



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:49 AM GMT

PDB ID : 3CBF
Title : Crystal structure of LysN, alpha-aminoadipate aminotransferase, from *Thermus thermophilus* HB27
Authors : Tomita, T.; Miyazaki, T.; Miyagawa, T.; Fushinobu, S.; Kuzuyama, T.; Nishiyama, M.
Deposited on : 2008-02-21
Resolution : 1.67 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

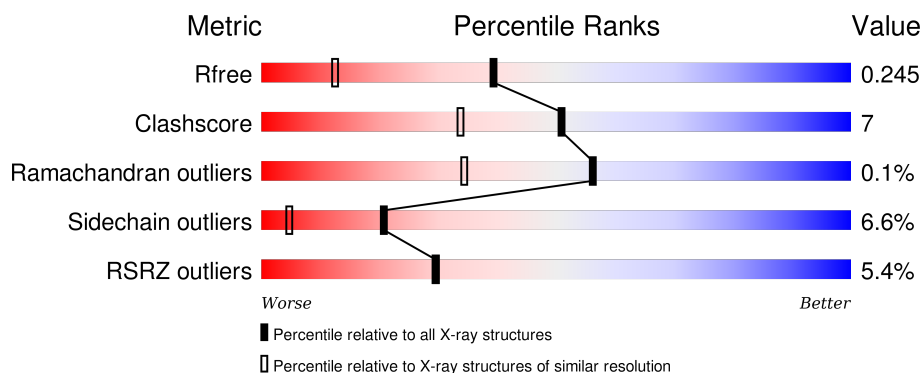
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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	4802 (1.70-1.66)
Clashscore	102246	5317 (1.70-1.66)
Ramachandran outliers	100387	5225 (1.70-1.66)
Sidechain outliers	100360	5224 (1.70-1.66)
RSRZ outliers	91569	4813 (1.70-1.66)

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	397	<div> <div>6%</div> <div>81%</div> <div>15%</div> <div>••</div> </div>
1	B	397	<div> <div>5%</div> <div>84%</div> <div>13%</div> <div>••</div> </div>

2 Entry composition [i](#)

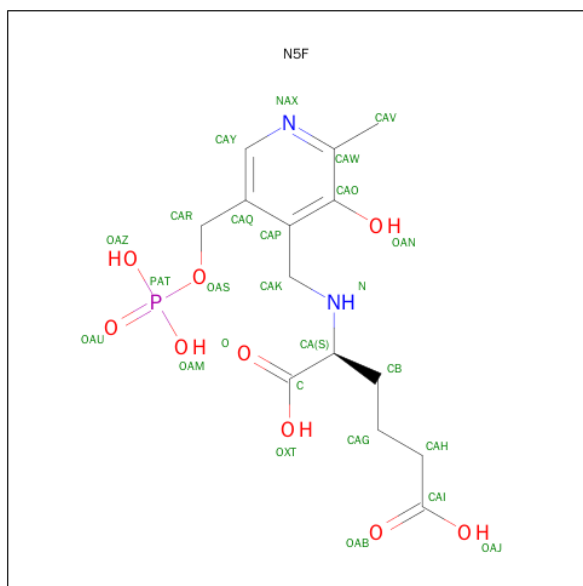
There are 3 unique types of molecules in this entry. The entry contains 6639 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alpha-aminodipate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	6	0
			3086	1987	542	548	9			
1	B	392	Total	C	N	O	S	0	3	0
			3070	1970	542	549	9			

- Molecule 2 is (2S)-2-[(3-HYDROXY-2-METHYL-5-[(PHOSPHONOOXY)METHYL]PYRIDIN-4-YL)METHYL]AMINO]HEXANEDIOIC ACID (three-letter code: N5F) (formula: C₁₄H₂₁N₂O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			26	14	2	9	1		
2	B	1	Total	C	N	O	P	0	0
			26	14	2	9	1		

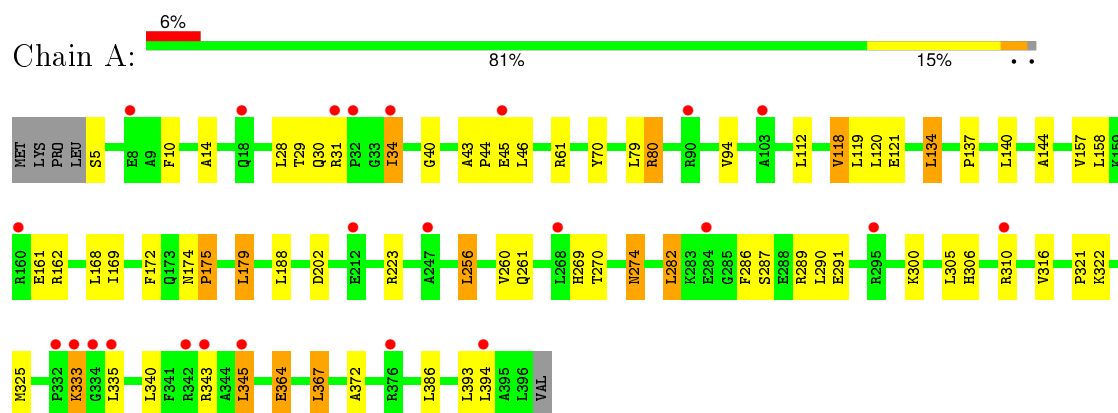
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	211	Total 211	O 211	0	0
3	B	220	Total 220	O 220	0	0

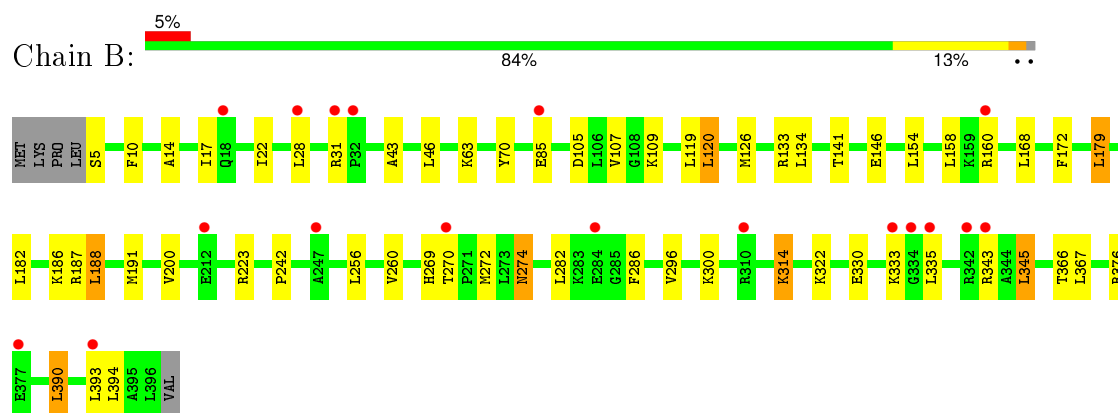
3 Residue-property plots [i](#)

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: Alpha-aminodipate aminotransferase



• Molecule 1: Alpha-aminodipate aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.28 Å 93.24 Å 150.88 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.69 – 1.67 34.68 – 1.67	Depositor EDS
% Data completeness (in resolution range)	96.8 (34.69-1.67) 96.7 (34.68-1.67)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 1.67 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.202 , 0.247 0.201 , 0.245	Depositor DCC
R_{free} test set	4415 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 49.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 88140 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6639	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.50 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.2938e-03.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: N5F

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	0.61	0/3170	0.75	4/4283 (0.1%)
1	B	0.62	0/3146	0.71	2/4252 (0.0%)
All	All	0.61	0/6316	0.73	6/8535 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	367	LEU	CA-CB-CG	6.92	131.21	115.30
1	A	80	ARG	NE-CZ-NH2	6.64	123.62	120.30
1	B	390	LEU	CA-CB-CG	5.81	128.66	115.30
1	A	80	ARG	NE-CZ-NH1	-5.81	117.40	120.30
1	A	61	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	B	188	LEU	CB-CG-CD2	-5.02	102.47	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3086	0	3182	46	0
1	B	3070	0	3137	44	0
2	A	26	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	26	0	17	1	0
3	A	211	0	0	4	0
3	B	220	0	0	12	0
All	All	6639	0	6352	86	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 7.

All (86) 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:105:ASP:OD2	3:B:773:HOH:O	1.61	1.14
1:A:140:LEU:HD11	1:A:161:GLU:HG2	1.33	1.06
1:A:140:LEU:CD1	1:A:161:GLU:HG2	2.01	0.89
1:B:46:LEU:HD11	1:B:296:VAL:HG21	1.56	0.86
1:B:272[A]:MET:HB2	3:B:693:HOH:O	1.79	0.81
1:B:133:ARG:NH1	3:B:639:HOH:O	2.19	0.74
1:B:272[B]:MET:HB2	3:B:693:HOH:O	1.90	0.71
1:A:29:THR:HG22	1:A:34:ILE:HD11	1.71	0.71
1:B:314:LYS:HE3	3:B:757:HOH:O	1.90	0.70
1:A:274:ASN:H	1:A:274:ASN:HD22	1.41	0.69
1:A:223:ARG:HD2	3:A:581:HOH:O	1.93	0.68
1:B:31:ARG:HD2	3:B:658:HOH:O	1.95	0.66
1:B:107:VAL:HG11	1:B:200:VAL:HG21	1.78	0.66
1:A:168:LEU:CD1	1:A:188:LEU:HD21	2.27	0.65
1:A:261:GLN:HE21	1:B:17:ILE:HG22	1.61	0.64
1:A:112:LEU:HD21	1:A:118[A]:VAL:HG13	1.79	0.64
1:B:5:SER:N	3:B:779:HOH:O	2.31	0.62
1:B:343:ARG:NE	1:B:393:LEU:HD13	2.14	0.62
1:B:274:ASN:H	1:B:274:ASN:HD22	1.46	0.62
1:A:112:LEU:CD2	1:A:118[A]:VAL:HG13	2.33	0.59
1:A:168:LEU:HD13	1:A:188:LEU:HD21	1.85	0.58
1:A:134:LEU:HD11	1:B:109:LYS:HD3	1.85	0.58
1:B:172:PHE:CE1	1:B:179:LEU:HG	2.39	0.58
1:B:223:ARG:NH2	3:B:788:HOH:O	2.18	0.57
1:B:322:LYS:HE2	3:B:616:HOH:O	2.03	0.57
1:A:28:LEU:HD21	1:A:345:LEU:HD21	1.87	0.56
1:B:274:ASN:HD22	1:B:274:ASN:N	2.03	0.56
1:B:168:LEU:HD13	1:B:188:LEU:HD21	1.87	0.56
1:A:306:HIS:HD2	1:A:310:ARG:HH11	1.53	0.54
1:B:119:LEU:HD11	1:B:154:LEU:CD1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:LYS:HE3	3:B:790:HOH:O	2.07	0.54
1:B:269:HIS:HD2	1:B:270:THR:O	1.91	0.53
1:A:274:ASN:N	1:A:274:ASN:HD22	2.07	0.53
1:B:22:ILE:HD12	1:B:126:MET:HG2	1.91	0.53
1:B:146:GLU:HG3	3:B:616:HOH:O	2.10	0.52
1:A:287:SER:O	1:A:291:GLU:HG3	2.10	0.51
1:A:343:ARG:NE	1:A:393:LEU:HD13	2.26	0.51
1:A:364:GLU:CD	1:A:364:GLU:H	2.14	0.51
1:A:118[A]:VAL:HG22	1:A:137:PRO:HB2	1.92	0.51
1:A:70:TYR:CZ	1:B:242:PRO:HB3	2.46	0.50
1:A:10:PHE:HB3	1:A:14:ALA:HB3	1.93	0.50
1:A:112:LEU:HD21	1:A:118[A]:VAL:CG1	2.42	0.50
1:A:29:THR:HA	1:A:34:ILE:HG12	1.95	0.49
1:A:40:GLY:HA3	1:A:325[B]:MET:HE1	1.95	0.49
1:B:376:ARG:NH1	1:B:376:ARG:HB3	2.27	0.49
1:B:376:ARG:HB3	1:B:376:ARG:HH11	1.78	0.49
1:A:305:LEU:HD11	1:A:321:PRO:HD2	1.93	0.49
1:B:187:ARG:NE	3:B:763:HOH:O	2.30	0.48
1:A:40:GLY:HA3	1:A:325[B]:MET:CE	2.44	0.47
1:B:120:LEU:O	1:B:141:THR:HA	2.13	0.47
1:B:70:TYR:HA	1:B:269:HIS:HE1	1.80	0.47
1:B:187:ARG:O	1:B:191:MET:HG3	2.14	0.47
1:B:28:LEU:HD21	1:B:345:LEU:HD21	1.96	0.46
1:B:343:ARG:HD2	1:B:393:LEU:HD22	1.98	0.45
1:B:10:PHE:HB3	1:B:14:ALA:HB3	1.98	0.45
1:A:261:GLN:HB2	1:B:17:ILE:CG2	2.47	0.45
1:A:269:HIS:HD2	1:A:270:THR:O	1.99	0.45
1:A:274:ASN:ND2	1:A:274:ASN:N	2.65	0.44
1:A:119:LEU:HD12	1:A:157:VAL:HG11	1.99	0.44
1:A:172:PHE:CE1	1:A:179[B]:LEU:HD13	2.52	0.44
1:B:43:ALA:HB2	1:B:300:LYS:HE3	2.01	0.43
1:A:256:LEU:HD13	1:A:260:VAL:HG23	2.01	0.43
2:B:501:N5F:N	2:B:501:N5F:OAN	2.52	0.43
1:B:70:TYR:HA	1:B:269:HIS:CE1	2.54	0.43
1:B:330:GLU:HG2	1:B:366:THR:HG22	2.01	0.42
1:A:31:ARG:HG2	3:A:699:HOH:O	2.18	0.42
1:A:289:ARG:NH1	3:A:694:HOH:O	2.35	0.42
1:A:169:ILE:HG12	1:A:202:ASP:HB3	2.01	0.42
1:B:274:ASN:ND2	1:B:274:ASN:N	2.66	0.42
1:B:10:PHE:HB3	1:B:14:ALA:CB	2.49	0.42
1:A:174:ASN:HA	1:A:175:PRO:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:LEU:HG	1:A:286:PHE:CD1	2.54	0.42
1:A:121:GLU:HB3	1:A:144:ALA:HB2	2.02	0.42
1:B:256:LEU:O	1:B:260:VAL:HG23	2.20	0.42
1:A:80:ARG:HD2	1:A:94:VAL:O	2.19	0.41
1:A:134:LEU:HD11	1:B:109:LYS:CD	2.49	0.41
1:A:325[B]:MET:HB3	1:A:372:ALA:HB2	2.02	0.41
1:A:43:ALA:HA	1:A:44:PRO:HD3	1.94	0.41
1:B:343:ARG:HE	1:B:393:LEU:HD13	1.85	0.41
1:A:306:HIS:CD2	1:A:310:ARG:HH11	2.36	0.41
1:A:80:ARG:CD	1:A:94:VAL:O	2.69	0.41
1:A:300[A]:LYS:NZ	3:A:643:HOH:O	2.54	0.41
1:A:343:ARG:HE	1:A:393:LEU:HD13	1.85	0.40
1:B:282:LEU:HD22	1:B:286:PHE:CD1	2.57	0.40
1:A:274:ASN:ND2	1:A:274:ASN:H	2.13	0.40
1:B:182:LEU:HG	1:B:186:LYS:HE2	2.04	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	396/397 (100%)	384 (97%)	11 (3%)	1 (0%)	46	25
1	B	393/397 (99%)	382 (97%)	11 (3%)	0	100	100
All	All	789/794 (99%)	766 (97%)	22 (3%)	1 (0%)	56	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	LYS

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	317/316 (100%)	287 (90%)	30 (10%)	11	2
1	B	314/316 (99%)	300 (96%)	14 (4%)	34	11
All	All	631/632 (100%)	587 (93%)	44 (7%)	21	4

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	30	GLN
1	A	34	ILE
1	A	45	GLU
1	A	46	LEU
1	A	79	LEU
1	A	118[A]	VAL
1	A	118[B]	VAL
1	A	120[A]	LEU
1	A	120[B]	LEU
1	A	134	LEU
1	A	158	LEU
1	A	162	ARG
1	A	175	PRO
1	A	179[A]	LEU
1	A	179[B]	LEU
1	A	256	LEU
1	A	274	ASN
1	A	282	LEU
1	A	290	LEU
1	A	316	VAL
1	A	322	LYS
1	A	333	LYS
1	A	335	LEU
1	A	340	LEU
1	A	345	LEU
1	A	364	GLU

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Mol	Chain	Res	Type
1	A	367	LEU
1	A	386	LEU
1	A	394	LEU
1	B	85	GLU
1	B	120	LEU
1	B	134	LEU
1	B	158	LEU
1	B	160	ARG
1	B	179	LEU
1	B	274	ASN
1	B	314	LYS
1	B	333	LYS
1	B	335	LEU
1	B	345	LEU
1	B	367	LEU
1	B	390	LEU
1	B	394	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	101	GLN
1	A	135	GLN
1	A	261	GLN
1	A	269	HIS
1	A	274	ASN
1	A	302	GLN
1	A	306	HIS
1	A	360	ASN
1	B	30	GLN
1	B	101	GLN
1	B	135	GLN
1	B	190	GLN
1	B	261	GLN
1	B	269	HIS
1	B	274	ASN
1	B	360	ASN

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 ⓘ

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	N5F	A	500	-	20,26,26	1.23	1 (5%)	24,36,36	1.75	6 (25%)
2	N5F	B	501	-	20,26,26	1.43	2 (10%)	24,36,36	1.53	4 (16%)

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	N5F	A	500	-	-	0/15/21/21	0/1/1/1
2	N5F	B	501	-	-	0/15/21/21	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	N5F	CA-N	2.44	1.51	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	N5F	CAK-CAP	4.34	1.56	1.51
2	B	501	N5F	CAK-CAP	4.76	1.57	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	N5F	OAM-PAT-OAS	-3.14	97.53	106.56
2	A	500	N5F	OAM-PAT-OAS	-2.68	98.85	106.56
2	A	500	N5F	CAQ-CAY-NAX	-2.12	120.18	123.86
2	A	500	N5F	CAO-CAP-CAQ	-2.07	116.63	118.82
2	B	501	N5F	OAS-PAT-OAU	2.04	112.32	107.14
2	A	500	N5F	CAY-NAX-CAW	2.09	123.54	119.28
2	A	500	N5F	CAY-CAQ-CAP	2.20	119.73	118.09
2	B	501	N5F	CAK-N-CA	2.33	117.38	113.81
2	B	501	N5F	CAK-CAP-CAQ	2.47	121.91	119.71
2	A	500	N5F	CAK-N-CA	5.47	122.17	113.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	N5F	1	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	392/397 (98%)	0.23	24 (6%) 25 24	13, 22, 35, 46	0
1	B	392/397 (98%)	0.12	18 (4%) 36 38	13, 21, 34, 41	0
All	All	784/794 (98%)	0.17	42 (5%) 29 29	13, 22, 35, 46	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	LYS	4.3
1	B	32	PRO	4.2
1	A	32	PRO	4.0
1	A	376	ARG	3.8
1	A	334	GLY	3.8
1	A	335	LEU	3.6
1	B	31	ARG	3.5
1	B	284	GLU	3.5
1	A	310	ARG	3.2
1	B	28	LEU	3.1
1	A	160	ARG	3.1
1	B	334	GLY	2.9
1	B	160	ARG	2.8
1	A	31	ARG	2.8
1	B	335	LEU	2.7
1	A	394	LEU	2.7
1	A	45	GLU	2.6
1	A	8	GLU	2.5
1	B	377	GLU	2.5
1	A	90	ARG	2.5
1	B	18	GLN	2.5
1	B	393	LEU	2.4
1	A	295	ARG	2.4
1	A	342	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	85	GLU	2.3
1	B	342	ARG	2.2
1	B	270	THR	2.2
1	A	18	GLN	2.2
1	B	343	ARG	2.1
1	A	247	ALA	2.1
1	A	332	PRO	2.1
1	A	343	ARG	2.1
1	B	310	ARG	2.1
1	A	103	ALA	2.1
1	B	333	LYS	2.1
1	B	247	ALA	2.1
1	A	268	LEU	2.1
1	A	212	GLU	2.0
1	A	345	LEU	2.0
1	A	34	ILE	2.0
1	A	284	GLU	2.0
1	B	212	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 carbohydrates 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. 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(Å ²)	Q<0.9
2	N5F	A	500	26/26	0.97	0.13	-0.05	14,18,20,21	0
2	N5F	B	501	26/26	0.97	0.12	-0.42	13,17,20,21	0

6.5 Other polymers

There are no such residues in this entry.