



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:08 PM UTC

PDB ID : 3WQZ / pdb_00003wqz
Title : Crystal structure of Archaeoglobus fulgidus alanyl-tRNA synthetase in complex with a tRNA(Ala) variant having A3.U70
Authors : Naganuma, M.; Sekine, S.; Yokoyama, S.
Deposited on : 2014-02-05
Resolution : 3.49 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

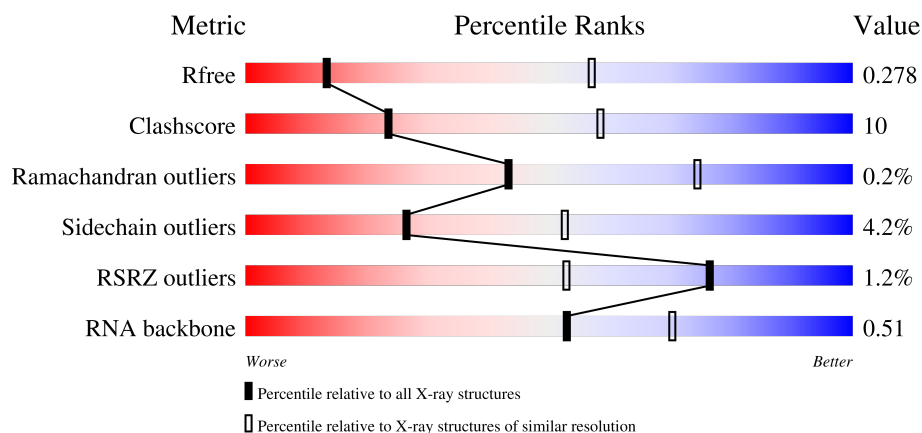
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.49 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}	180053	1083 (3.52-3.44)
Clashscore	190562	1139 (3.52-3.44)
Ramachandran outliers	187476	1111 (3.52-3.44)
Sidechain outliers	187428	1112 (3.52-3.44)
RSRZ outliers	180081	1082 (3.52-3.44)
RNA backbone	3983	1001 (3.94-3.02)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	906	73% 26% .
1	B	906	73% 26% .
2	C	75	53% 27% 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16078 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.

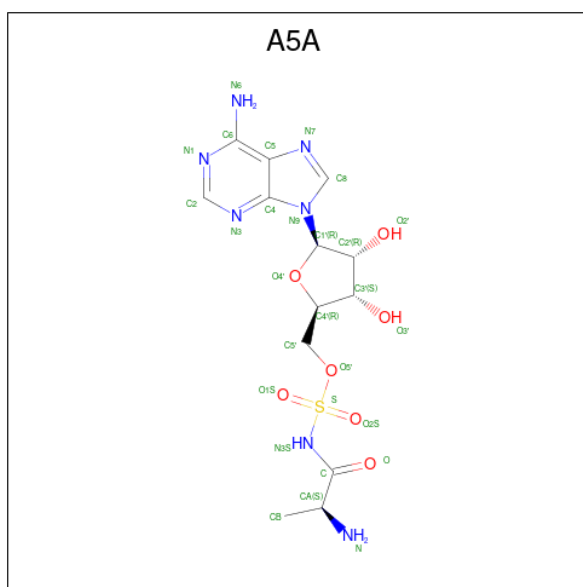
- Molecule 1 is a protein called Alanine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	905	Total	C	N	O	S	0	0	0
			7209	4573	1248	1357	31			
1	B	904	Total	C	N	O	S	0	0	0
			7203	4571	1247	1353	32			

- Molecule 2 is a RNA chain called RNA (75-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	75	Total	C	N	O	P	0	0	0
			1608	715	295	523	75			

- Molecule 3 is '5'-O-(N-(L-ALANYL)-SULFAMOYL)ADENOSINE (CCD ID: A5A) (formula: C₁₃H₁₉N₇O₇S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			28	13	7	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			28	13	7	7	1		

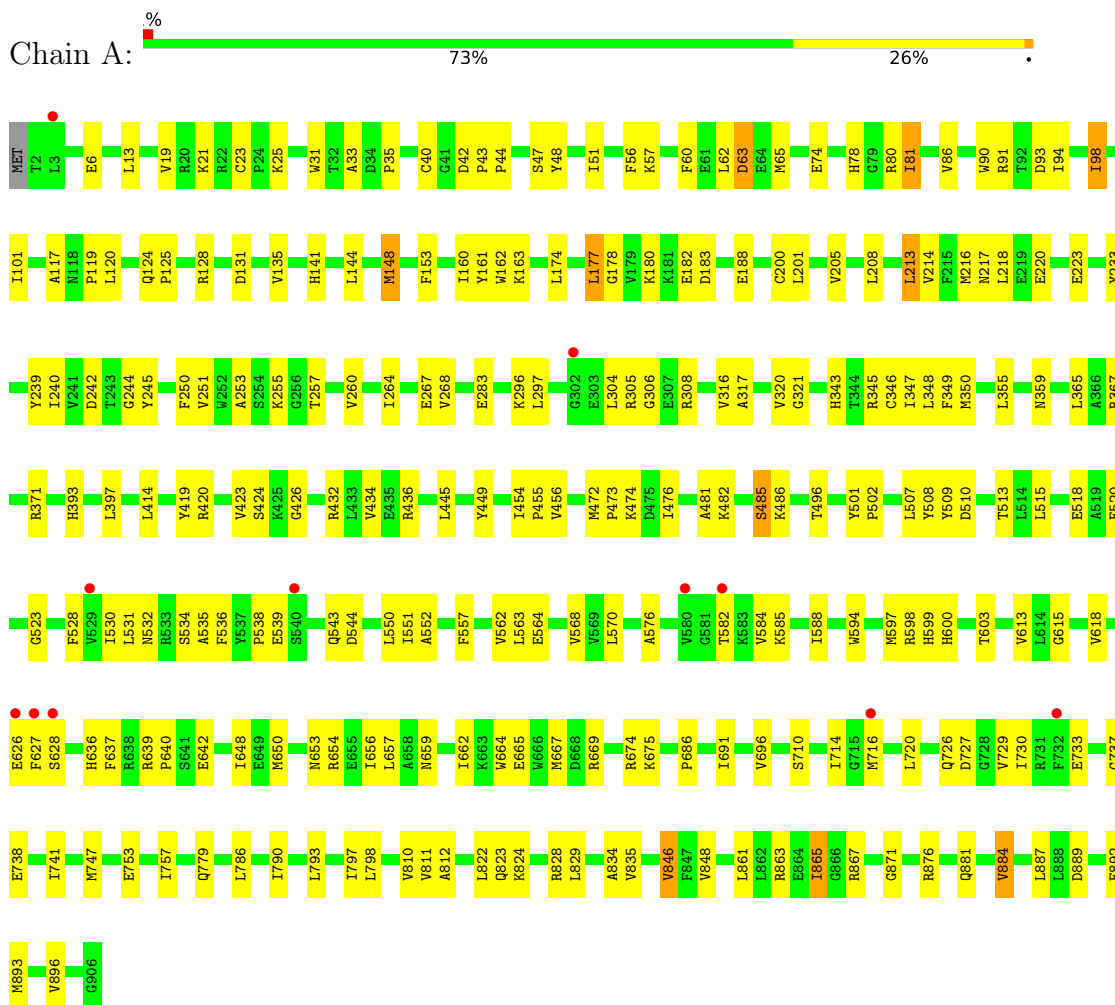
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

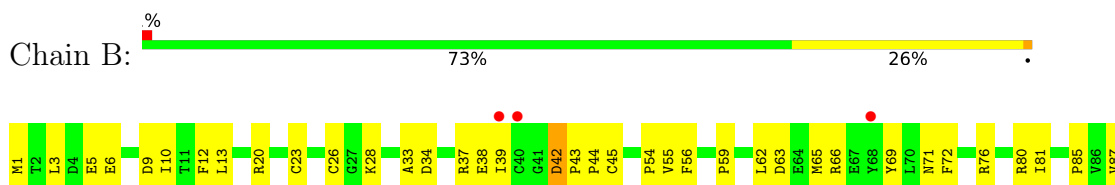
3 Residue-property plots

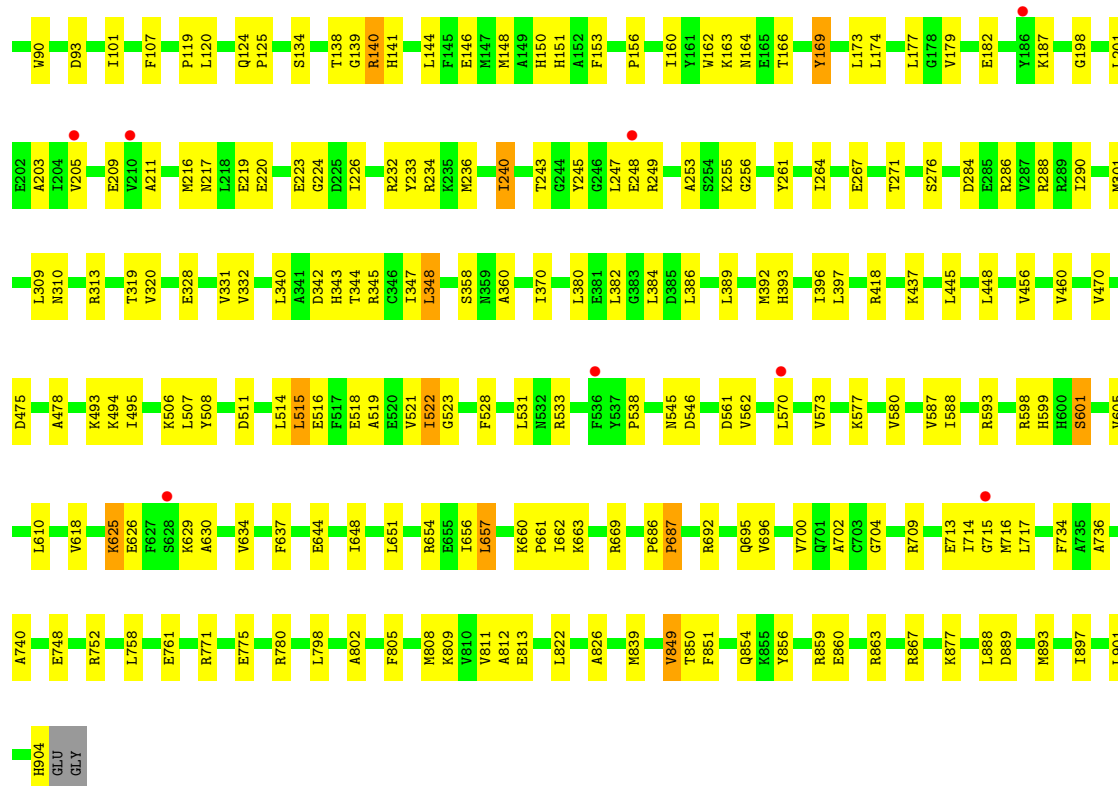
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Alanine-tRNA ligase



• Molecule 1: Alanine-tRNA ligase





• Molecule 2: RNA (75-MER)

Chain C: 53% 27% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.61Å 169.68Å 176.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.74 – 3.49 42.74 – 3.49	Depositor EDS
% Data completeness (in resolution range)	99.8 (42.74-3.49) 99.8 (42.74-3.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.241 , 0.277 0.245 , 0.278	Depositor DCC
R_{free} test set	1996 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å ²)	100.8	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.037 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16078	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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: ZN, A5A

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	0.28	0/7347	0.74	2/9909 (0.0%)
1	B	0.30	0/7341	0.73	2/9902 (0.0%)
2	C	0.22	1/1797 (0.1%)	0.38	0/2800
All	All	0.28	1/16485 (0.0%)	0.70	4/22611 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1601	G	OP3-P	5.99	1.60	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	ASP	CA-C-N	6.34	126.91	120.38
1	A	42	ASP	C-N-CA	6.34	126.91	120.38
1	B	169	TYR	N-CA-C	6.05	118.66	111.33
1	B	43	PRO	N-CA-C	5.12	116.94	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7209	0	7200	151	0
1	B	7203	0	7203	154	0
2	C	1608	0	816	29	0
3	A	28	0	19	2	0
3	B	28	0	19	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	16078	0	15257	320	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 10.

All (320) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:599:HIS:HD2	1:B:625:LYS:HE3	1.35	0.90
1:A:482:LYS:HA	2:C:1676:A:H61	1.38	0.86
1:B:626:GLU:HB3	1:B:629:LYS:HB2	1.63	0.80
1:A:640:PRO:HD3	1:A:730:ILE:HD13	1.67	0.75
1:A:636:HIS:HB3	1:A:730:ILE:HD12	1.69	0.74
1:B:345:ARG:HH21	1:B:397:LEU:HD21	1.53	0.72
1:B:33:ALA:HB3	1:B:182:GLU:HA	1.72	0.72
1:B:382:LEU:HG	1:B:384:LEU:H	1.53	0.72
1:A:531:LEU:HD21	1:A:534:SER:HB2	1.72	0.70
1:B:148:MET:HB2	1:B:245:TYR:HB2	1.74	0.70
1:B:138:THR:HG23	1:B:140:ARG:H	1.56	0.70
1:B:290:ILE:HD13	1:B:320:VAL:HG11	1.73	0.70
1:B:198:GLY:HA3	1:B:216:MET:HA	1.73	0.69
1:B:1:MET:HG2	1:B:226:ILE:HD11	1.74	0.69
2:C:1634:U:H4'	2:C:1635:G:O5'	1.93	0.68
2:C:1675:C:H3'	2:C:1676:A:H2'	1.76	0.67
1:B:625:LYS:HA	1:B:630:ALA:HA	1.76	0.67
1:A:162:TRP:CG	1:A:163:LYS:H	2.13	0.67
1:A:509:TYR:O	1:A:664:TRP:NE1	2.28	0.67
1:A:445:LEU:HD21	1:A:456:VAL:HG13	1.77	0.66
1:A:823:GLN:NE2	2:C:1620:G:OP2	2.29	0.66
1:B:709:ARG:NH2	1:B:713:GLU:OE2	2.28	0.66
1:B:65:MET:HG3	1:B:148:MET:HE1	1.77	0.66
1:B:344:THR:HG21	1:B:389:LEU:HB2	1.76	0.66
1:A:669:ARG:NH2	1:A:686:PRO:O	2.29	0.65
1:B:224:GLY:HA3	1:B:232:ARG:HD2	1.76	0.65
1:B:599:HIS:CE1	1:B:630:ALA:HB1	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:GLU:HB3	1:B:236:MET:HE2	1.79	0.65
2:C:1636:C:H1'	2:C:1637:G:OP2	1.98	0.64
1:A:876:ARG:NH1	2:C:1620:G:OP1	2.31	0.64
1:B:310:ASN:HA	1:B:313:ARG:HB2	1.79	0.64
1:A:304:LEU:HD21	1:A:308:ARG:HH21	1.62	0.63
1:A:481:ALA:O	2:C:1676:A:N6	2.31	0.63
1:A:220:GLU:CD	2:C:1674:C:H42	2.07	0.62
1:B:71:ASN:OD1	1:B:80:ARG:NH2	2.26	0.62
1:B:276:SER:HB2	1:B:380:LEU:HB3	1.79	0.62
1:B:546:ASP:OD2	1:B:593:ARG:NH1	2.30	0.62
1:B:651:LEU:HA	1:B:654:ARG:HE	1.65	0.62
1:B:692:ARG:HD3	1:B:704:GLY:HA2	1.81	0.62
1:B:736:ALA:HA	1:B:740:ALA:HB2	1.81	0.62
1:A:482:LYS:HA	2:C:1676:A:N6	2.12	0.62
1:B:139:GLY:HA2	1:B:261:TYR:HE1	1.63	0.62
1:B:34:ASP:HB2	1:B:182:GLU:HB2	1.83	0.61
1:B:839:MET:HE1	1:B:888:LEU:HB3	1.82	0.61
1:A:220:GLU:OE1	2:C:1674:C:N4	2.31	0.61
1:B:219:GLU:N	1:B:234:ARG:O	2.32	0.61
1:A:515:LEU:HB3	1:A:588:ILE:HB	1.84	0.60
1:A:420:ARG:NH1	1:A:424:SER:OG	2.34	0.60
1:A:63:ASP:OD1	1:A:63:ASP:N	2.34	0.59
1:B:802:ALA:HB2	1:B:811:VAL:HB	1.83	0.59
1:A:117:ALA:H	1:A:120:LEU:HD21	1.67	0.59
1:B:717:LEU:HD11	1:B:734:PHE:HD2	1.67	0.59
1:A:656:ILE:HG22	1:A:714:ILE:HD11	1.86	0.58
1:A:60:PHE:HB3	1:A:65:MET:HG2	1.86	0.57
1:B:508:TYR:HB2	1:B:593:ARG:HH22	1.69	0.57
1:B:826:ALA:HB1	1:B:851:PHE:HB3	1.86	0.57
1:A:544:ASP:OD1	1:A:600:HIS:NE2	2.35	0.57
1:B:37:ARG:NH2	1:B:38:GLU:O	2.38	0.57
1:A:81:ILE:HG12	1:A:120:LEU:HD22	1.87	0.57
1:A:214:VAL:HB	1:A:242:ASP:HB3	1.87	0.57
1:B:798:LEU:HD22	1:B:813:GLU:HG3	1.87	0.57
1:A:90:TRP:CD1	1:A:91:ARG:HG3	2.40	0.56
1:B:124:GLN:NE2	1:B:125:PRO:O	2.38	0.56
1:B:538:PRO:HB3	1:B:562:VAL:HG22	1.86	0.56
1:B:860:GLU:HG2	1:B:863:ARG:HH12	1.69	0.56
1:A:101:ILE:HG12	1:A:216:MET:HE1	1.87	0.56
1:B:119:PRO:HG3	1:B:160:ILE:HG21	1.88	0.56
1:A:74:GLU:OE2	1:A:80:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:VAL:HG22	1:A:141:HIS:HB3	1.88	0.56
1:A:510:ASP:HA	1:A:664:TRP:HE1	1.69	0.56
2:C:1646:G:O2'	2:C:1648:C:OP2	2.22	0.56
1:A:33:ALA:HB3	1:A:182:GLU:HA	1.88	0.56
1:B:573:VAL:O	1:B:577:LYS:NZ	2.37	0.55
1:B:81:ILE:HD13	1:B:120:LEU:HB2	1.88	0.55
1:B:515:LEU:HG	1:B:588:ILE:HB	1.89	0.55
1:A:557:PHE:HE2	1:A:576:ALA:HB3	1.71	0.55
1:A:798:LEU:HB3	1:A:811:VAL:HG11	1.88	0.55
1:B:26:CYS:SG	1:B:28:LYS:NZ	2.74	0.55
1:B:162:TRP:CG	1:B:163:LYS:H	2.24	0.54
1:A:538:PRO:HA	1:A:562:VAL:HG22	1.90	0.54
1:B:56:PHE:HE1	1:B:177:LEU:HD13	1.72	0.54
1:B:812:ALA:HB1	1:B:893:MET:HE2	1.90	0.54
1:A:62:LEU:HD23	1:A:251:VAL:HG21	1.89	0.54
2:C:1621:A:C2	2:C:1648:C:C2	2.96	0.54
1:A:367:ARG:O	1:A:371:ARG:HG2	2.08	0.54
1:A:317:ALA:O	1:A:321:GLY:N	2.40	0.54
1:A:162:TRP:CD1	1:A:163:LYS:HG2	2.43	0.53
1:B:209:GLU:O	1:B:249:ARG:NH1	2.40	0.53
1:B:717:LEU:HD11	1:B:734:PHE:HB2	1.90	0.53
1:A:812:ALA:HB1	1:A:893:MET:HE2	1.89	0.53
1:B:822:LEU:HD23	1:B:849:VAL:HB	1.90	0.53
1:A:473:PRO:HB3	1:A:476:ILE:HD13	1.90	0.53
2:C:1609:A:O2'	2:C:1610:G:N7	2.41	0.53
1:A:520:GLU:OE2	1:A:532:ASN:ND2	2.41	0.53
1:B:150:HIS:HE1	1:B:166:THR:HG21	1.74	0.53
1:B:148:MET:HE3	1:B:247:LEU:HG	1.90	0.52
1:B:599:HIS:CD2	1:B:625:LYS:HE3	2.27	0.52
1:A:283:GLU:N	1:A:283:GLU:OE1	2.42	0.52
1:A:539:GLU:HB2	1:A:543:GLN:O	2.09	0.52
1:B:610:LEU:HD23	1:B:648:ILE:HD12	1.91	0.52
1:B:340:LEU:HD11	1:B:386:LEU:HD21	1.92	0.52
1:B:460:VAL:HG13	1:B:470:VAL:HG11	1.92	0.52
1:A:726:GLN:HG2	1:A:729:VAL:HB	1.92	0.51
1:A:78:HIS:HA	1:A:119:PRO:HG2	1.92	0.51
1:A:642:GLU:OE2	1:B:752:ARG:NH2	2.43	0.51
1:B:328:GLU:HA	1:B:331:VAL:HG22	1.92	0.51
1:B:301:MET:HE3	1:B:309:LEU:HD11	1.93	0.51
1:B:531:LEU:HD23	1:B:533:ARG:H	1.74	0.51
1:B:445:LEU:HD13	1:B:456:VAL:HG13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1616:C:O2'	2:C:1618:G:OP2	2.25	0.51
1:A:13:LEU:HD13	1:A:31:TRP:CD2	2.46	0.50
1:A:686:PRO:HG2	1:A:691:ILE:HD12	1.93	0.50
1:B:10:ILE:HG13	1:B:12:PHE:H	1.76	0.50
1:A:823:GLN:HG3	1:A:881:GLN:HE21	1.75	0.50
1:B:343:HIS:O	1:B:347:ILE:HG12	2.12	0.50
1:B:59:PRO:HB3	1:B:255:LYS:HA	1.94	0.50
1:B:69:TYR:CE2	1:B:148:MET:HB3	2.47	0.50
2:C:1647:C:H2'	2:C:1650:C:OP1	2.11	0.50
1:B:493:LYS:NZ	1:B:494:LYS:O	2.45	0.49
1:A:829:LEU:HB3	1:A:834:ALA:HB3	1.94	0.49
3:A:1001:A5A:O5'	3:A:1001:A5A:H8	2.11	0.49
1:A:810:VAL:HG12	1:A:835:VAL:HB	1.94	0.49
2:C:1632:U:H2'	2:C:1633:U:O4'	2.11	0.49
1:A:31:TRP:NE1	1:A:188:GLU:OE1	2.44	0.49
1:A:848:VAL:HG11	1:A:865:ILE:HD11	1.95	0.49
1:B:358:SER:OG	1:B:360:ALA:O	2.27	0.49
1:A:538:PRO:HG2	1:A:564:GLU:HB3	1.95	0.48
1:A:260:VAL:O	1:A:264:ILE:HG12	2.12	0.48
1:B:644:GLU:O	1:B:648:ILE:HG12	2.14	0.48
1:A:824:LYS:HE3	1:A:828:ARG:HH22	1.77	0.48
1:B:651:LEU:HB2	1:B:654:ARG:HH21	1.78	0.48
1:A:25:LYS:HE3	1:A:43:PRO:HD3	1.94	0.48
1:A:846:VAL:HG21	1:A:887:LEU:HD23	1.95	0.48
1:B:85:PRO:HG2	1:B:90:TRP:HZ3	1.76	0.48
1:A:432:ARG:HB3	1:A:436:ARG:HH12	1.79	0.48
1:B:599:HIS:CE1	1:B:630:ALA:CB	2.96	0.48
1:A:871:GLY:HA3	1:A:884:VAL:HG22	1.96	0.48
1:B:601:SER:HB3	1:B:714:ILE:HD11	1.95	0.48
1:A:543:GLN:HG2	1:A:626:GLU:HA	1.96	0.48
1:B:162:TRP:CD1	1:B:163:LYS:HG2	2.49	0.48
1:B:808:MET:HE3	1:B:854:GLN:HG3	1.95	0.48
1:B:150:HIS:CE1	1:B:243:THR:HG21	2.48	0.48
1:A:346:CYS:O	1:A:350:MET:HG3	2.14	0.47
1:A:657:LEU:HD13	1:B:598:ARG:HH12	1.79	0.47
1:A:793:LEU:O	1:A:797:ILE:HG12	2.14	0.47
1:B:601:SER:O	1:B:605:VAL:HG23	2.14	0.47
1:A:6:GLU:OE2	1:A:217:ASN:ND2	2.47	0.47
1:A:267:GLU:CD	1:A:267:GLU:H	2.22	0.47
1:A:650:MET:O	1:A:654:ARG:HG2	2.14	0.47
1:B:66:ARG:HA	1:B:148:MET:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:MET:N	1:B:245:TYR:O	2.47	0.47
1:B:545:ASN:ND2	1:B:561:ASP:OD1	2.42	0.47
1:A:343:HIS:O	1:A:347:ILE:HG12	2.13	0.47
1:B:267:GLU:O	1:B:271:THR:OG1	2.32	0.47
2:C:1675:C:H5'	2:C:1676:A:H2'	1.97	0.47
1:A:508:TYR:HB3	1:A:535:ALA:HA	1.96	0.47
1:A:613:VAL:HG11	1:A:648:ILE:HG13	1.97	0.47
1:A:753:GLU:O	1:A:757:ILE:HG12	2.14	0.47
1:B:519:ALA:HB3	1:B:531:LEU:HD21	1.97	0.47
1:B:203:ALA:HB3	1:B:211:ALA:HB3	1.97	0.47
1:A:93:ASP:OD1	1:A:94:ILE:N	2.46	0.47
1:B:808:MET:HE1	1:B:901:LEU:HD11	1.97	0.47
1:A:162:TRP:CG	1:A:163:LYS:N	2.82	0.47
1:A:674:ARG:HG3	1:A:675:LYS:HG3	1.96	0.47
1:B:56:PHE:HE2	1:B:253:ALA:HB3	1.80	0.47
2:C:1633:U:H2'	2:C:1634:U:H5'	1.97	0.47
1:B:669:ARG:NH1	1:B:686:PRO:O	2.48	0.46
2:C:1608:U:H4'	2:C:1648:C:H4'	1.97	0.46
1:A:255:LYS:HB3	1:A:257:THR:HG23	1.97	0.46
1:B:805:PHE:HD2	1:B:901:LEU:HD23	1.80	0.46
1:A:180:LYS:NZ	1:A:183:ASP:OD2	2.39	0.46
1:B:522:ILE:HA	1:B:580:VAL:HG23	1.97	0.46
1:B:516:GLU:HG2	1:B:587:VAL:HA	1.97	0.46
1:A:304:LEU:HD21	1:A:308:ARG:HD2	1.97	0.46
1:A:665:GLU:HG3	1:A:667:MET:HE2	1.97	0.46
1:A:485:SER:HB3	2:C:1676:A:H2	1.81	0.46
1:A:720:LEU:N	1:A:733:GLU:O	2.45	0.46
1:B:138:THR:HG21	1:B:141:HIS:ND1	2.30	0.46
1:B:867:ARG:HA	1:B:867:ARG:HD3	1.66	0.46
1:A:297:LEU:HD13	1:A:316:VAL:HB	1.98	0.46
1:B:125:PRO:HA	1:B:146:GLU:HA	1.97	0.46
1:A:98:ILE:HG22	1:A:128:ARG:HG2	1.97	0.46
1:B:656:ILE:HD12	1:B:714:ILE:HB	1.97	0.46
1:A:86:VAL:HG11	1:A:349:PHE:HB3	1.98	0.45
1:A:432:ARG:HB3	1:A:436:ARG:NH1	2.31	0.45
1:A:551:ILE:HG12	1:A:552:ALA:H	1.81	0.45
1:B:223:GLU:HB3	1:B:234:ARG:HD3	1.97	0.45
1:A:43:PRO:HA	1:A:44:PRO:HA	1.64	0.45
1:A:160:ILE:HG22	1:A:161:TYR:HD1	1.81	0.45
1:B:217:ASN:O	1:B:236:MET:HG2	2.16	0.45
1:B:521:VAL:HG12	1:B:523:GLY:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:786:LEU:O	1:A:790:ILE:HG12	2.17	0.45
1:B:55:VAL:HG22	1:B:179:VAL:HG22	1.99	0.45
1:B:859:ARG:HH21	1:B:877:LYS:HG3	1.82	0.45
1:A:518:GLU:HA	1:A:585:LYS:HD2	1.98	0.45
1:A:530:ILE:HD12	1:A:531:LEU:H	1.82	0.45
1:A:594:TRP:HB3	1:A:598:ARG:NH1	2.31	0.45
1:A:889:ASP:HB3	1:A:892:GLU:HG3	1.98	0.45
1:B:101:ILE:HD13	1:B:151:HIS:CD2	2.52	0.45
1:B:511:ASP:HB3	1:B:514:LEU:HG	1.98	0.45
1:B:856:TYR:CE2	1:B:904:HIS:HB2	2.52	0.45
1:B:717:LEU:HD11	1:B:734:PHE:CD2	2.48	0.44
1:B:686:PRO:HG3	1:B:702:ALA:HB1	1.99	0.44
1:B:72:PHE:O	1:B:76:ARG:HG2	2.18	0.44
1:B:662:ILE:HG23	1:B:696:VAL:HG22	1.99	0.44
1:A:544:ASP:CG	1:A:600:HIS:HE2	2.25	0.44
1:A:599:HIS:O	1:A:603:THR:OG1	2.24	0.44
1:A:653:ASN:O	1:A:656:ILE:HG12	2.18	0.44
1:A:367:ARG:HH11	1:A:371:ARG:NH2	2.16	0.44
1:A:420:ARG:HA	1:A:423:VAL:HG12	2.00	0.44
1:A:881:GLN:OE1	2:C:1619:G:O2'	2.33	0.44
1:B:758:LEU:O	2:C:1647:C:N4	2.51	0.44
1:A:65:MET:HE2	1:A:250:PHE:HB3	2.00	0.44
1:A:568:VAL:HG12	1:A:570:LEU:HD23	2.00	0.44
1:A:627:PHE:O	1:A:628:SER:OG	2.31	0.44
1:B:56:PHE:CD1	1:B:177:LEU:HB3	2.52	0.44
1:A:659:ASN:OD1	1:A:710:SER:HB2	2.17	0.43
1:B:348:LEU:HD12	1:B:393:HIS:HB3	2.00	0.43
1:A:19:VAL:HG13	1:A:21:LYS:HD3	2.00	0.43
1:B:893:MET:O	1:B:897:ILE:HG12	2.19	0.43
1:A:371:ARG:HD2	1:A:419:TYR:CD2	2.53	0.43
1:A:639:ARG:HA	1:A:640:PRO:HD3	1.85	0.43
1:B:10:ILE:HG12	1:B:13:LEU:HG	1.99	0.43
1:B:28:LYS:HE2	1:B:187:LYS:HD2	1.99	0.43
1:B:618:VAL:HG13	1:B:634:VAL:HB	2.00	0.43
1:B:662:ILE:HA	1:B:695:GLN:O	2.18	0.43
1:B:771:ARG:NH1	1:B:775:GLU:OE2	2.51	0.43
2:C:1674:C:H3'	2:C:1675:C:H5''	2.00	0.43
1:A:6:GLU:O	1:A:163:LYS:NZ	2.39	0.43
1:B:56:PHE:HD1	1:B:177:LEU:HB3	1.83	0.43
2:C:1643:G:H2'	2:C:1644:A:C8	2.54	0.43
1:A:153:PHE:CD2	1:A:240:ILE:HD12	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:HB2	1:A:213:LEU:HD11	1.99	0.43
1:B:516:GLU:HG2	1:B:587:VAL:HG22	2.01	0.43
1:B:657:LEU:HD12	1:B:657:LEU:HA	1.91	0.43
1:B:859:ARG:H	1:B:859:ARG:HG2	1.64	0.43
1:B:124:GLN:HA	1:B:125:PRO:HD3	1.86	0.43
1:B:134:SER:O	1:B:138:THR:HG22	2.19	0.43
1:B:162:TRP:CD1	1:B:163:LYS:HZ2	2.36	0.43
1:A:51:ILE:HD12	1:A:296:LYS:HA	2.01	0.43
1:A:449:TYR:CD1	1:A:455:PRO:HA	2.53	0.43
1:A:56:PHE:HE2	1:A:253:ALA:HB3	1.83	0.43
1:B:10:ILE:HD12	1:B:164:ASN:HA	2.01	0.43
1:A:268:VAL:HG21	1:A:393:HIS:CE1	2.54	0.42
1:B:507:LEU:HD11	1:B:533:ARG:HG2	2.00	0.42
1:B:656:ILE:HG21	1:B:715:GLY:O	2.20	0.42
1:A:552:ALA:HA	1:A:584:VAL:HB	2.01	0.42
1:B:54:PRO:HG3	1:B:256:GLY:HA3	2.01	0.42
1:B:811:VAL:HG13	1:B:851:PHE:HZ	1.84	0.42
1:B:220:GLU:HA	1:B:233:TYR:HA	2.01	0.42
2:C:1636:C:HO2'	2:C:1637:G:P	2.42	0.42
1:A:244:GLY:HA3	3:A:1001:A5A:HB1	2.01	0.42
1:A:359:ASN:OD1	1:A:726:GLN:HB2	2.20	0.42
1:A:538:PRO:HB3	1:A:563:LEU:C	2.44	0.42
1:A:543:GLN:HB3	1:A:544:ASP:H	1.59	0.42
1:A:218:LEU:HB3	1:A:233:TYR:HB3	2.01	0.42
1:A:305:ARG:NH1	1:A:306:GLY:O	2.53	0.42
1:A:472:MET:HE2	1:A:474:LYS:HG2	2.02	0.42
1:A:486:LYS:HB3	1:A:486:LYS:HE2	1.81	0.42
1:A:426:GLY:HA3	1:A:454:ILE:HD11	2.01	0.42
2:C:1636:C:O2'	2:C:1637:G:OP1	2.33	0.42
1:A:57:LYS:HE2	1:A:178:GLY:HA2	2.02	0.42
1:A:345:ARG:HB2	1:A:393:HIS:CE1	2.55	0.42
1:A:615:GLY:O	1:A:618:VAL:HG22	2.20	0.42
1:A:81:ILE:H	1:A:81:ILE:HG13	1.72	0.42
1:A:863:ARG:O	1:A:867:ARG:HG2	2.19	0.42
1:A:536:PHE:CZ	1:A:588:ILE:HG13	2.55	0.41
1:B:475:ASP:HB2	1:B:478:ALA:HB3	2.02	0.41
1:B:716:MET:HE3	1:B:716:MET:HB2	1.94	0.41
1:B:860:GLU:HG2	1:B:863:ARG:NH1	2.34	0.41
1:A:47:SER:HB2	1:A:296:LYS:O	2.20	0.41
1:A:501:TYR:CE2	1:A:523:GLY:HA3	2.55	0.41
1:A:550:LEU:N	1:A:557:PHE:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:737:GLY:O	1:A:741:ILE:HG13	2.21	0.41
1:A:501:TYR:HA	1:A:502:PRO:HD3	1.74	0.41
1:A:662:ILE:HG23	1:A:696:VAL:HA	2.02	0.41
1:A:510:ASP:HA	1:A:664:TRP:NE1	2.34	0.41
1:B:107:PHE:HE2	1:B:687:PRO:HA	1.86	0.41
1:B:267:GLU:HB2	1:B:396:ILE:HD11	2.02	0.41
1:B:284:ASP:O	1:B:288:ARG:HG3	2.21	0.41
1:B:286:ARG:O	1:B:290:ILE:HG12	2.21	0.41
1:B:386:LEU:HD23	1:B:386:LEU:HA	1.90	0.41
1:A:432:ARG:NH2	2:C:1614:A:OP1	2.54	0.41
1:B:418:ARG:NH2	1:B:637:PHE:O	2.40	0.41
1:B:506:LYS:C	1:B:507:LEU:HD12	2.45	0.41
2:C:1636:C:O2'	2:C:1637:G:P	2.79	0.41
1:A:564:GLU:HA	1:A:570:LEU:HG	2.02	0.41
1:A:738:GLU:HA	1:A:741:ILE:HD12	2.02	0.41
1:B:695:GLN:HG2	1:B:700:VAL:HG22	2.02	0.41
1:A:177:LEU:HD12	1:A:177:LEU:HA	1.82	0.41
1:A:345:ARG:HE	1:A:397:LEU:HD21	1.84	0.41
1:B:660:LYS:HA	1:B:661:PRO:HD3	1.94	0.41
1:B:717:LEU:HA	1:B:717:LEU:HD12	1.75	0.41
1:A:25:LYS:HD3	1:A:25:LYS:HA	1.78	0.41
1:A:48:TYR:HE1	1:A:208:LEU:HD13	1.86	0.41
1:A:316:VAL:O	1:A:320:VAL:HG22	2.21	0.41
1:A:865:ILE:HG22	1:A:896:VAL:HG11	2.02	0.41
1:B:42:ASP:HB3	1:B:44:PRO:HD2	2.03	0.41
1:B:248:GLU:HG3	1:B:264:ILE:HD13	2.03	0.41
1:B:528:PHE:CG	1:B:570:LEU:HD23	2.55	0.41
1:B:630:ALA:HB3	1:B:734:PHE:O	2.21	0.41
1:A:414:LEU:HD23	1:A:637:PHE:HB2	2.02	0.41
1:A:747:MET:SD	1:B:748:GLU:HG2	2.60	0.41
1:B:23:CYS:SG	1:B:26:CYS:HB3	2.61	0.41
1:A:124:GLN:NE2	1:A:125:PRO:O	2.54	0.40
1:A:148:MET:HG3	1:A:245:TYR:O	2.21	0.40
1:A:594:TRP:HA	1:A:597:MET:HE2	2.02	0.40
1:A:779:GLN:HE22	1:B:780:ARG:NH1	2.19	0.40
1:B:3:LEU:O	1:B:6:GLU:HG2	2.21	0.40
2:C:1675:C:H5'	2:C:1676:A:C2'	2.51	0.40
1:A:716:MET:HE2	1:A:716:MET:HB3	2.00	0.40
1:B:5:GLU:O	1:B:9:ASP:N	2.49	0.40
1:B:56:PHE:CE1	1:B:177:LEU:HD13	2.54	0.40
1:B:856:TYR:HE2	1:B:904:HIS:HB2	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:LEU:HD13	1:B:598:ARG:NH1	2.36	0.40
1:B:62:LEU:HD12	1:B:63:ASP:N	2.37	0.40
1:B:889:ASP:O	1:B:893:MET:HG3	2.21	0.40
1:B:153:PHE:CD2	1:B:240:ILE:HD13	2.56	0.40
1:B:493:LYS:NZ	1:B:495:ILE:HG12	2.36	0.40
3:B:1001:A5A:O5'	3:B:1001:A5A:H8	2.21	0.40

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	903/906 (100%)	863 (96%)	39 (4%)	1 (0%)	48	79
1	B	902/906 (100%)	864 (96%)	36 (4%)	2 (0%)	43	74
All	All	1805/1812 (100%)	1727 (96%)	75 (4%)	3 (0%)	43	74

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	156	PRO
1	A	35	PRO
1	B	687	PRO

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	766/767 (100%)	735 (96%)	31 (4%)	28	54
1	B	766/767 (100%)	733 (96%)	33 (4%)	26	52
All	All	1532/1534 (100%)	1468 (96%)	64 (4%)	26	52

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	CYS
1	A	40	CYS
1	A	63	ASP
1	A	81	ILE
1	A	98	ILE
1	A	131	ASP
1	A	144	LEU
1	A	148	MET
1	A	174	LEU
1	A	177	LEU
1	A	200	CYS
1	A	205	VAL
1	A	213	LEU
1	A	223	GLU
1	A	239	TYR
1	A	348	LEU
1	A	355	LEU
1	A	365	LEU
1	A	434	VAL
1	A	485	SER
1	A	496	THR
1	A	507	LEU
1	A	513	THR
1	A	528	PHE
1	A	582	THR
1	A	727	ASP
1	A	822	LEU
1	A	846	VAL
1	A	861	LEU
1	A	865	ILE
1	A	884	VAL
1	B	20	ARG
1	B	39	ILE
1	B	42	ASP
1	B	45	CYS

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Mol	Chain	Res	Type
1	B	87	VAL
1	B	93	ASP
1	B	140	ARG
1	B	144	LEU
1	B	169	TYR
1	B	173	LEU
1	B	174	LEU
1	B	201	LEU
1	B	205	VAL
1	B	240	ILE
1	B	319	THR
1	B	332	VAL
1	B	342	ASP
1	B	348	LEU
1	B	370	ILE
1	B	392	MET
1	B	437	LYS
1	B	448	LEU
1	B	515	LEU
1	B	518	GLU
1	B	522	ILE
1	B	601	SER
1	B	625	LYS
1	B	657	LEU
1	B	663	LYS
1	B	761	GLU
1	B	809	LYS
1	B	849	VAL
1	B	850	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	HIS
1	A	604	HIS
1	A	636	HIS
1	A	823	GLN
1	B	150	HIS
1	B	151	HIS
1	B	175	ASN
1	B	452	HIS
1	B	596	HIS

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Mol	Chain	Res	Type
1	B	599	HIS
1	B	620	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	74/75 (98%)	24 (32%)	5 (6%)

All (24) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	1603	A
2	C	1609	A
2	C	1613	C
2	C	1615	G
2	C	1616	C
2	C	1618	G
2	C	1619	G
2	C	1620	G
2	C	1621	A
2	C	1622	G
2	C	1629	G
2	C	1635	G
2	C	1636	C
2	C	1637	G
2	C	1638	A
2	C	1647	C
2	C	1648	C
2	C	1649	G
2	C	1652	G
2	C	1658	A
2	C	1660	U
2	C	1674	C
2	C	1675	C
2	C	1676	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	1616	C
2	C	1621	A

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Mol	Chain	Res	Type
2	C	1634	U
2	C	1636	C
2	C	1647	C

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	A5A	A	1001	-	29,30,30	2.62	11 (37%)	42,45,45	2.55	14 (33%)
3	A5A	B	1001	-	29,30,30	2.59	11 (37%)	42,45,45	2.51	14 (33%)

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
3	A5A	A	1001	-	-	5/18/35/35	0/3/3/3
3	A5A	B	1001	-	-	3/18/35/35	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1001	A5A	O5'-S	-6.11	1.47	1.60
3	A	1001	A5A	O5'-S	-6.05	1.47	1.60
3	A	1001	A5A	O1S-S	5.64	1.47	1.42
3	B	1001	A5A	O1S-S	5.63	1.47	1.42
3	A	1001	A5A	C6-N6	5.01	1.47	1.34
3	B	1001	A5A	C6-N6	4.98	1.46	1.34
3	A	1001	A5A	C-N3S	3.97	1.44	1.37
3	A	1001	A5A	O-C	-3.92	1.15	1.23
3	B	1001	A5A	O-C	-3.87	1.16	1.23
3	A	1001	A5A	C2'-C3'	-3.81	1.43	1.53
3	B	1001	A5A	C2'-C3'	-3.81	1.43	1.53
3	B	1001	A5A	C-N3S	3.78	1.44	1.37
3	A	1001	A5A	O2S-S	3.54	1.45	1.42
3	B	1001	A5A	O2S-S	3.49	1.45	1.42
3	A	1001	A5A	S-N3S	3.43	1.65	1.59
3	B	1001	A5A	S-N3S	3.21	1.65	1.59
3	A	1001	A5A	C3'-C4'	-2.93	1.45	1.53
3	B	1001	A5A	C3'-C4'	-2.91	1.45	1.53
3	A	1001	A5A	CA-N	-2.47	1.40	1.48
3	B	1001	A5A	CA-N	-2.47	1.40	1.48
3	B	1001	A5A	C2'-C1'	-2.04	1.47	1.53
3	A	1001	A5A	C2'-C1'	-2.00	1.47	1.53

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	A5A	O2S-S-O1S	-8.12	108.69	120.85
3	B	1001	A5A	O2S-S-O1S	-7.50	109.62	120.85
3	A	1001	A5A	C5-C4-N3	-5.82	118.70	126.72
3	B	1001	A5A	N3-C2-N1	-5.74	119.89	128.58
3	A	1001	A5A	N3-C2-N1	-5.58	120.14	128.58
3	B	1001	A5A	C5-C4-N3	-5.52	119.12	126.72
3	A	1001	A5A	O5'-C5'-C4'	4.84	116.19	107.57
3	B	1001	A5A	O5'-C5'-C4'	4.43	115.47	107.57
3	A	1001	A5A	N3-C4-N9	4.00	133.97	127.17
3	A	1001	A5A	C2-N3-C4	3.93	121.43	111.83
3	B	1001	A5A	C2-N3-C4	3.89	121.33	111.83
3	B	1001	A5A	N3-C4-N9	3.78	133.60	127.17
3	B	1001	A5A	N9-C8-N7	-3.62	108.80	113.94
3	A	1001	A5A	C4-C5-N7	-3.56	106.51	110.58
3	A	1001	A5A	C5-N7-C8	3.56	109.05	103.45
3	A	1001	A5A	N9-C8-N7	-3.53	108.92	113.94
3	B	1001	A5A	C4-C5-N7	-3.53	106.55	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1001	A5A	C5-N7-C8	3.52	108.98	103.45
3	B	1001	A5A	O4'-C1'-N9	2.84	113.54	108.09
3	B	1001	A5A	C4-N9-C8	2.53	108.40	105.74
3	B	1001	A5A	CA-C-N3S	2.50	119.89	114.46
3	B	1001	A5A	C2-N1-C6	2.43	122.72	118.73
3	A	1001	A5A	C4-N9-C8	2.35	108.20	105.74
3	B	1001	A5A	C2'-C3'-C4'	2.35	107.14	102.61
3	A	1001	A5A	O4'-C1'-N9	2.34	112.58	108.09
3	A	1001	A5A	C2-N1-C6	2.22	122.38	118.73
3	A	1001	A5A	CA-C-N3S	2.21	119.27	114.46
3	A	1001	A5A	C2'-C3'-C4'	2.19	106.83	102.61

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	A5A	C5'-O5'-S-N3S
3	A	1001	A5A	C5'-O5'-S-O2S
3	A	1001	A5A	C3'-C4'-C5'-O5'
3	B	1001	A5A	C5'-O5'-S-N3S
3	A	1001	A5A	C5'-O5'-S-O1S
3	A	1001	A5A	C-N3S-S-O2S
3	B	1001	A5A	C5'-O5'-S-O2S
3	B	1001	A5A	C5'-O5'-S-O1S

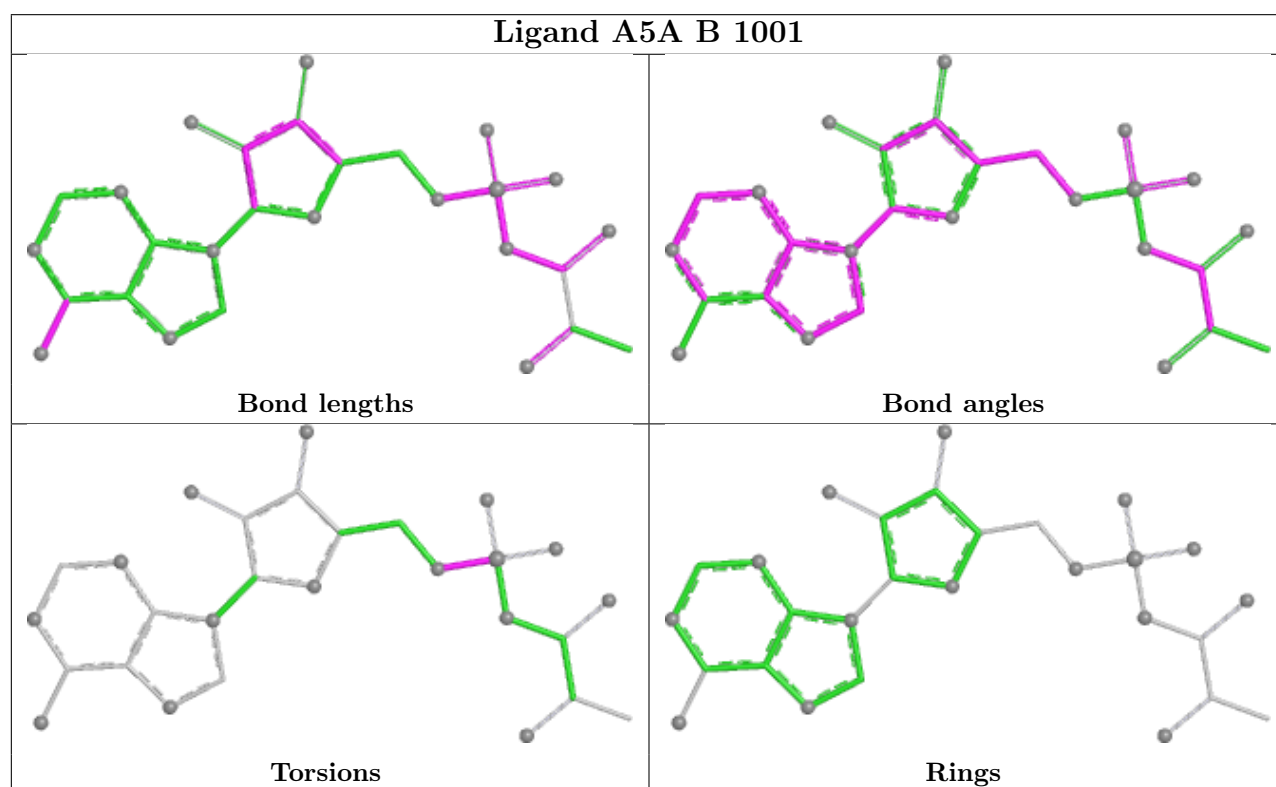
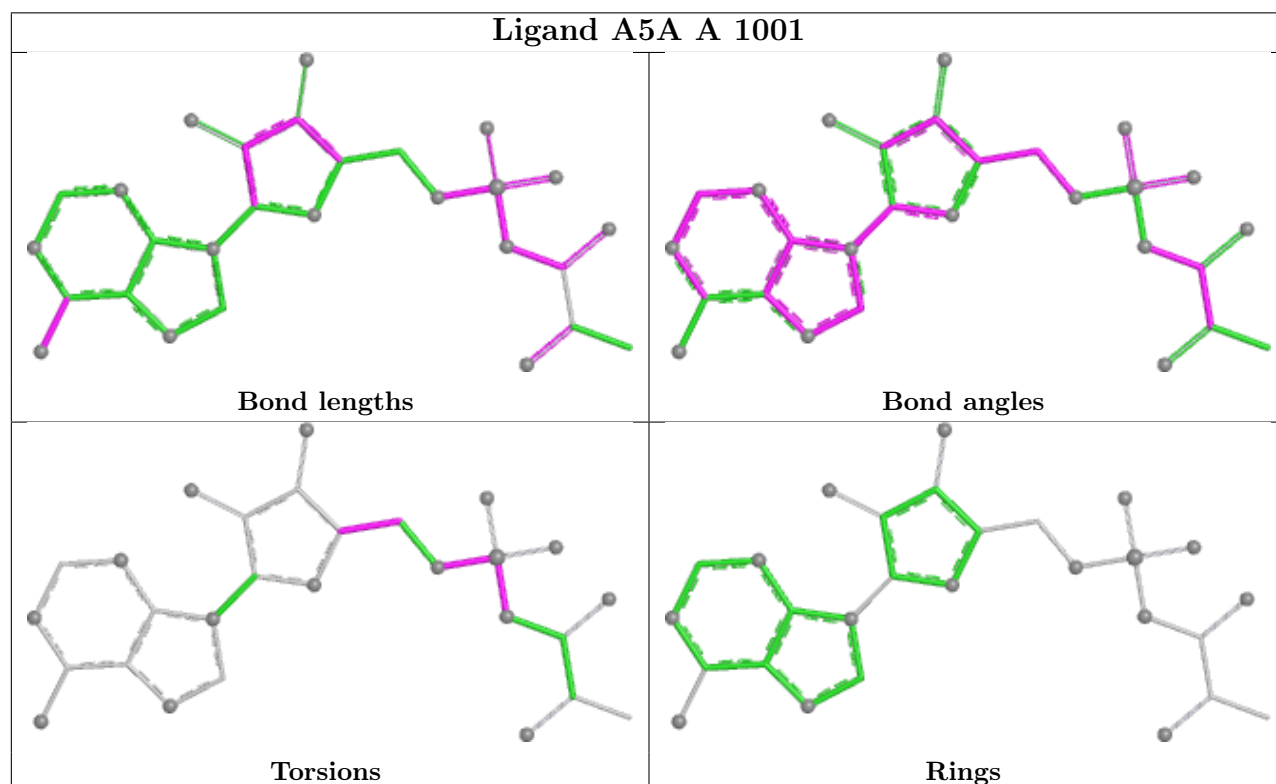
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	A5A	2	0
3	B	1001	A5A	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9	
1	A	905/906 (99%)	-0.03	11 (1%)	76	53	45, 111, 199, 233	0
1	B	904/906 (99%)	-0.03	11 (1%)	76	53	49, 122, 194, 246	0
2	C	75/75 (100%)	-0.27	0	100	100	59, 90, 162, 213	0
All	All	1884/1887 (99%)	-0.04	22 (1%)	76	53	45, 116, 197, 246	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	628	SER	4.6
1	B	570	LEU	4.1
1	A	529	VAL	3.8
1	A	627	PHE	3.3
1	B	536	PHE	2.6
1	B	68	TYR	2.6
1	A	732	PHE	2.6
1	B	248	GLU	2.6
1	B	628	SER	2.5
1	A	3	LEU	2.5
1	A	302	GLY	2.4
1	B	186	TYR	2.4
1	B	210	VAL	2.3
1	B	39	ILE	2.3
1	A	716	MET	2.3
1	B	715	GLY	2.2
1	A	582	THR	2.2
1	B	40	CYS	2.1
1	A	580	VAL	2.1
1	A	540	SER	2.1
1	B	205	VAL	2.1
1	A	626	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

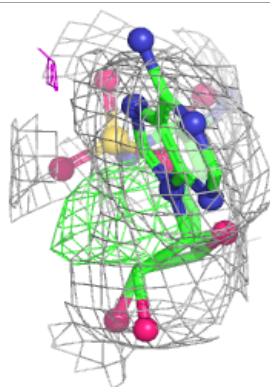
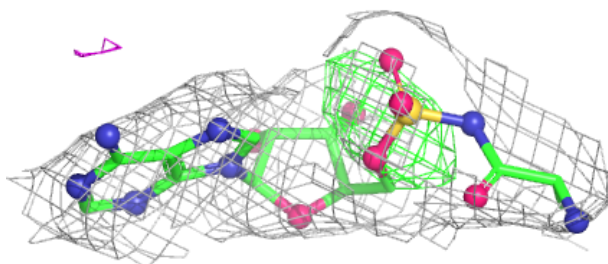
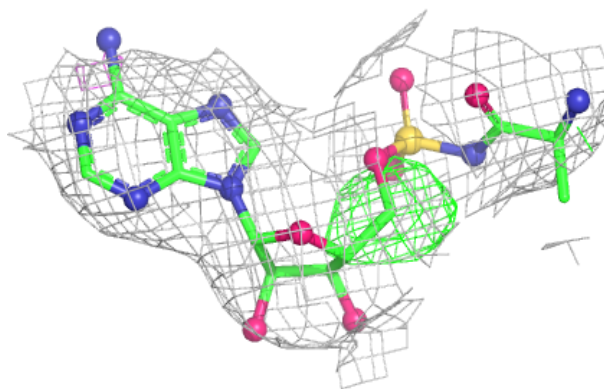
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	A5A	B	1001	28/28	0.90	0.11	86,117,135,148	0
3	A5A	A	1001	28/28	0.94	0.11	94,107,119,123	0
4	ZN	A	1002	1/1	0.94	0.08	119,119,119,119	0
4	ZN	B	1002	1/1	0.97	0.06	109,109,109,109	0

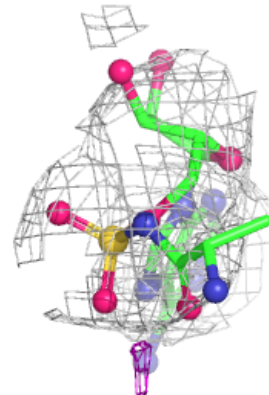
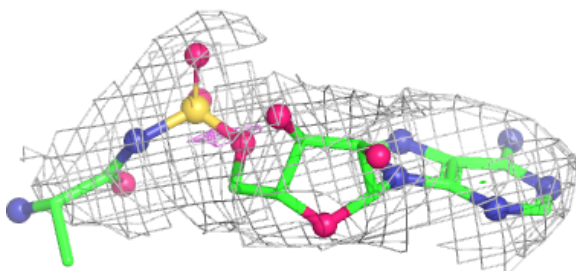
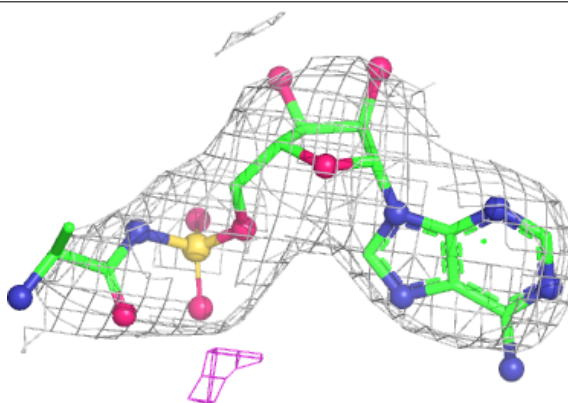
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around A5A B 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around A5A A 1001:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.