



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:01 AM GMT

PDB ID : 3D2M
Title : Crystal structure of N-acetylglutamate synthase from *Neisseria gonorrhoeae*
complexed with coenzyme A and L-glutamate
Authors : Shi, D.; Min, L.; Jin, Z.; Allewell, N.M.; Tuchman, M.
Deposited on : 2008-05-08
Resolution : 2.21 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

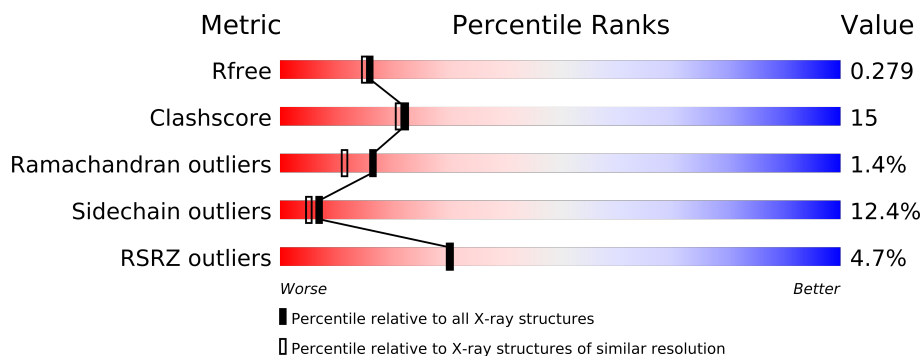
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
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 2.21 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}	66092	3340 (2.24-2.20)
Clashscore	79885	4208 (2.24-2.20)
Ramachandran outliers	78287	4135 (2.24-2.20)
Sidechain outliers	78261	4136 (2.24-2.20)
RSRZ outliers	66119	3341 (2.24-2.20)

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.

Mol	Chain	Length	Quality of chain
1	A	456	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3366 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.

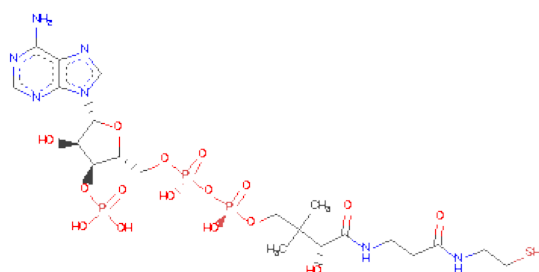
- Molecule 1 is a protein called Putative acetylglutamate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3227	2012	595	611	9			

There are 23 discrepancies between the modelled and reference sequences:

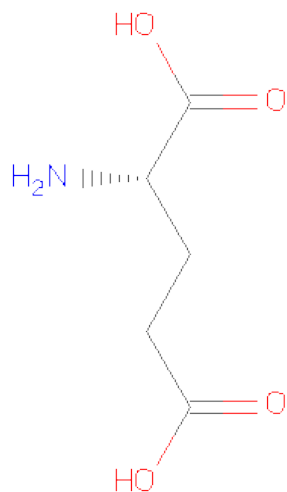
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q5FAK7
A	-18	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-17	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-16	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-15	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-14	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-13	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-12	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-11	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-10	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-9	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-8	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-7	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-6	LEU	-	EXPRESSION TAG	UNP Q5FAK7
A	-5	VAL	-	EXPRESSION TAG	UNP Q5FAK7
A	-4	PRO	-	EXPRESSION TAG	UNP Q5FAK7
A	-3	ARG	-	EXPRESSION TAG	UNP Q5FAK7
A	-2	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-1	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	0	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	312	ILE	VAL	ENGINEERED	UNP Q5FAK7
A	336	ASN	ASP	ENGINEERED	UNP Q5FAK7
A	427	SER	PRO	ENGINEERED	UNP Q5FAK7

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	
			48	21	7	16	3	1	

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O		
			10	5	1	4	0	0

- Molecule 4 is water.

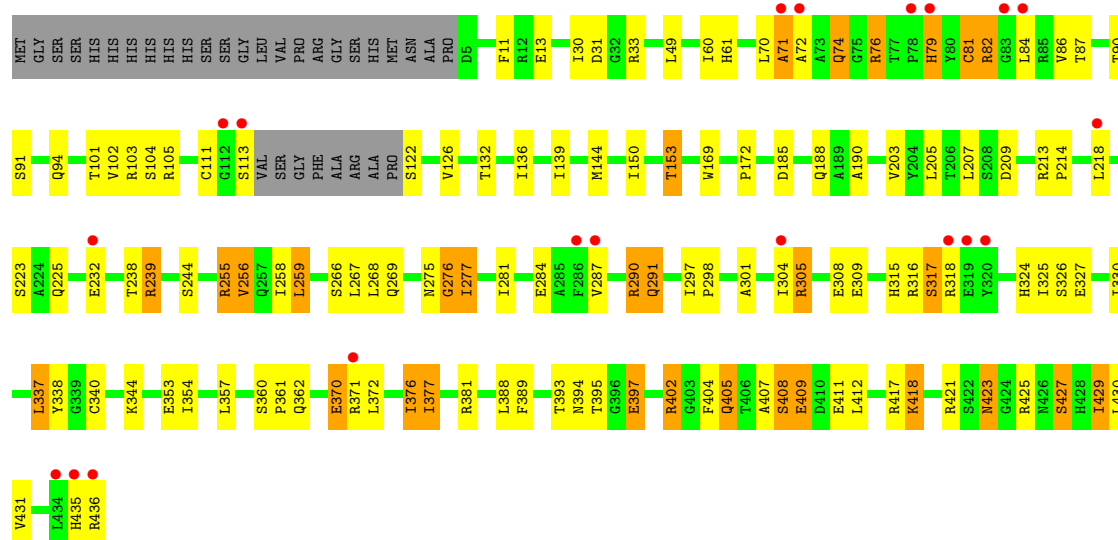
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	81	Total	O	0	0
			81	81		

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: Putative acetylglutamate synthase

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 1 2	Depositor
Cell constants a, b, c, α , β , γ	98.80Å 98.80Å 90.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.21 49.40 – 2.21	Depositor EDS
% Data completeness (in resolution range)	96.7 (20.00-2.21) 96.7 (49.40-2.21)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.229 , 0.280 0.232 , 0.279	Depositor DCC
R_{free} test set	1247 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	49.0	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.5	EDS
Estimated twinning fraction	0.045 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 24540 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3366	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: COA

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	0.93	4/3280 (0.1%)	0.88	3/4433 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	79	HIS	CE1-NE2	15.24	1.67	1.32
1	A	79	HIS	CG-CD2	14.54	1.60	1.35
1	A	79	HIS	CG-ND1	9.90	1.60	1.38
1	A	232	GLU	CG-CD	5.08	1.59	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	259	LEU	CB-CG-CD2	-5.95	100.88	111.00
1	A	79	HIS	ND1-CG-CD2	5.45	116.43	108.80
1	A	79	HIS	CG-CD2-NE2	-5.25	99.23	109.20

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	3227	0	3208	96	0
2	A	48	0	32	2	0
3	A	10	0	5	2	0
4	A	81	0	0	5	0
All	All	3366	0	3245	97	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 15.

All (97) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:79:HIS:NE2	1:A:79:HIS:CE1	1.67	1.40
1:A:91:SER:HA	1:A:94:GLN:HE21	1.18	1.07
1:A:370:GLU:OE2	1:A:402:ARG:HD3	1.69	0.93
1:A:389:PHE:HD1	1:A:429:ILE:HD11	1.36	0.91
1:A:316:ARG:O	1:A:317:SER:HB3	1.77	0.84
1:A:91:SER:HA	1:A:94:GLN:NE2	1.91	0.84
1:A:304:ILE:HD11	1:A:340:CYS:SG	2.19	0.82
1:A:389:PHE:HD1	1:A:429:ILE:CD1	1.92	0.82
1:A:389:PHE:CD1	1:A:429:ILE:HD11	2.15	0.81
1:A:33:ARG:CZ	1:A:207:LEU:HD22	2.14	0.77
1:A:287:VAL:HG23	1:A:287:VAL:O	1.83	0.77
1:A:377:ILE:CD1	1:A:381:ARG:HH21	2.03	0.71
1:A:31:ASP:OD2	1:A:33:ARG:HD3	1.91	0.70
1:A:287:VAL:HG11	1:A:371:ARG:HD3	1.74	0.69
1:A:393:THR:HG23	1:A:394:ASN:ND2	2.07	0.69
1:A:290:ARG:HD2	1:A:291:GLN:O	1.94	0.66
1:A:301:ALA:O	1:A:305:ARG:HG3	1.95	0.66
1:A:150:ILE:HG21	1:A:153:THR:HG22	1.78	0.65
1:A:305:ARG:HA	1:A:308:GLU:HG2	1.77	0.65
1:A:417:ARG:O	1:A:421:ARG:HG3	1.97	0.65
1:A:74:GLN:HG2	1:A:76:ARG:HE	1.62	0.64
1:A:418:LYS:NZ	1:A:421:ARG:HB2	2.13	0.64
1:A:287:VAL:HG21	1:A:371:ARG:HD3	1.81	0.63
1:A:239:ARG:HG2	1:A:239:ARG:HH11	1.63	0.62
1:A:318:ARG:HD2	4:A:491:HOH:O	2.00	0.62
1:A:213:ARG:HB3	1:A:214:PRO:HD2	1.81	0.61
1:A:136:ILE:HG21	1:A:139:ILE:HD11	1.83	0.60
1:A:305:ARG:HB2	1:A:305:ARG:HH11	1.67	0.60
1:A:84:LEU:HD13	1:A:136:ILE:HD13	1.83	0.59
1:A:287:VAL:CG2	1:A:287:VAL:O	2.50	0.59
1:A:225:GLN:HA	4:A:511:HOH:O	2.01	0.58
1:A:404:PHE:HB3	1:A:430:LEU:HB3	1.86	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:409:GLU:OE2	1:A:421:ARG:HG2	2.05	0.57
1:A:397:GLU:HA	1:A:397:GLU:OE1	2.05	0.57
1:A:354:ILE:HB	1:A:376:ILE:HD11	1.86	0.57
1:A:377:ILE:HD11	1:A:381:ARG:HH21	1.69	0.56
1:A:284:GLU:O	1:A:284:GLU:HG2	2.05	0.56
1:A:139:ILE:HD12	1:A:144:MET:HG3	1.88	0.56
1:A:239:ARG:NH2	4:A:443:HOH:O	2.29	0.55
1:A:389:PHE:CE1	1:A:431:VAL:HG22	2.41	0.55
1:A:239:ARG:HG2	1:A:239:ARG:NH1	2.22	0.54
1:A:324:HIS:O	1:A:327:GLU:HG2	2.07	0.53
1:A:330:ILE:HB	1:A:337:LEU:CD2	2.39	0.52
2:A:437:COA:H62	2:A:437:COA:O9P	2.10	0.51
1:A:305:ARG:HH11	1:A:305:ARG:CB	2.23	0.51
1:A:90:THR:O	1:A:94:GLN:HG3	2.11	0.51
1:A:291:GLN:HE22	1:A:326:SER:HA	1.76	0.51
1:A:223:SER:HB2	1:A:284:GLU:OE2	2.11	0.51
1:A:266:SER:O	1:A:277:ILE:HD11	2.11	0.51
1:A:427:SER:OG	3:A:438:GLU:OE2	2.07	0.50
1:A:389:PHE:CD1	1:A:431:VAL:HG22	2.46	0.49
1:A:393:THR:HG23	1:A:394:ASN:HD22	1.76	0.49
1:A:33:ARG:NH2	1:A:207:LEU:HD22	2.26	0.49
1:A:389:PHE:CD1	1:A:429:ILE:CD1	2.83	0.49
1:A:297:ILE:N	1:A:298:PRO:HD2	2.28	0.48
1:A:377:ILE:HD11	1:A:381:ARG:NH2	2.28	0.48
1:A:71:ALA:O	1:A:72:ALA:C	2.53	0.48
1:A:377:ILE:HG22	1:A:388:LEU:HD22	1.95	0.47
1:A:423:ASN:HB3	1:A:425:ARG:H	1.80	0.47
1:A:425:ARG:NH2	3:A:438:GLU:HG2	2.29	0.47
1:A:395:THR:HG22	1:A:395:THR:O	2.15	0.46
1:A:405:GLN:HB2	1:A:405:GLN:HE21	1.64	0.46
1:A:275:ASN:O	1:A:276:GLY:O	2.34	0.46
1:A:381:ARG:HD3	1:A:435:HIS:O	2.17	0.45
1:A:315:HIS:HD2	1:A:316:ARG:O	1.98	0.45
1:A:337:LEU:HD13	1:A:338:TYR:N	2.31	0.45
1:A:256:VAL:HG13	1:A:281:ILE:HB	1.98	0.45
1:A:101:THR:HG22	1:A:105:ARG:HD2	1.98	0.45
1:A:60:ILE:HD12	1:A:190:ALA:HA	1.99	0.45
1:A:209:ASP:O	1:A:218:LEU:HD11	2.17	0.45
1:A:87:THR:HG23	1:A:91:SER:HB2	1.97	0.45
1:A:81:CYS:C	1:A:82:ARG:HG2	2.37	0.44
1:A:287:VAL:HG11	1:A:371:ARG:CD	2.47	0.43
1:A:417:ARG:HD3	1:A:421:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:258:ILE:O	1:A:259:LEU:HD23	2.19	0.43
1:A:61:HIS:CE1	1:A:172:PRO:HD3	2.54	0.43
1:A:255:ARG:HB2	1:A:255:ARG:HE	1.56	0.43
1:A:354:ILE:HD12	1:A:376:ILE:HG12	2.01	0.43
1:A:86:VAL:HG22	1:A:144:MET:SD	2.59	0.42
1:A:185:ASP:OD1	1:A:188:GLN:HB2	2.19	0.42
1:A:330:ILE:O	1:A:330:ILE:HG13	2.19	0.42
1:A:84:LEU:O	1:A:144:MET:HE1	2.19	0.42
1:A:203:VAL:HG12	1:A:205:LEU:HD12	2.01	0.42
1:A:103:ARG:HG3	1:A:169:TRP:CD1	2.54	0.42
1:A:357:LEU:O	2:A:437:COA:N4P	2.45	0.42
1:A:291:GLN:HG2	4:A:469:HOH:O	2.19	0.42
1:A:372:LEU:O	1:A:376:ILE:HG23	2.20	0.41
1:A:408:SER:O	1:A:411:GLU:HB2	2.20	0.41
1:A:30:ILE:O	1:A:61:HIS:HA	2.20	0.41
1:A:412:LEU:HD21	1:A:429:ILE:HD13	2.02	0.41
1:A:418:LYS:HZ1	1:A:421:ARG:HB2	1.85	0.41
1:A:258:ILE:C	1:A:259:LEU:HD23	2.41	0.41
1:A:325:ILE:HD12	1:A:325:ILE:HA	1.97	0.41
1:A:132:THR:HG23	4:A:479:HOH:O	2.20	0.40
1:A:344:LYS:HE3	1:A:344:LYS:HB3	1.68	0.40
1:A:407:ALA:HB3	1:A:429:ILE:HG13	2.03	0.40
1:A:360:SER:HA	1:A:361:PRO:HD3	1.95	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	420/456 (92%)	398 (95%)	16 (4%)	6 (1%)	16 11

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	276	GLY
1	A	317	SER
1	A	71	ALA
1	A	74	GLN
1	A	81	CYS
1	A	277	ILE

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	330/355 (93%)	289 (88%)	41 (12%)	7 5

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	PHE
1	A	13	GLU
1	A	49	LEU
1	A	70	LEU
1	A	76	ARG
1	A	82	ARG
1	A	102	VAL
1	A	104	SER
1	A	111	CYS
1	A	113	SER
1	A	122	SER
1	A	126	VAL
1	A	153	THR
1	A	238	THR
1	A	239	ARG
1	A	244	SER
1	A	255	ARG
1	A	256	VAL
1	A	267	LEU
1	A	268	LEU
1	A	269	GLN
1	A	290	ARG

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Mol	Chain	Res	Type
1	A	291	GLN
1	A	305	ARG
1	A	309	GLU
1	A	337	LEU
1	A	353	GLU
1	A	362	GLN
1	A	370	GLU
1	A	376	ILE
1	A	377	ILE
1	A	397	GLU
1	A	402	ARG
1	A	405	GLN
1	A	408	SER
1	A	409	GLU
1	A	418	LYS
1	A	423	ASN
1	A	427	SER
1	A	429	ILE
1	A	436	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	161	GLN
1	A	166	ASN
1	A	183	ASN
1	A	188	GLN
1	A	198	GLN
1	A	254	HIS
1	A	275	ASN
1	A	291	GLN
1	A	315	HIS
1	A	362	GLN
1	A	364	GLN
1	A	394	ASN
1	A	405	GLN
1	A	423	ASN

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 ⓘ

2 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	COA	A	437	-	50,50,50	1.85	9 (18%)	75,75,75	2.53	19 (25%)
3	GLU	A	438	-	9,9,9	0.95	0	11,11,11	1.14	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
2	COA	A	437	-	1/1/11/13	1/48/64/64	0/1/3/3
3	GLU	A	438	-	-	0/9/9/9	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	437	COA	O4B-C1B	5.50	1.49	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	437	COA	C3P-N4P	-5.10	1.34	1.46
2	A	437	COA	P1A-O3A	4.71	1.68	1.59
2	A	437	COA	P3B-O7A	4.05	1.64	1.51
2	A	437	COA	C2P-C3P	-2.75	1.39	1.51
2	A	437	COA	P2A-O6A	2.67	1.71	1.59
2	A	437	COA	P3B-O3B	2.62	1.67	1.59
2	A	437	COA	C4A-N9A	-2.60	1.33	1.37
2	A	437	COA	P3B-O8A	2.18	1.62	1.54

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	437	COA	O4B-C1B-N9A	11.43	119.07	108.44
2	A	437	COA	N3A-C2A-N1A	-9.05	121.15	128.71
2	A	437	COA	C2P-C3P-N4P	6.45	126.89	112.45
2	A	437	COA	N3A-C4A-N9A	4.98	134.42	125.43
2	A	437	COA	C2B-C1B-N9A	-4.25	102.35	113.27
2	A	437	COA	O9A-P3B-O8A	4.06	123.42	107.61
2	A	437	COA	C3P-N4P-C5P	4.04	131.06	122.84
2	A	437	COA	O4B-C1B-C2B	-3.44	101.50	106.77
2	A	437	COA	C6P-C5P-N4P	-3.41	110.31	116.50
2	A	437	COA	O8A-P3B-O3B	-3.39	97.32	107.09
2	A	437	COA	OAP-CAP-C9P	-3.18	102.57	110.76
2	A	437	COA	C4B-O4B-C1B	-3.16	106.32	109.75
2	A	437	COA	C6P-C7P-N8P	-2.88	105.66	111.87
2	A	437	COA	C5A-C4A-N3A	-2.67	119.88	125.70
2	A	437	COA	O5P-C5P-N4P	2.40	127.70	122.94
2	A	437	COA	O4B-C4B-C5B	-2.39	100.82	109.36
2	A	437	COA	C2A-N3A-C4A	2.30	120.55	114.01
2	A	437	COA	O9P-C9P-N8P	2.20	127.51	123.05
3	A	438	GLU	CB-CA-C	-2.11	105.98	110.98
2	A	437	COA	CDP-CBP-CAP	2.08	112.44	108.82

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	437	COA	CAP

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	437	COA	C2P-C3P-N4P-C5P

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 ⓘ

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	424/456 (92%)	0.39	20 (4%) 30 30	25, 45, 57, 69	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	PHE	6.1
1	A	113	SER	4.6
1	A	436	ARG	4.6
1	A	218	LEU	3.7
1	A	320	TYR	3.2
1	A	319	GLU	3.1
1	A	435	HIS	3.1
1	A	78	PRO	3.0
1	A	304	ILE	2.9
1	A	318	ARG	2.7
1	A	84	LEU	2.5
1	A	72	ALA	2.5
1	A	232	GLU	2.4
1	A	71	ALA	2.2
1	A	83	GLY	2.2
1	A	79	HIS	2.2
1	A	434	LEU	2.2
1	A	287	VAL	2.1
1	A	112	GLY	2.1
1	A	371	ARG	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	COA	A	437	48/48	0.13	-0.56	45,55,65,66	0
3	GLU	A	438	10/10	0.10	-1.06	47,55,56,57	0

6.5 Other polymers

There are no such residues in this entry.