



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2016 – 07:15 PM EST

PDB ID : 5KOD
Title : Crystal Structure of GH3.5 Acyl Acid Amido Synthetase from Arabidopsis thaliana
Authors : Jez, J.M.; Westfall, C.S.; Zubieta, C.
Deposited on : 2016-06-30
Resolution : 2.20 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

<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

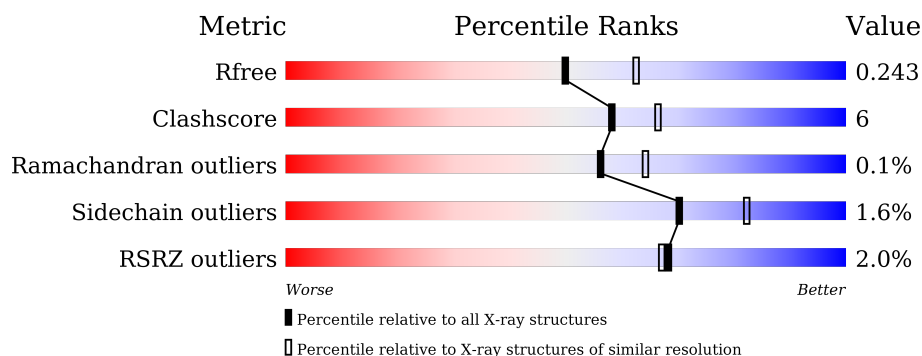
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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. 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.

Mol	Chain	Length	Quality of chain
1	A	612	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>6%</div> </div> </div>
1	B	612	<div> <div>0%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>6%</div> </div> </div>
1	C	612	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>8%</div> </div> </div>
1	D	612	<div> <div>0%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	IAC	A	702	-	-	-	X
3	IAC	B	702	-	-	-	X
3	IAC	C	702	-	-	-	X
3	IAC	D	702	-	-	-	X
4	SO4	B	703	-	-	-	X
4	SO4	B	704	-	-	-	X

2 Entry composition [i](#)

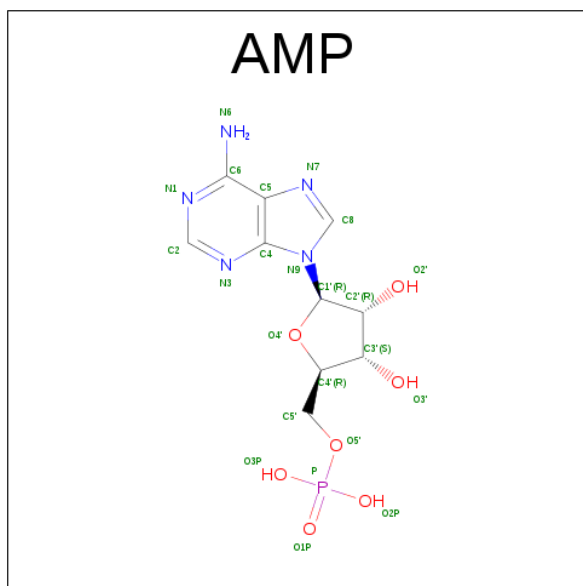
There are 5 unique types of molecules in this entry. The entry contains 19306 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Indole-3-acetic acid-amido synthetase GH3.5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	573	Total	C	N	O	S	0	3	0
			4565	2920	750	870	25			
1	B	573	Total	C	N	O	S	0	0	0
			4570	2924	749	872	25			
1	C	566	Total	C	N	O	S	0	2	0
			4507	2882	740	860	25			
1	D	566	Total	C	N	O	S	0	1	0
			4509	2888	739	856	26			

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



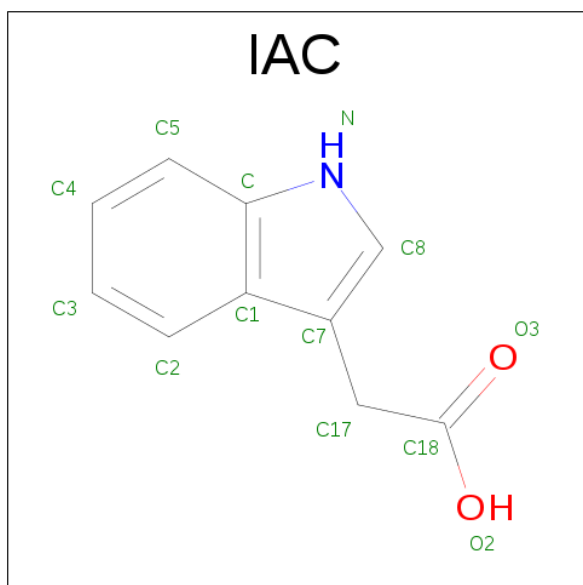
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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

- Molecule 3 is 1H-INDOL-3-YLACETIC ACID (three-letter code: IAC) (formula: C₁₀H₉NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	10	1	2		
3	B	1	Total	C	N	O	0	0
			13	10	1	2		
3	C	1	Total	C	N	O	0	0
			13	10	1	2		
3	D	1	Total	C	N	O	0	0
			13	10	1	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

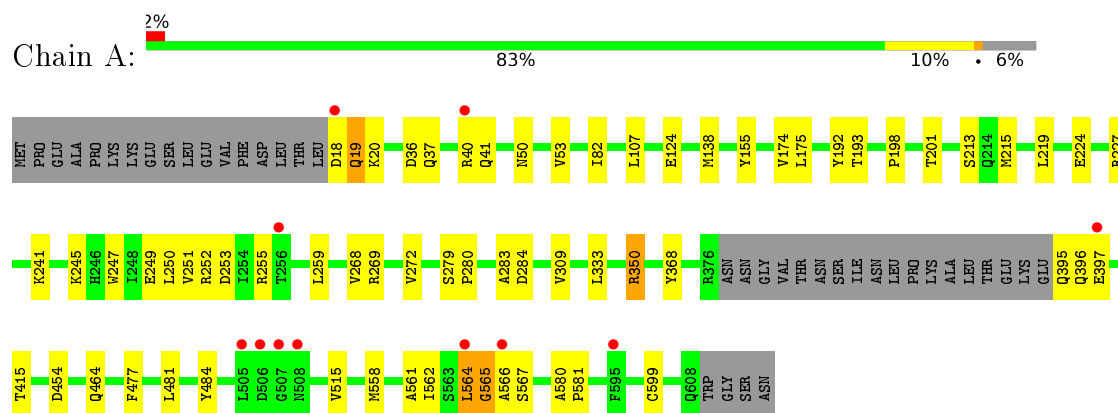
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	282	Total	O	0	0
			282	282		
5	B	260	Total	O	0	0
			260	260		
5	C	215	Total	O	0	0
			215	215		
5	D	244	Total	O	0	0
			244	244		

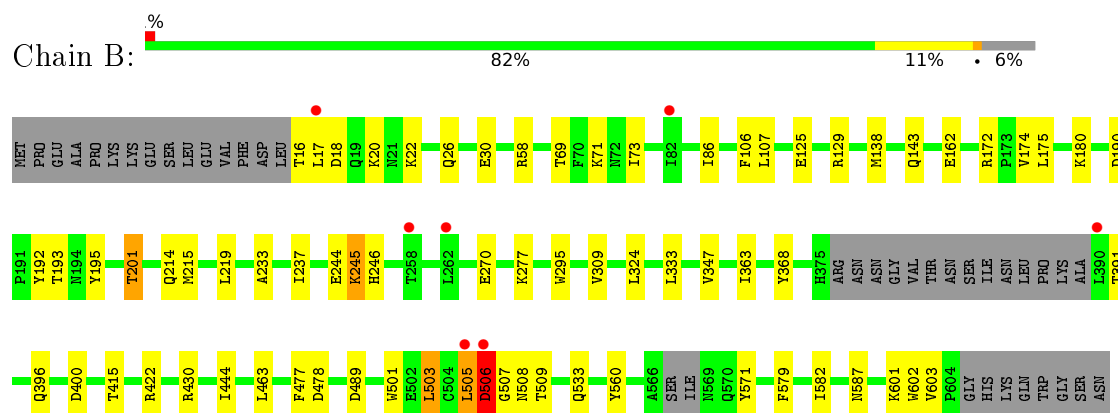
3 Residue-property plots

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.

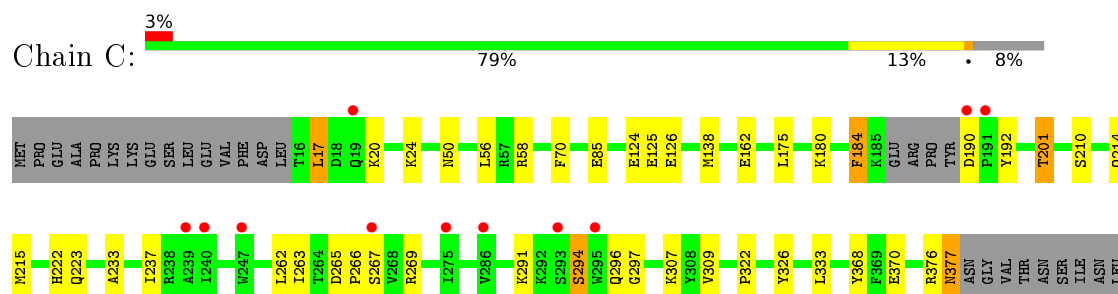
- Molecule 1: Indole-3-acetic acid-amido synthetase GH3.5

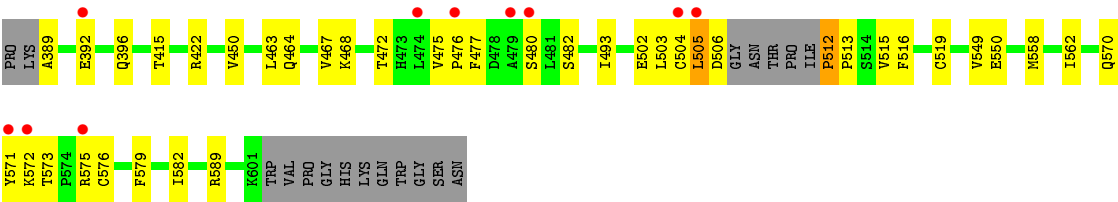


- Molecule 1: Indole-3-acetic acid-amido synthetase GH3.5

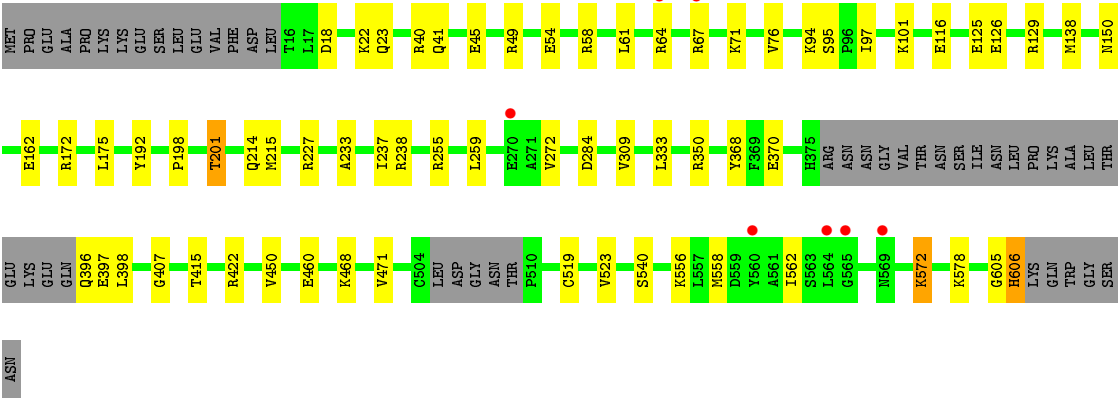
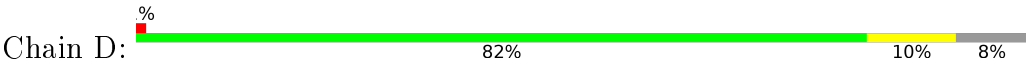


- Molecule 1: Indole-3-acetic acid-amido synthetase GH3.5





● Molecule 1: Indole-3-acetic acid-amido synthetase GH3.5



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.61Å 143.52Å 102.32Å 90.00° 114.72° 90.00°	Depositor
Resolution (Å)	42.16 – 2.20 42.16 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.5 (42.16-2.20) 89.5 (42.16-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.205 , 0.245 0.206 , 0.243	Depositor DCC
R_{free} test set	5417 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19306	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: AMP, SO4, IAC

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	0.45	0/4679	0.58	0/6352
1	B	0.53	2/4673 (0.0%)	0.62	5/6342 (0.1%)
1	C	0.57	2/4609 (0.0%)	0.69	8/6250 (0.1%)
1	D	0.45	0/4616	0.59	3/6266 (0.0%)
All	All	0.50	4/18577 (0.0%)	0.62	16/25210 (0.1%)

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	C	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	571	TYR	C-N	6.33	1.48	1.34
1	B	501	TRP	NE1-CE2	-5.60	1.30	1.37
1	C	513	PRO	N-CD	5.24	1.55	1.47
1	C	476	PRO	N-CD	5.18	1.55	1.47

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	184	PHE	O-C-N	-16.38	96.49	122.70
1	C	184	PHE	C-N-CA	10.63	148.26	121.70
1	C	184	PHE	CA-C-N	8.44	135.77	117.20
1	C	505	LEU	CA-CB-CG	-6.89	99.46	115.30
1	C	512	PRO	C-N-CD	6.48	142.01	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	603	VAL	C-N-CD	6.08	141.18	128.40
1	B	601	LYS	C-N-CA	5.89	136.42	121.70
1	B	509	THR	C-N-CD	5.79	140.56	128.40
1	D	605	GLY	N-CA-C	5.69	127.32	113.10
1	D	398	LEU	CA-CB-CG	-5.67	102.26	115.30
1	C	17	LEU	CB-CG-CD1	5.67	120.63	111.00
1	C	475	VAL	C-N-CD	5.59	140.15	128.40
1	C	573	THR	C-N-CD	5.46	139.87	128.40
1	B	503	LEU	CB-CG-CD2	5.44	120.25	111.00
1	B	601	LYS	O-C-N	-5.15	114.45	122.70
1	D	572	LYS	CB-CG-CD	-5.07	98.41	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	184	PHE	Mainchain

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	4565	0	4547	57	0
1	B	4570	0	4563	38	0
1	C	4507	0	4510	68	3
1	D	4509	0	4495	52	3
2	A	23	0	12	0	0
2	B	23	0	12	0	0
2	C	23	0	12	0	0
2	D	23	0	12	0	0
3	A	13	0	8	2	0
3	B	13	0	8	3	0
3	C	13	0	8	2	0
3	D	13	0	8	2	0
4	B	10	0	0	0	0
5	A	282	0	0	9	1
5	B	260	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	215	0	0	5	1
5	D	244	0	0	6	0
All	All	19306	0	18195	215	4

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 (215) 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:480:SER:OG	1:C:504:CYS:CA	1.65	1.43
1:C:480:SER:OG	1:C:504:CYS:CB	1.77	1.31
1:C:480:SER:OG	1:C:504:CYS:C	1.70	1.29
1:A:19:GLN:HB2	5:A:1029:HOH:O	1.14	1.23
1:C:480:SER:OG	1:C:504:CYS:O	1.57	1.18
1:A:19:GLN:CG	5:A:1029:HOH:O	1.66	1.15
1:C:480:SER:OG	1:C:504:CYS:HB2	1.35	1.09
1:A:18:ASP:O	1:A:19:GLN:NE2	1.87	1.07
1:C:480:SER:CB	1:C:504:CYS:HB2	1.86	1.05
1:A:561:ALA:O	1:A:564:LEU:O	1.80	0.99
1:D:578:LYS:NZ	5:D:801:HOH:O	1.98	0.97
1:A:562:ILE:HG23	1:A:566:ALA:HB1	1.50	0.93
1:A:19:GLN:HG2	1:A:20:LYS:H	1.36	0.90
1:B:489:ASP:OD2	5:B:802:HOH:O	1.93	0.86
1:A:562:ILE:O	1:A:566:ALA:HB2	1.77	0.83
1:C:480:SER:N	1:C:504:CYS:O	2.14	0.80
1:C:480:SER:OG	1:C:504:CYS:N	2.16	0.78
1:A:562:ILE:HG23	1:A:566:ALA:CB	2.13	0.78
1:D:407:GLY:O	5:D:802:HOH:O	2.01	0.78
3:B:702:IAC:N	5:B:801:HOH:O	1.81	0.77
1:B:175:LEU:HG	3:B:702:IAC:H171	1.68	0.76
1:B:18:ASP:OD2	1:B:22:LYS:HE3	1.85	0.76
1:D:192:TYR:O	1:D:227:ARG:NH2	2.20	0.74
1:D:350:ARG:NH2	5:D:804:HOH:O	2.21	0.74
1:A:36:ASP:OD2	1:A:40:ARG:NH1	2.19	0.74
1:D:76:VAL:HG23	1:D:396:GLN:HB3	1.71	0.73
1:A:19:GLN:HG3	5:A:1029:HOH:O	1.51	0.72
1:C:125:GLU:HB2	5:C:883:HOH:O	1.89	0.72
1:B:162:GLU:OE1	1:B:180:LYS:NZ	2.22	0.71
1:C:263:ILE:HD11	1:C:269:ARG:HG2	1.71	0.71
1:C:570:GLN:OE1	1:C:570:GLN:N	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:LEU:HG	3:D:702:IAC:H171	1.74	0.69
1:C:482:SER:HB2	1:C:504:CYS:SG	2.33	0.69
1:C:17:LEU:HD11	1:C:192:TYR:CE2	2.29	0.68
1:C:296:GLN:OE1	1:C:297:GLY:N	2.28	0.67
1:A:198:PRO:O	1:A:201:THR:HG22	1.93	0.67
1:C:322:PRO:HD2	5:C:830:HOH:O	1.94	0.66
1:C:20:LYS:HZ1	1:C:24:LYS:HG2	1.61	0.66
1:B:125:GLU:OE1	1:B:129:ARG:NH2	2.30	0.65
1:A:561:ALA:O	1:A:565:GLY:O	2.14	0.65
1:A:155:TYR:OH	1:A:227:ARG:NH1	2.29	0.65
1:D:54:GLU:OE2	1:D:58:ARG:NH2	2.30	0.65
1:C:558:MET:O	1:C:562:ILE:HG12	1.97	0.64
1:C:480:SER:CB	1:C:504:CYS:O	2.46	0.64
1:C:480:SER:O	1:C:503:LEU:HB3	1.98	0.64
1:A:193:THR:O	5:A:801:HOH:O	2.15	0.64
1:A:19:GLN:CG	1:A:20:LYS:H	2.03	0.63
1:A:259:LEU:HD23	1:A:269:ARG:HB2	1.81	0.63
1:B:270:GLU:CD	1:D:23:GLN:HE21	2.02	0.62
3:B:702:IAC:C8	5:B:801:HOH:O	2.37	0.62
1:A:175:LEU:HG	3:A:702:IAC:H171	1.80	0.62
1:A:19:GLN:CB	5:A:1029:HOH:O	1.64	0.62
1:C:138:MET:HG3	1:C:192:TYR:HB3	1.81	0.62
1:A:454:ASP:OD1	5:A:802:HOH:O	2.16	0.62
1:D:558:MET:O	1:D:562:ILE:HG12	2.00	0.60
1:C:263:ILE:HD11	1:C:269:ARG:HH11	1.66	0.60
1:A:252:ARG:NH1	1:A:253:ASP:OD1	2.35	0.60
1:C:175:LEU:HG	3:C:702:IAC:H171	1.84	0.60
1:C:201:THR:CG2	1:C:214:GLN:HG2	2.31	0.60
1:C:296:GLN:O	1:C:326:TYR:O	2.20	0.59
1:D:40:ARG:HG2	1:D:67:ARG:HH21	1.66	0.59
1:A:18:ASP:CG	1:A:19:GLN:H	2.06	0.59
1:C:480:SER:O	1:C:503:LEU:CA	2.51	0.59
1:A:464:GLN:NE2	1:A:484:TYR:OH	2.35	0.58
1:D:162:GLU:HG3	1:D:172:ARG:HB3	1.85	0.58
1:A:255:ARG:NH2	1:A:284:ASP:OD1	2.36	0.58
1:B:245:LYS:HG3	1:B:246:HIS:CD2	2.39	0.58
1:D:150:ASN:ND2	5:D:803:HOH:O	2.19	0.58
1:C:392:GLU:O	1:C:396:GLN:HG3	2.04	0.57
1:D:396:GLN:O	1:D:422:ARG:NH2	2.37	0.57
1:D:40:ARG:HH11	1:D:40:ARG:HG3	1.70	0.57
1:A:268:VAL:O	1:A:269:ARG:HG2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:GLN:O	1:B:422:ARG:NH2	2.38	0.57
1:D:255:ARG:NH2	1:D:284:ASP:OD1	2.38	0.56
1:A:224:GLU:OE2	5:A:803:HOH:O	2.18	0.56
1:A:350:ARG:HH11	1:A:350:ARG:HG2	1.69	0.56
1:D:61:LEU:O	1:D:64:ARG:HG3	2.06	0.56
1:C:480:SER:O	1:C:503:LEU:HA	2.06	0.56
1:B:26:GLN:O	1:B:30:GLU:HG3	2.05	0.56
1:C:512:PRO:HG2	1:C:515:VAL:HG23	1.87	0.56
1:C:477:PHE:CD1	1:C:477:PHE:N	2.73	0.56
1:C:20:LYS:NZ	1:C:24:LYS:HE2	2.21	0.56
1:D:138:MET:HG3	1:D:192:TYR:HB3	1.87	0.56
1:C:20:LYS:NZ	1:C:24:LYS:HG2	2.20	0.55
1:A:215:MET:O	1:A:215:MET:HE3	2.06	0.55
1:D:450:VAL:HG21	1:D:460:GLU:HG3	1.89	0.55
1:A:395:GLN:HG3	1:A:395:GLN:O	2.06	0.54
1:A:37:GLN:O	1:A:41:GLN:HG3	2.08	0.54
1:B:245:LYS:HG3	1:B:246:HIS:NE2	2.22	0.54
1:C:464:GLN:HE21	1:C:575:ARG:HE	1.54	0.54
1:D:238:ARG:HD3	1:D:540:SER:HA	1.90	0.54
1:D:40:ARG:NH1	1:D:40:ARG:HG3	2.22	0.54
1:A:201:THR:OG1	1:A:213:SER:OG	2.17	0.54
1:C:516:PHE:O	1:C:519:CYS:HB2	2.07	0.53
1:C:370:GLU:OE1	1:C:422:ARG:HD2	2.09	0.53
1:B:190:ASP:HB3	1:B:193:THR:HG22	1.90	0.53
1:D:201:THR:HG23	1:D:214:GLN:HG2	1.91	0.53
1:C:389:ALA:N	5:C:809:HOH:O	2.41	0.53
1:D:116:GLU:HG3	1:D:606:HIS:HD2	1.73	0.53
1:A:215:MET:HE3	1:A:219:LEU:HG	1.91	0.52
1:A:19:GLN:CG	1:A:20:LYS:N	2.73	0.52
1:C:502:GLU:HG3	1:C:549:VAL:HG23	1.92	0.52
1:D:126:GLU:OE2	1:D:129:ARG:NH1	2.41	0.52
1:C:20:LYS:HZ3	1:C:24:LYS:HE2	1.74	0.52
1:B:587:ASN:O	5:B:803:HOH:O	2.19	0.52
1:C:162:GLU:OE2	1:C:180:LYS:NZ	2.44	0.51
1:C:480:SER:O	1:C:503:LEU:CB	2.58	0.51
1:A:241:LYS:HE3	1:A:245:LYS:HE3	1.93	0.51
1:B:270:GLU:CD	1:D:23:GLN:NE2	2.64	0.51
1:B:233:ALA:O	1:B:237:ILE:HG12	2.10	0.51
1:D:18:ASP:O	1:D:22:LYS:HG2	2.11	0.50
1:C:368:TYR:HB3	1:C:415:THR:HB	1.93	0.50
1:C:58:ARG:NH1	1:C:85:GLU:OE2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:MET:HE2	1:B:219:LEU:HG	1.93	0.49
1:A:245:LYS:HD2	5:A:1030:HOH:O	2.13	0.49
1:B:138:MET:HG3	1:B:192:TYR:HB3	1.94	0.49
1:C:233:ALA:O	1:C:237:ILE:HG12	2.11	0.49
3:C:702:IAC:H8	5:C:817:HOH:O	2.12	0.49
1:D:45:GLU:HG2	1:D:49:ARG:HE	1.77	0.49
1:C:215:MET:HE3	1:C:215:MET:O	2.13	0.49
1:D:519:CYS:O	1:D:523:VAL:HG23	2.13	0.49
1:D:259:LEU:HD13	1:D:272:VAL:HG11	1.94	0.48
1:A:558:MET:O	1:A:562:ILE:HD12	2.14	0.48
1:B:162:GLU:HG3	1:B:172:ARG:HB3	1.95	0.48
1:D:116:GLU:CD	1:D:606:HIS:CD2	2.88	0.48
1:D:309:VAL:HB	1:D:333:LEU:HD23	1.96	0.47
1:A:252:ARG:HG2	1:A:252:ARG:HH11	1.80	0.47
1:B:478:ASP:O	1:B:506:ASP:HA	2.14	0.47
1:B:507:GLY:O	1:B:508:ASN:HB2	2.14	0.47
1:A:269:ARG:HA	1:A:272:VAL:HB	1.96	0.47
1:B:533:GLN:HB2	1:B:602:TRP:NE1	2.30	0.47
1:B:201:THR:CG2	1:B:214:GLN:HG2	2.45	0.47
1:C:70:PHE:CE2	1:C:422:ARG:HD3	2.50	0.46
1:A:107:LEU:HD22	1:A:174:VAL:HA	1.97	0.46
1:A:309:VAL:HB	1:A:333:LEU:HD23	1.98	0.46
1:D:201:THR:CG2	1:D:214:GLN:HG2	2.46	0.46
1:B:309:VAL:HB	1:B:333:LEU:HD23	1.96	0.46
1:C:464:GLN:HE21	1:C:575:ARG:NE	2.14	0.46
1:D:233:ALA:O	1:D:237:ILE:HG12	2.16	0.46
1:A:138:MET:HG3	1:A:192:TYR:HB3	1.98	0.46
1:A:18:ASP:C	1:A:19:GLN:HE21	2.16	0.46
1:A:259:LEU:HD23	1:A:269:ARG:CB	2.44	0.46
1:C:294:SER:HB2	1:C:296:GLN:H	1.81	0.46
1:C:265:ASP:HA	1:C:266:PRO:HD3	1.83	0.46
1:A:558:MET:O	1:A:562:ILE:CD1	2.64	0.45
1:A:175:LEU:HG	3:A:702:IAC:H2	1.98	0.45
1:B:347:VAL:HG22	1:B:363:ILE:HD11	1.96	0.45
1:B:477:PHE:O	1:B:506:ASP:HB2	2.16	0.45
1:D:370:GLU:OE2	1:D:422:ARG:NH1	2.49	0.45
1:D:606:HIS:HB3	5:D:1012:HOH:O	2.17	0.45
1:C:480:SER:O	1:C:504:CYS:N	2.50	0.45
1:D:76:VAL:CG2	1:D:396:GLN:HB3	2.45	0.45
1:D:468:LYS:HA	1:D:468:LYS:HD2	1.73	0.45
1:B:579:PHE:HB3	1:B:582:ILE:HD12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:480:SER:CB	1:C:504:CYS:CB	2.68	0.45
1:C:512:PRO:HG2	1:C:515:VAL:CG2	2.47	0.45
1:B:195:TYR:HB3	5:B:953:HOH:O	2.17	0.45
1:D:368:TYR:HB3	1:D:415:THR:HB	1.99	0.45
1:D:101:LYS:NZ	1:D:125:GLU:OE2	2.50	0.45
1:D:95:SER:O	1:D:97:ILE:HG13	2.17	0.45
1:B:190:ASP:HB3	1:B:193:THR:CG2	2.47	0.44
1:C:210:SER:O	1:C:214:GLN:HG3	2.17	0.44
1:C:579:PHE:HB3	1:C:582:ILE:HD12	1.99	0.44
1:B:143:GLN:O	1:C:307:LYS:NZ	2.47	0.44
1:C:309:VAL:HB	1:C:333:LEU:HD23	2.00	0.44
1:D:468:LYS:O	1:D:471:VAL:HG22	2.18	0.44
1:D:94:LYS:HB2	1:D:94:LYS:HE3	1.86	0.44
1:C:377:ASN:ND2	1:C:377:ASN:C	2.71	0.44
1:A:477:PHE:CE2	1:A:515:VAL:HG21	2.52	0.43
1:D:198:PRO:O	1:D:201:THR:HG22	2.18	0.43
1:C:237:ILE:CG2	1:C:493:ILE:HD13	2.47	0.43
1:A:368:TYR:HB3	1:A:415:THR:HB	2.00	0.43
1:B:368:TYR:HB3	1:B:415:THR:HB	2.00	0.43
1:C:222:HIS:CE1	1:C:223:GLN:HG3	2.53	0.43
1:C:50:ASN:O	1:C:56:LEU:HD22	2.17	0.43
1:D:578:LYS:HD2	1:D:578:LYS:HA	1.69	0.43
1:B:244:GLU:HA	1:B:295:TRP:CH2	2.53	0.43
1:C:570:GLN:N	1:C:570:GLN:CD	2.72	0.43
1:D:397:GLU:HA	1:D:397:GLU:OE1	2.17	0.43
1:D:41:GLN:O	1:D:45:GLU:HB2	2.18	0.43
1:A:249:GLU:HG3	5:A:807:HOH:O	2.17	0.42
1:A:50:ASN:O	1:A:53:VAL:HG22	2.20	0.42
1:B:107:LEU:HD22	1:B:174:VAL:HA	2.00	0.42
1:C:237:ILE:HG22	1:C:493:ILE:HD13	2.01	0.42
1:C:190:ASP:OD2	1:C:192:TYR:HB2	2.20	0.42
1:D:556:LYS:HE2	1:D:556:LYS:HB3	1.84	0.42
1:A:18:ASP:CG	1:A:19:GLN:N	2.72	0.42
1:A:193:THR:HG22	1:A:193:THR:O	2.20	0.42
1:C:20:LYS:HZ1	1:C:24:LYS:CG	2.28	0.42
1:C:262:LEU:HA	1:C:262:LEU:HD23	1.82	0.42
1:A:247:TRP:HA	1:A:250:LEU:HD12	2.01	0.42
1:B:233:ALA:HB1	1:B:324:LEU:HD11	2.02	0.42
1:C:450:VAL:HG13	1:C:576:CYS:HB2	2.02	0.42
1:C:550:GLU:HB2	1:C:589:ARG:HG3	2.01	0.42
1:D:162:GLU:HG2	5:D:822:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:THR:HG23	1:D:214:GLN:CG	2.49	0.42
1:B:71:LYS:HE3	1:B:400:ASP:OD2	2.19	0.41
1:D:71:LYS:HB3	1:D:397:GLU:OE2	2.21	0.41
1:B:16:THR:O	1:B:17:LEU:HB3	2.20	0.41
1:D:116:GLU:HG3	1:D:606:HIS:CD2	2.54	0.41
1:B:190:ASP:O	1:B:193:THR:HG22	2.20	0.41
1:C:512:PRO:HD2	1:C:515:VAL:HG21	2.01	0.41
1:D:175:LEU:CG	3:D:702:IAC:H171	2.45	0.41
1:B:69:THR:HG23	1:B:73:ILE:HD12	2.03	0.41
1:A:397:GLU:OE2	1:A:397:GLU:HA	2.21	0.41
1:B:86:ILE:HG23	1:B:106:PHE:CE1	2.56	0.41
1:B:430:ARG:HB2	1:B:444:ILE:HD11	2.03	0.41
1:A:580:ALA:HB3	1:A:581:PRO:HD3	2.04	0.40
1:A:251:VAL:HG13	1:A:283:ALA:HB1	2.02	0.40
1:A:481:LEU:HD21	1:A:484:TYR:HB3	2.03	0.40
1:A:350:ARG:NH1	1:A:350:ARG:HG2	2.36	0.40
1:A:279:SER:HA	1:A:280:PRO:HD2	1.94	0.40
1:C:126:GLU:OE1	5:C:801:HOH:O	2.22	0.40
1:C:463:LEU:O	1:C:467:VAL:HG23	2.22	0.40

All (4) 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:C:377:ASN:CB	1:D:572:LYS:CE[1_556]	2.02	0.18
1:C:377:ASN:CB	1:D:572:LYS:CD[1_556]	2.10	0.10
1:C:377:ASN:CB	1:D:572:LYS:NZ[1_556]	2.11	0.09
5:A:901:HOH:O	5:C:861:HOH:O[1_655]	2.16	0.04

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	572/612 (94%)	561 (98%)	10 (2%)	1 (0%)	52	59
1	B	567/612 (93%)	554 (98%)	11 (2%)	2 (0%)	39	42
1	C	560/612 (92%)	547 (98%)	13 (2%)	0	100	100
1	D	561/612 (92%)	551 (98%)	10 (2%)	0	100	100
All	All	2260/2448 (92%)	2213 (98%)	44 (2%)	3 (0%)	56	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	505	LEU
1	A	565	GLY
1	B	506	ASP

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	522/557 (94%)	514 (98%)	8 (2%)	72	84
1	B	523/557 (94%)	512 (98%)	11 (2%)	61	74
1	C	516/557 (93%)	503 (98%)	13 (2%)	55	67
1	D	515/557 (92%)	513 (100%)	2 (0%)	93	97
All	All	2076/2228 (93%)	2042 (98%)	34 (2%)	70	82

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	82	ILE
1	A	124	GLU
1	A	350	ARG
1	A	396	GLN
1	A	564	LEU
1	A	567	SER
1	A	599	CYS

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Mol	Chain	Res	Type
1	B	20	LYS
1	B	58	ARG
1	B	201	THR
1	B	245	LYS
1	B	277	LYS
1	B	391	THR
1	B	463	LEU
1	B	503	LEU
1	B	505	LEU
1	B	506	ASP
1	B	560	TYR
1	C	124	GLU
1	C	201	THR
1	C	267	SER
1	C	291	LYS
1	C	294	SER
1	C	376	ARG
1	C	377	ASN
1	C	468	LYS
1	C	472	THR
1	C	505	LEU
1	C	506	ASP
1	C	571	TYR
1	C	572	LYS
1	D	201	THR
1	D	606	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	464	GLN
1	B	23	GLN
1	C	377	ASN
1	C	464	GLN
1	D	23	GLN
1	D	606	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

10 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	AMP	A	701	-	22,25,25	0.90	1 (4%)	22,38,38	2.11	4 (18%)
3	IAC	A	702	-	10,14,14	2.66	6 (60%)	7,19,19	1.75	1 (14%)
2	AMP	B	701	-	22,25,25	0.92	1 (4%)	22,38,38	1.95	3 (13%)
3	IAC	B	702	-	10,14,14	2.72	6 (60%)	7,19,19	1.59	1 (14%)
4	SO4	B	703	-	4,4,4	0.16	0	6,6,6	0.56	0
4	SO4	B	704	-	4,4,4	0.19	0	6,6,6	0.14	0
2	AMP	C	701	-	22,25,25	0.93	1 (4%)	22,38,38	1.81	2 (9%)
3	IAC	C	702	-	10,14,14	2.68	6 (60%)	7,19,19	1.28	0
2	AMP	D	701	-	22,25,25	0.85	1 (4%)	22,38,38	2.11	3 (13%)
3	IAC	D	702	-	10,14,14	2.67	6 (60%)	7,19,19	1.85	1 (14%)

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	AMP	A	701	-	-	0/6/26/26	0/3/3/3
3	IAC	A	702	-	-	0/2/4/4	0/2/2/2
2	AMP	B	701	-	-	0/6/26/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IAC	B	702	-	-	0/2/4/4	0/2/2/2
4	SO4	B	703	-	-	0/0/0/0	0/0/0/0
4	SO4	B	704	-	-	0/0/0/0	0/0/0/0
2	AMP	C	701	-	-	0/6/26/26	0/3/3/3
3	IAC	C	702	-	-	0/2/4/4	0/2/2/2
2	AMP	D	701	-	-	0/6/26/26	0/3/3/3
3	IAC	D	702	-	-	0/2/4/4	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	IAC	C5-C	-3.18	1.36	1.41
3	C	702	IAC	C5-C	-3.18	1.36	1.41
3	B	702	IAC	C8-C7	-3.16	1.28	1.37
3	B	702	IAC	C5-C	-3.13	1.36	1.41
3	D	702	IAC	C8-C7	-3.04	1.29	1.37
3	A	702	IAC	C8-C7	-2.91	1.29	1.37
3	D	702	IAC	C5-C	-2.86	1.36	1.41
3	C	702	IAC	C8-C7	-2.78	1.29	1.37
3	A	702	IAC	C1-C	2.23	1.48	1.42
3	B	702	IAC	C1-C	2.30	1.48	1.42
3	D	702	IAC	C1-C	2.52	1.49	1.42
3	C	702	IAC	C1-C	2.56	1.49	1.42
2	D	701	AMP	C5-C4	2.70	1.46	1.40
2	C	701	AMP	C5-C4	2.90	1.47	1.40
2	B	701	AMP	C5-C4	3.05	1.47	1.40
2	A	701	AMP	C5-C4	3.10	1.47	1.40
3	A	702	IAC	C4-C3	3.13	1.45	1.38
3	D	702	IAC	C4-C3	3.21	1.46	1.38
3	B	702	IAC	C4-C3	3.34	1.46	1.38
3	D	702	IAC	C-N	3.39	1.49	1.38
3	C	702	IAC	C4-C3	3.40	1.46	1.38
3	C	702	IAC	C-N	3.43	1.49	1.38
3	B	702	IAC	C-N	3.47	1.49	1.38
3	A	702	IAC	C-N	3.59	1.50	1.38
3	C	702	IAC	C3-C2	4.21	1.46	1.36
3	A	702	IAC	C3-C2	4.33	1.46	1.36
3	D	702	IAC	C3-C2	4.34	1.46	1.36
3	B	702	IAC	C3-C2	4.36	1.46	1.36

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	AMP	N3-C2-N1	-8.00	122.59	128.87
2	D	701	AMP	N3-C2-N1	-7.74	122.79	128.87
2	B	701	AMP	N3-C2-N1	-7.51	122.97	128.87
2	C	701	AMP	N3-C2-N1	-6.88	123.47	128.87
2	D	701	AMP	C1'-N9-C4	-3.77	122.59	126.81
3	D	702	IAC	C3-C4-C5	-3.20	115.83	120.45
2	A	701	AMP	C1'-N9-C4	-2.98	123.48	126.81
3	A	702	IAC	C3-C4-C5	-2.92	116.24	120.45
3	B	702	IAC	C3-C4-C5	-2.17	117.33	120.45
2	B	701	AMP	O3P-P-O2P	2.07	115.06	107.44
2	B	701	AMP	C2-N1-C6	2.09	122.50	118.77
2	A	701	AMP	O3P-P-O2P	2.09	115.12	107.44
2	D	701	AMP	C2-N1-C6	2.14	122.58	118.77
2	C	701	AMP	O3P-P-O2P	2.24	115.65	107.44
2	A	701	AMP	C2-N1-C6	2.93	124.00	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	702	IAC	2	0
3	B	702	IAC	3	0
3	C	702	IAC	2	0
3	D	702	IAC	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, 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	573/612 (93%)	-0.24	11 (1%) 70 68	16, 27, 48, 70	0
1	B	573/612 (93%)	-0.24	7 (1%) 81 80	13, 27, 48, 68	0
1	C	566/612 (92%)	-0.12	21 (3%) 45 44	18, 31, 59, 79	0
1	D	566/612 (92%)	-0.29	7 (1%) 81 80	16, 27, 50, 68	0
All	All	2278/2448 (93%)	-0.22	46 (2%) 68 67	13, 28, 51, 79	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	571	TYR	6.5
1	C	480	SER	5.3
1	D	564	LEU	4.6
1	A	508	ASN	4.2
1	A	564	LEU	4.0
1	C	295	TRP	3.7
1	C	190	ASP	3.7
1	B	390	LEU	3.6
1	C	267	SER	3.5
1	A	256	THR	3.4
1	C	293	SER	3.4
1	C	479	ALA	3.3
1	D	569	ASN	3.3
1	B	505	LEU	3.3
1	C	474	LEU	3.3
1	B	506	ASP	3.1
1	C	505	LEU	3.1
1	A	506	ASP	2.9
1	D	270	GLU	2.8
1	A	18	ASP	2.8
1	C	275	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	17	LEU	2.7
1	C	476	PRO	2.7
1	C	247	TRP	2.7
1	C	504	CYS	2.6
1	C	286	VAL	2.6
1	C	239	ALA	2.6
1	A	505	LEU	2.5
1	A	507	GLY	2.5
1	D	67	ARG	2.5
1	C	191	PRO	2.4
1	C	19	GLN	2.4
1	C	572	LYS	2.4
1	A	595	PHE	2.4
1	D	560	TYR	2.4
1	C	575	ARG	2.3
1	A	566	ALA	2.3
1	C	240	ILE	2.3
1	C	392	GLU	2.2
1	A	397	GLU	2.2
1	B	82	ILE	2.2
1	D	64	ARG	2.1
1	D	565	GLY	2.1
1	B	262	LEU	2.0
1	B	258	THR	2.0
1	A	40	ARG	2.0

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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	IAC	A	702	13/13	0.88	0.30	9.74	9,35,41,42	0
4	SO4	B	704	5/5	0.84	0.22	7.35	72,76,77,78	0
4	SO4	B	703	5/5	0.77	0.24	7.33	47,48,57,62	0
3	IAC	C	702	13/13	0.84	0.25	5.07	34,44,52,53	0
3	IAC	D	702	13/13	0.88	0.24	3.36	10,33,41,43	0
3	IAC	B	702	13/13	0.89	0.23	2.78	5,29,35,38	0
2	AMP	A	701	23/23	0.97	0.12	0.37	12,18,23,27	0
2	AMP	B	701	23/23	0.97	0.13	0.02	12,16,19,27	0
2	AMP	C	701	23/23	0.97	0.12	-0.06	12,17,25,29	0
2	AMP	D	701	23/23	0.97	0.11	-0.66	10,16,22,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.