	0	0

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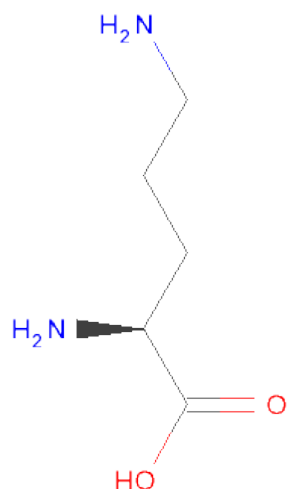
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Cl	0	0
			3	3		
5	F	1	Total	Cl	0	0
			1	1		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



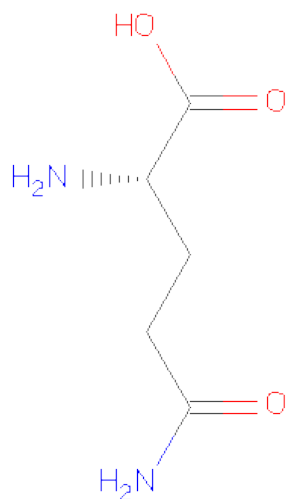
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	O	P	0	0
			5	4	1		
6	E	1	Total	O	P	0	0
			5	4	1		
6	G	1	Total	O	P	0	0
			5	4	1		
6	A	1	Total	O	P	0	0
			5	4	1		
6	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is L-ORNITHINE (three-letter code: ORN) (formula: C₅H₁₂N₂O₂).



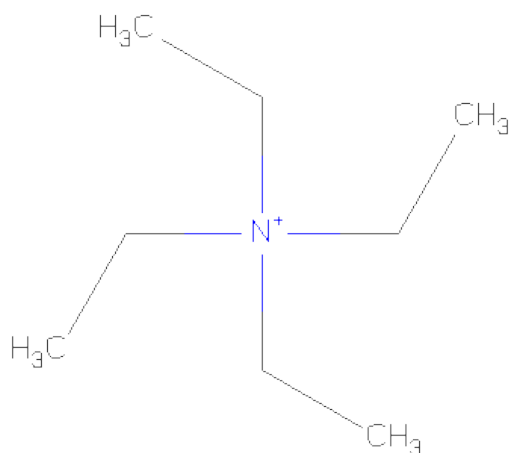
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			9	5	2	2		
7	E	1	Total	C	N	O	0	0
			9	5	2	2		
7	G	1	Total	C	N	O	0	0
			9	5	2	2		
7	A	1	Total	C	N	O	0	0
			9	5	2	2		

- Molecule 8 is GLUTAMINE (three-letter code: GLN) (formula: C₅H₁₀N₂O₃).



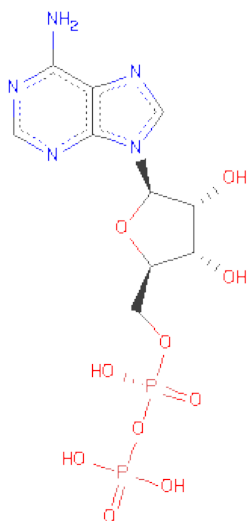
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	D	1	Total	C	N	O	0	0
			10	5	2	3		
8	C	1	Total	C	N	O	0	0
			10	5	2	3		
8	F	1	Total	C	N	O	0	0
			10	5	2	3		
8	E	1	Total	C	N	O	0	0
			10	5	2	3		
8	H	1	Total	C	N	O	0	0
			10	5	2	3		
8	G	1	Total	C	N	O	0	0
			10	5	2	3		
8	B	1	Total	C	N	O	0	0
			10	5	2	3		
8	A	1	Total	C	N	O	0	0
			10	5	2	3		

- Molecule 9 is TETRAETHYLAMMONIUM ION (three-letter code: NET) (formula: $C_8H_{20}N$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	N	0	0
			9	8	1		
9	E	1	Total	C	N	0	0
			9	8	1		
9	G	1	Total	C	N	0	0
			9	8	1		
9	A	1	Total	C	N	0	0
			9	8	1		

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
10	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	699	Total	O	0	0
			699	699		
11	B	231	Total	O	0	0
			231	231		

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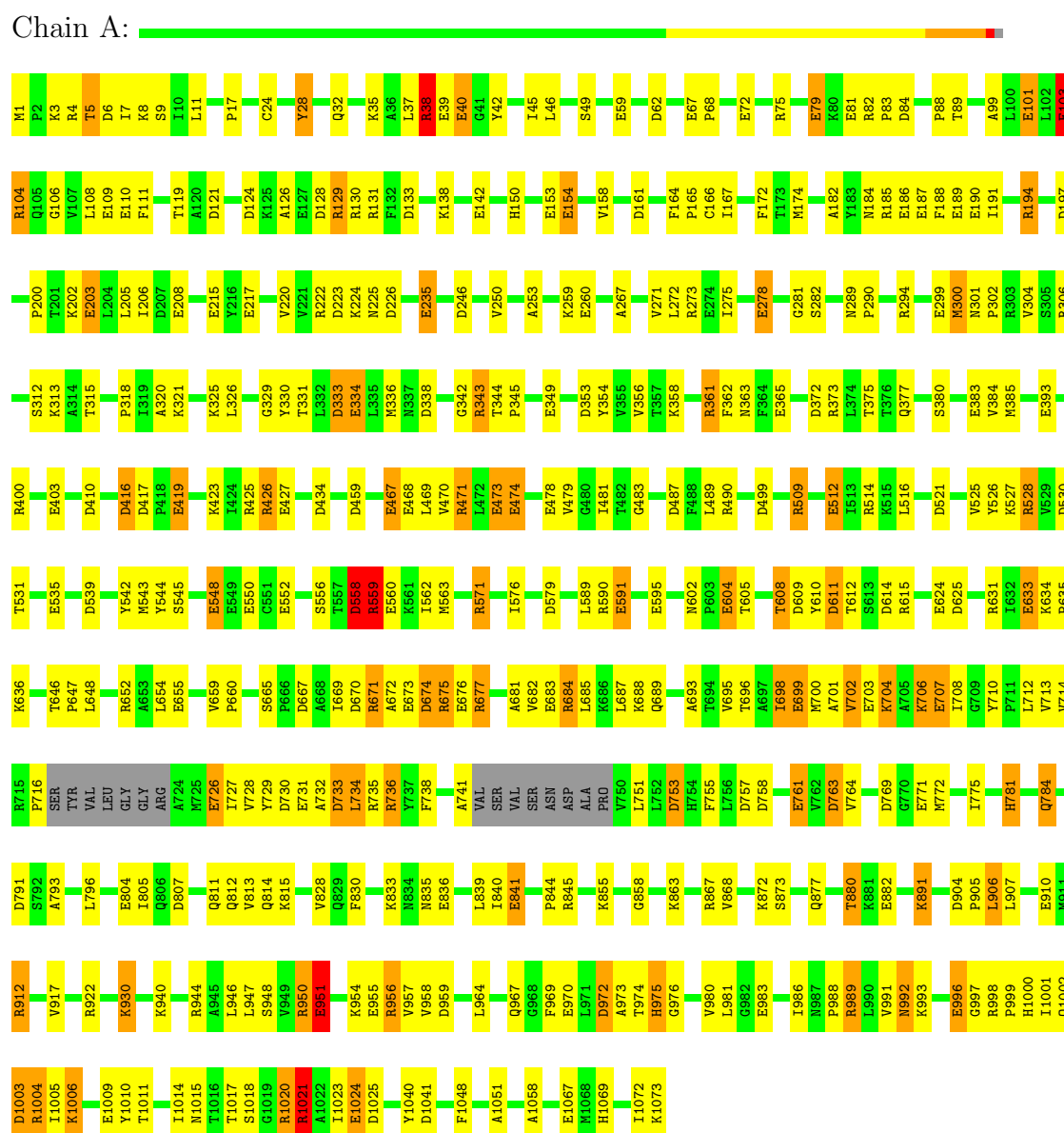
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	C	706	Total 706	O 706	0	0
11	D	250	Total 250	O 250	0	0
11	E	754	Total 754	O 754	0	0
11	F	231	Total 231	O 231	0	0
11	G	622	Total 622	O 622	0	0
11	H	173	Total 173	O 173	0	0

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.

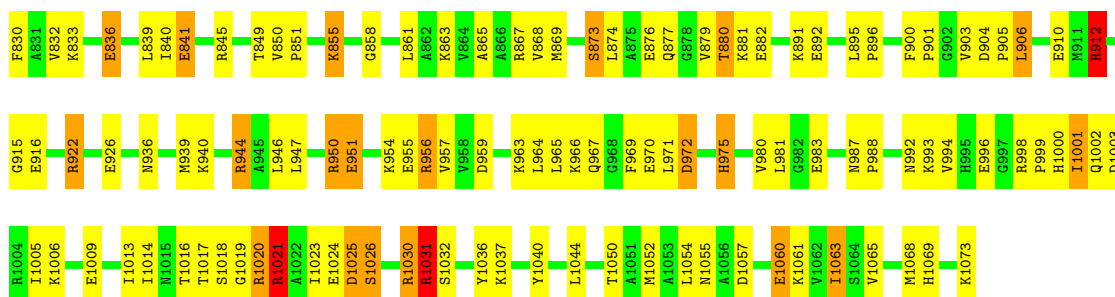
Note EDS was not executed.

• Molecule 1: CARBAMOYL PHOSPHATE SYNTHETASE: LARGE SUBUNIT



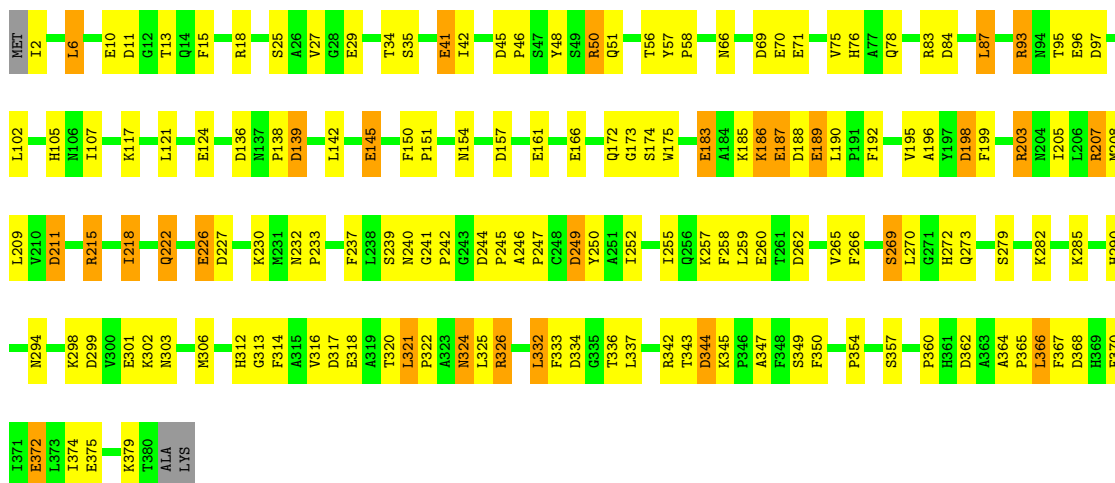
• Molecule 1: CARBAMOYL PHOSPHATE SYNTHETASE: LARGE SUBUNIT





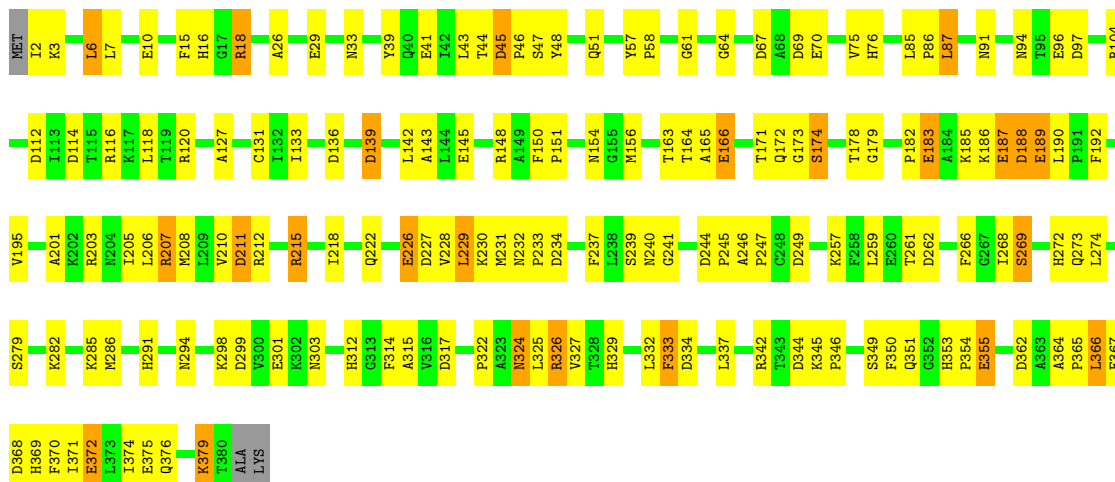
• Molecule 2: CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT

Chain B:



• Molecule 2: CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT

Chain D:



• Molecule 2: CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT

Chain F:



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	152.50Å 164.40Å 332.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10	Depositor
% Data completeness (in resolution range)	98.4 (30.00-2.10)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.188 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	48477	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

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: ADP, CL, K, MN, ORN, NET, PO4

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	1.04	72/8345 (0.9%)	1.41	128/11276 (1.1%)
1	C	1.04	77/8346 (0.9%)	1.38	112/11281 (1.0%)
1	E	1.05	68/8377 (0.8%)	1.40	124/11320 (1.1%)
1	G	1.01	79/8322 (0.9%)	1.39	118/11249 (1.0%)
2	B	0.90	18/2957 (0.6%)	1.32	40/4016 (1.0%)
2	D	0.94	15/2957 (0.5%)	1.38	44/4016 (1.1%)
2	F	0.92	15/2957 (0.5%)	1.37	43/4016 (1.1%)
2	H	0.91	18/2957 (0.6%)	1.33	35/4016 (0.9%)
All	All	1.01	362/45218 (0.8%)	1.39	644/61190 (1.1%)

The worst 5 of 362 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	419[A]	GLU	CD-OE2	-10.50	1.14	1.25
1	C	419[B]	GLU	CD-OE2	-10.50	1.14	1.25
1	C	110	GLU	CD-OE1	-10.46	1.14	1.25
1	C	1009	GLU	CD-OE2	9.29	1.35	1.25
1	A	109	GLU	CD-OE2	8.80	1.35	1.25

The worst 5 of 644 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	514	ARG	NE-CZ-NH2	-12.65	113.97	120.30
1	G	75	ARG	NE-CZ-NH2	-12.58	114.01	120.30
1	G	265	ARG	NE-CZ-NH1	12.54	126.57	120.30
2	D	120	ARG	NE-CZ-NH1	12.14	126.37	120.30
1	E	343	ARG	NE-CZ-NH1	11.54	126.07	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8195	0	8247	239	0
1	C	8192	0	8230	247	0
1	E	8211	0	8245	225	0
1	G	8180	0	8214	291	0
2	B	2895	0	2861	91	0
2	D	2895	0	2861	98	0
2	F	2895	0	2861	107	0
2	H	2895	0	2861	134	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
3	E	3	0	0	0	0
3	G	3	0	0	0	0
4	A	7	0	0	0	0
4	B	1	0	0	0	0
4	C	7	0	0	0	0
4	D	1	0	0	0	0
4	E	7	0	0	0	0
4	F	1	0	0	0	0
4	G	7	0	0	0	0
4	H	1	0	0	0	0
5	A	3	0	0	1	0
5	B	1	0	0	0	0
5	C	3	0	0	2	0
5	D	1	0	0	0	0
5	E	3	0	0	0	0
5	F	1	0	0	0	0
5	G	3	0	0	3	0
5	H	1	0	0	0	0
6	A	5	0	0	0	0
6	C	5	0	0	0	0
6	E	10	0	0	0	0
6	G	5	0	0	0	0
7	A	9	0	11	1	0
7	C	9	0	11	1	0
7	E	9	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	9	0	11	0	0
8	A	10	0	7	0	0
8	B	10	0	7	3	0
8	C	10	0	7	0	0
8	D	10	0	7	2	0
8	E	10	0	7	0	0
8	F	10	0	7	3	0
8	G	10	0	7	0	0
8	H	10	0	7	2	0
9	A	9	0	20	0	0
9	C	9	0	20	1	0
9	E	9	0	20	2	0
9	G	9	0	20	0	0
10	A	54	0	24	0	0
10	C	54	0	24	1	0
10	E	54	0	24	4	0
10	G	54	0	24	2	0
11	A	699	0	0	14	0
11	B	231	0	0	4	0
11	C	706	0	0	19	0
11	D	250	0	0	5	0
11	E	754	0	0	23	0
11	F	231	0	0	4	0
11	G	622	0	0	20	0
11	H	173	0	0	4	0
All	All	48477	0	44656	1411	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

The worst 5 of 1411 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:808:VAL:HA	1:E:811[B]:GLN:HE21	1.12	1.11
2:H:133:ILE:HD12	2:H:143:ALA:HB2	1.28	1.10
1:A:695:VAL:HG13	1:A:700:MET:HB3	1.36	1.08
1:C:695:VAL:HG11	1:C:701:ALA:HB2	1.38	1.04
2:H:187:GLU:HG2	2:H:215:ARG:HD2	1.35	1.03

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	1058/1073 (99%)	1004 (95%)	51 (5%)	3 (0%)	50	49
1	C	1059/1073 (99%)	1005 (95%)	50 (5%)	4 (0%)	43	39
1	E	1062/1073 (99%)	1004 (94%)	56 (5%)	2 (0%)	56	57
1	G	1056/1073 (98%)	991 (94%)	59 (6%)	6 (1%)	33	28
2	B	377/382 (99%)	362 (96%)	15 (4%)	0	100	100
2	D	377/382 (99%)	357 (95%)	18 (5%)	2 (0%)	38	33
2	F	377/382 (99%)	358 (95%)	19 (5%)	0	100	100
2	H	377/382 (99%)	353 (94%)	22 (6%)	2 (0%)	38	33
All	All	5743/5820 (99%)	5434 (95%)	290 (5%)	19 (0%)	50	49

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	558	ASP
1	E	954	LYS
1	G	558	ASP
1	G	873	SER
1	A	975	HIS

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	871/878 (99%)	810 (93%)	61 (7%)	21	17
1	C	872/878 (99%)	805 (92%)	67 (8%)	18	13
1	E	875/878 (100%)	817 (93%)	58 (7%)	24	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	869/878 (99%)	796 (92%)	73 (8%)	16	10
2	B	308/310 (99%)	277 (90%)	31 (10%)	11	6
2	D	308/310 (99%)	289 (94%)	19 (6%)	26	21
2	F	308/310 (99%)	280 (91%)	28 (9%)	14	8
2	H	308/310 (99%)	283 (92%)	25 (8%)	17	12
All	All	4719/4752 (99%)	4357 (92%)	362 (8%)	18	13

5 of 362 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	154	ASN
1	E	591	GLU
1	G	1061	LYS
2	D	257	LYS
1	E	103	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	154	ASN
1	E	689	GLN
1	G	1035	GLN
2	D	222	GLN
1	E	105	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 89 ligands modelled in this entry, 60 are monoatomic - leaving 29 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$
10	ADP	A	4000	3	29,29,29	1.24	3 (10%)	45,45,45	0.96	0
6	PO4	A	4006	3,4	4,4,4	1.39	0	6,6,6	0.34	0
10	ADP	A	4007	3,4	29,29,29	1.15	2 (6%)	45,45,45	1.15	4 (8%)
7	ORN	A	4011	-	8,8,8	0.94	0	9,9,9	1.45	1 (11%)
8	GLN	A	4013	-	9,9,9	1.22	1 (11%)	11,11,11	1.03	0
9	NET	A	4014	-	8,8,8	0.63	0	10,10,10	0.50	0
8	GLN	B	4012	-	9,9,9	1.08	1 (11%)	11,11,11	1.73	4 (36%)
10	ADP	C	4023	3	29,29,29	1.21	3 (10%)	45,45,45	0.93	2 (4%)
6	PO4	C	4028	3,4	4,4,4	1.76	2 (50%)	6,6,6	0.35	0
10	ADP	C	4029	3,4	29,29,29	1.44	4 (13%)	45,45,45	1.19	5 (11%)
7	ORN	C	4033	-	8,8,8	0.98	1 (12%)	9,9,9	1.10	0
8	GLN	C	4035	-	9,9,9	1.16	1 (11%)	11,11,11	1.09	1 (9%)
9	NET	C	4036	-	8,8,8	0.49	0	10,10,10	0.42	0
8	GLN	D	4034	-	9,9,9	1.21	1 (11%)	11,11,11	2.25	3 (27%)
10	ADP	E	4045	3	29,29,29	1.23	3 (10%)	45,45,45	1.20	2 (4%)
6	PO4	E	4050	3,4	4,4,4	1.40	0	6,6,6	0.34	0
10	ADP	E	4051	3,4	29,29,29	1.18	4 (13%)	45,45,45	0.99	3 (6%)
7	ORN	E	4055	-	8,8,8	0.92	0	9,9,9	0.67	0
8	GLN	E	4057	-	9,9,9	1.28	1 (11%)	11,11,11	1.45	3 (27%)
9	NET	E	4058	-	8,8,8	0.49	0	10,10,10	0.67	0
6	PO4	E	4067	-	4,4,4	0.71	0	6,6,6	0.31	0
8	GLN	F	4056	-	9,9,9	1.35	2 (22%)	11,11,11	1.73	3 (27%)
10	ADP	G	4068	3	29,29,29	1.10	2 (6%)	45,45,45	1.28	7 (15%)
6	PO4	G	4073	3,4	4,4,4	1.13	0	6,6,6	0.34	0
10	ADP	G	4074	3,4	29,29,29	1.35	5 (17%)	45,45,45	1.07	2 (4%)
7	ORN	G	4078	-	8,8,8	0.69	0	9,9,9	1.05	1 (11%)
8	GLN	G	4080	-	9,9,9	1.23	1 (11%)	11,11,11	0.87	0
9	NET	G	4081	-	8,8,8	0.60	0	10,10,10	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GLN	H	4079	-	9,9,9	1.18	1 (11%)	11,11,11	1.60	1 (9%)

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
10	ADP	A	4000	3	-	0/16/32/32	0/1/3/3
6	PO4	A	4006	3,4	-	0/0/0/0	0/0/0/0
10	ADP	A	4007	3,4	-	0/16/32/32	0/1/3/3
7	ORN	A	4011	-	-	0/8/8/8	0/0/0/0
8	GLN	A	4013	-	-	0/9/9/9	0/0/0/0
9	NET	A	4014	-	-	0/12/12/12	0/0/0/0
8	GLN	B	4012	-	-	0/9/9/9	0/0/0/0
10	ADP	C	4023	3	-	0/16/32/32	0/1/3/3
6	PO4	C	4028	3,4	-	0/0/0/0	0/0/0/0
10	ADP	C	4029	3,4	-	0/16/32/32	0/1/3/3
7	ORN	C	4033	-	-	0/8/8/8	0/0/0/0
8	GLN	C	4035	-	-	0/9/9/9	0/0/0/0
9	NET	C	4036	-	-	0/12/12/12	0/0/0/0
8	GLN	D	4034	-	-	0/9/9/9	0/0/0/0
10	ADP	E	4045	3	-	0/16/32/32	0/1/3/3
6	PO4	E	4050	3,4	-	0/0/0/0	0/0/0/0
10	ADP	E	4051	3,4	-	0/16/32/32	0/1/3/3
7	ORN	E	4055	-	-	0/8/8/8	0/0/0/0
8	GLN	E	4057	-	-	0/9/9/9	0/0/0/0
9	NET	E	4058	-	-	0/12/12/12	0/0/0/0
6	PO4	E	4067	-	-	0/0/0/0	0/0/0/0
8	GLN	F	4056	-	-	0/9/9/9	0/0/0/0
10	ADP	G	4068	3	-	0/16/32/32	0/1/3/3
6	PO4	G	4073	3,4	-	0/0/0/0	0/0/0/0
10	ADP	G	4074	3,4	-	0/16/32/32	0/1/3/3
7	ORN	G	4078	-	-	0/8/8/8	0/0/0/0
8	GLN	G	4080	-	-	0/9/9/9	0/0/0/0
9	NET	G	4081	-	-	0/12/12/12	0/0/0/0
8	GLN	H	4079	-	-	0/9/9/9	0/0/0/0

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	4029	ADP	PB-O3A	4.78	1.68	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	G	4074	ADP	O3'-C3'	3.63	1.51	1.43
10	C	4029	ADP	O3'-C3'	3.52	1.51	1.43
10	E	4051	ADP	PB-O3A	3.49	1.66	1.60
10	A	4000	ADP	PA-O3A	-3.31	1.53	1.59

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	4034	GLN	CG-CB-CA	-5.17	104.78	114.43
10	E	4045	ADP	O4'-C1'-N9	4.37	112.50	108.44
8	F	4056	GLN	CG-CB-CA	-3.77	107.39	114.43
10	C	4029	ADP	O4'-C1'-N9	-3.75	104.95	108.44
8	D	4034	GLN	CB-CA-C	-3.57	102.53	110.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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