



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 03:21 PM GMT

PDB ID : 2CDQ
Title : CRYSTAL STRUCTURE OF ARABIDOPSIS THALIANA ASPARTATE KINASE COMPLEXED WITH LYSINE AND S-ADENOSYLMETHIONINE
Authors : Mas-Droux, C.; Curien, G.; Robert-Genthon, M.; Laurencin, M.; Ferrer, J.L.; Dumas, R.
Deposited on : 2006-01-26
Resolution : 2.85 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>

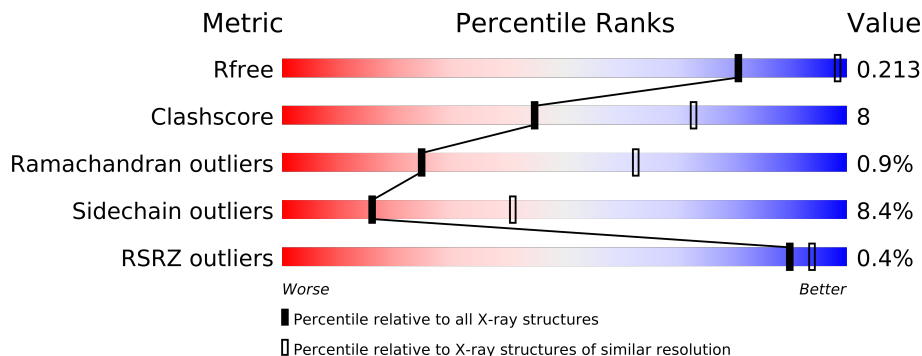
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.85 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	1524 (2.90-2.82)
Clashscore	79885	1879 (2.90-2.82)
Ramachandran outliers	78287	1824 (2.90-2.82)
Sidechain outliers	78261	1827 (2.90-2.82)
RSRZ outliers	66119	1526 (2.90-2.82)

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	510	
1	B	510	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	LYS	A	601	-	X
2	LYS	B	601	-	X

2 Entry composition i

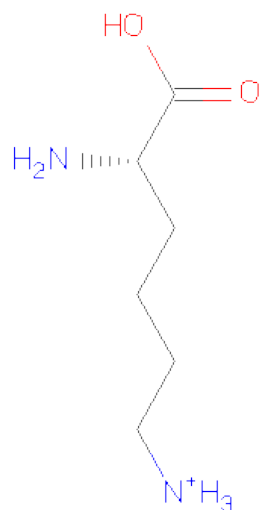
There are 5 unique types of molecules in this entry. The entry contains 7522 atoms, of which 0 are hydrogen and 0 are deuterium.

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 ASPARTOKINASE.

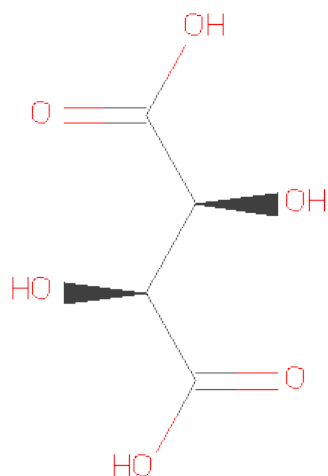
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	0	0
			3616	2311	598	691	16			
1	B	470	Total	C	N	O	S	0	0	0
			3616	2311	598	691	16			

- Molecule 2 is LYSINE (three-letter code: LYS) (formula: $\text{C}_6\text{H}_{15}\text{N}_2\text{O}_2$).



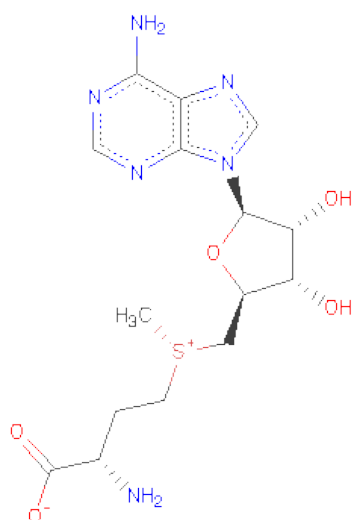
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 3 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		

- Molecule 4 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 5 is water.

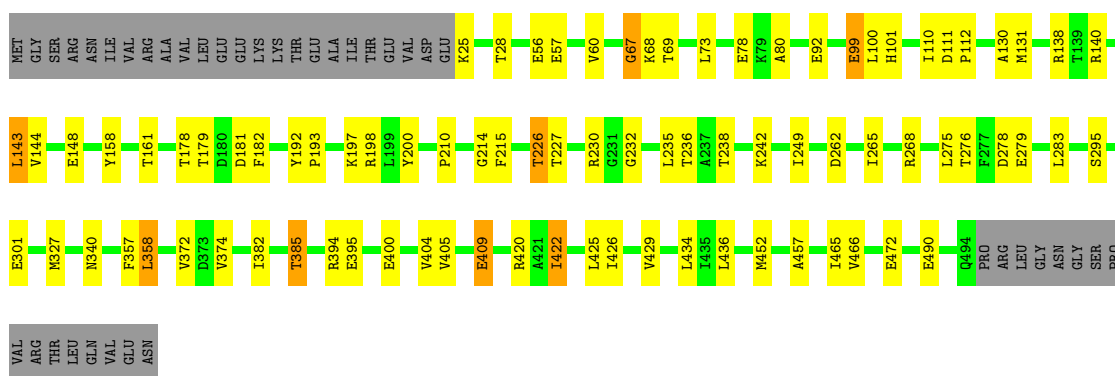
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	96	Total	O	0	0
			96	96		
5	B	80	Total	O	0	0
			80	80		

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.

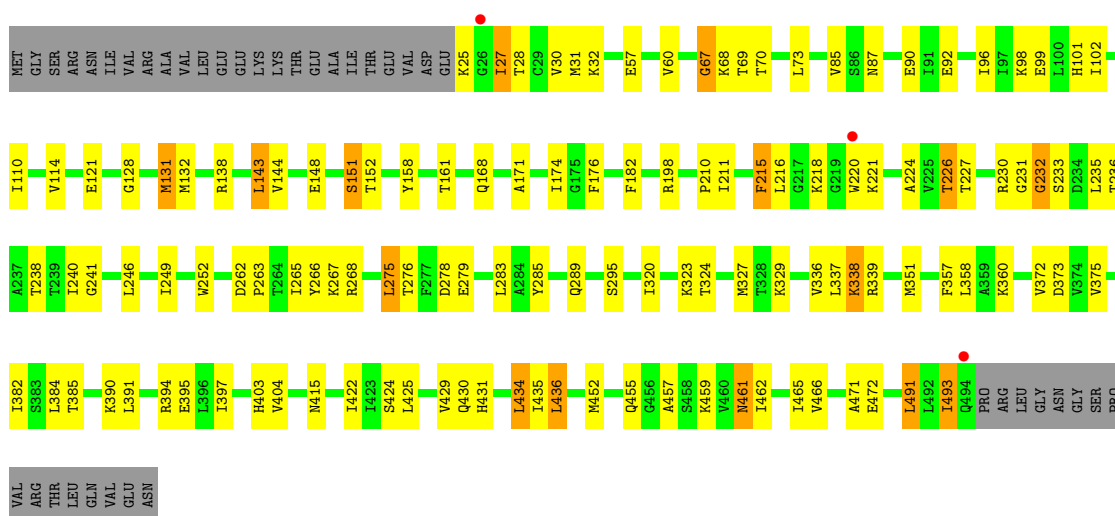
• Molecule 1: ASPARTOKINASE

Chain A:



• Molecule 1: ASPARTOKINASE

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	117.34Å 117.34Å 255.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.67 – 2.85 15.67 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (15.67-2.85) 96.7 (15.67-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.202 , 0.244 0.194 , 0.213	Depositor DCC
R_{free} test set	2042 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	67.4	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 22.4	EDS
Estimated twinning fraction	0.470 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	2 of 40648 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7522	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: SAM, TAR

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	0.38	0/3673	0.54	0/4977
1	B	0.38	0/3673	0.56	1/4977 (0.0%)
All	All	0.38	0/7346	0.55	1/9954 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	434	LEU	CA-CB-CG	5.22	127.32	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3616	0	3721	55	0
1	B	3616	0	3721	69	0
2	A	20	0	24	9	0
2	B	20	0	24	9	0
3	A	10	0	4	0	0
3	B	10	0	4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	27	0	22	0	0
4	B	27	0	22	1	0
5	A	96	0	0	5	0
5	B	80	0	0	3	0
All	All	7522	0	7542	126	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 8.

All (126) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:178:THR:HG21	1:A:226:THR:HG21	1.28	1.11
1:B:230:ARG:HH11	1:B:230:ARG:HG2	1.39	0.86
1:A:262:ASP:HB3	1:A:265:ILE:HD12	1.58	0.85
1:A:230:ARG:HH11	1:A:230:ARG:HG2	1.46	0.80
1:A:265:ILE:HG23	1:A:472:GLU:HG3	1.70	0.74
1:A:242:LYS:HE3	1:A:301:GLU:HG3	1.69	0.74
1:A:374:VAL:H	1:A:385:THR:HG22	1.52	0.73
1:B:372:VAL:HG11	1:B:384:LEU:HD22	1.71	0.72
1:A:385:THR:HG23	5:A:2061:HOH:O	1.89	0.72
1:A:178:THR:HG22	1:A:179:THR:O	1.90	0.71
1:A:490:GLU:HG2	1:A:490:GLU:O	1.92	0.70
1:B:385:THR:HG21	1:B:422:ILE:HD11	1.72	0.70
1:A:214:GLY:O	1:A:236:THR:OG1	2.07	0.69
1:B:372:VAL:N	2:B:600:LYS:OXT	2.25	0.68
1:A:357:PHE:H	2:B:600:LYS:N	1.92	0.67
1:A:394:ARG:HG2	1:A:395:GLU:O	1.95	0.67
1:B:455:GLN:HE21	1:B:462:ILE:HB	1.60	0.67
1:B:236:THR:O	1:B:240:ILE:HG12	1.97	0.65
2:A:600:LYS:HD3	1:B:351:MET:HE3	1.78	0.65
1:B:230:ARG:HH11	1:B:230:ARG:CG	2.12	0.62
1:A:372:VAL:O	2:A:600:LYS:HG3	1.99	0.62
1:B:73:LEU:HB3	1:B:143:LEU:HD22	1.82	0.62
1:A:276:THR:HG22	1:A:278:ASP:H	1.64	0.61
1:A:372:VAL:N	2:A:600:LYS:OXT	2.31	0.61
1:B:110:ILE:HD11	1:B:158:TYR:HA	1.82	0.60
1:A:69:THR:HG21	1:A:101:HIS:HE1	1.65	0.60
1:B:276:THR:HG22	1:B:278:ASP:H	1.67	0.60
1:A:452:MET:HB3	1:A:465:ILE:HB	1.84	0.59
1:A:358:LEU:HD22	2:B:600:LYS:HA	1.84	0.58
1:A:232:GLY:HA3	2:A:601:LYS:HD3	1.86	0.58
1:B:98:LYS:O	1:B:102:ILE:HG12	2.04	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:394:ARG:HD2	1:B:395:GLU:O	2.04	0.58
1:B:238:THR:HA	1:B:249:ILE:HD13	1.84	0.58
1:B:436:LEU:HD11	1:B:462:ILE:HD13	1.85	0.57
1:B:215:PHE:HB3	1:B:232:GLY:HA3	1.85	0.57
2:B:601:LYS:NZ	5:B:2079:HOH:O	2.26	0.57
1:A:178:THR:CG2	1:A:226:THR:HG21	2.20	0.57
1:A:238:THR:HA	1:A:249:ILE:HD13	1.87	0.56
1:B:138:ARG:HG3	1:B:182:PHE:CZ	2.41	0.56
1:B:337:LEU:HD11	1:B:471:ALA:HB1	1.87	0.56
1:B:230:ARG:HG2	1:B:230:ARG:NH1	2.17	0.53
2:B:601:LYS:N	2:B:601:LYS:HD3	2.25	0.52
1:B:215:PHE:O	1:B:227:THR:HA	2.09	0.52
1:A:230:ARG:HH11	1:A:230:ARG:CG	2.19	0.52
1:B:285:TYR:HE2	1:B:391:LEU:HD11	1.75	0.52
1:B:92:GLU:O	1:B:96:ILE:HG12	2.10	0.52
1:B:60:VAL:HG22	1:B:210:PRO:HG2	1.92	0.51
1:B:241:GLY:HA2	1:B:246:LEU:HD12	1.92	0.51
1:B:373:ASP:HB3	1:B:385:THR:HG22	1.93	0.50
1:B:375:VAL:HG22	1:B:384:LEU:CD2	2.41	0.50
1:B:431:HIS:O	1:B:435:ILE:HG12	2.11	0.50
1:A:73:LEU:HB3	1:A:143:LEU:HD22	1.93	0.49
1:B:338:LYS:HB2	1:B:422:ILE:HB	1.93	0.49
1:B:266:TYR:CE1	1:B:268:ARG:HB2	2.48	0.49
1:B:372:VAL:O	2:B:600:LYS:HG3	2.13	0.48
1:B:218:LYS:O	1:B:224:ALA:O	2.32	0.48
1:A:110:ILE:HD11	1:A:158:TYR:HB2	1.95	0.48
1:B:394:ARG:O	4:B:1500:SAM:H8	2.13	0.48
1:B:336:VAL:HB	1:B:424:SER:HB2	1.95	0.47
2:A:600:LYS:N	1:B:357:PHE:H	2.12	0.47
1:A:69:THR:HG21	1:A:101:HIS:CE1	2.48	0.47
1:B:461:ASN:C	1:B:461:ASN:HD22	2.18	0.47
1:A:400:GLU:O	1:A:404:VAL:HG23	2.15	0.47
1:A:138:ARG:HG3	1:A:182:PHE:CZ	2.49	0.47
1:B:452:MET:HB3	1:B:465:ILE:HB	1.97	0.47
1:B:73:LEU:HD13	1:B:144:VAL:HA	1.97	0.47
1:A:67:GLY:O	1:A:68:LYS:HB2	2.16	0.47
2:A:600:LYS:N	1:B:357:PHE:CB	2.78	0.46
1:B:70:THR:HG21	2:B:601:LYS:HB2	1.96	0.46
1:B:152:THR:HG22	1:B:211:ILE:HG22	1.97	0.46
1:A:158:TYR:O	1:A:161:THR:HB	2.15	0.46
1:B:276:THR:HB	1:B:279:GLU:HG3	1.97	0.46
1:B:171:ALA:O	1:B:176:PHE:HB2	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:385:THR:CG2	5:A:2061:HOH:O	2.57	0.46
1:B:67:GLY:O	1:B:68:LYS:HB2	2.15	0.46
1:A:230:ARG:HG2	1:A:230:ARG:NH1	2.23	0.46
1:A:148:GLU:OE1	2:A:601:LYS:N	2.49	0.46
1:B:262:ASP:HB3	1:B:265:ILE:HD13	1.96	0.46
1:A:357:PHE:CB	2:B:600:LYS:N	2.79	0.46
1:B:158:TYR:O	1:B:161:THR:HB	2.16	0.46
1:B:31:MET:HG2	1:B:252:TRP:HE1	1.81	0.46
1:A:405:VAL:O	1:A:409:GLU:HB2	2.16	0.46
1:A:235:LEU:HD13	1:A:295:SER:HA	1.98	0.45
1:B:230:ARG:CG	1:B:230:ARG:NH1	2.73	0.45
1:A:192:TYR:HB2	1:A:193:PRO:HD3	1.99	0.45
1:B:128:GLY:O	1:B:132:MET:HG2	2.17	0.45
1:B:148:GLU:HA	1:B:151:SER:HB2	1.98	0.45
1:A:276:THR:HB	1:A:279:GLU:HG3	1.98	0.44
1:A:215:PHE:O	1:A:227:THR:HA	2.17	0.44
1:A:283:LEU:HD13	1:A:426:ILE:HG13	1.99	0.44
1:A:140:ARG:O	1:A:144:VAL:HG13	2.17	0.44
1:B:215:PHE:HB3	1:B:232:GLY:CA	2.47	0.44
1:B:327:MET:HE1	5:B:2032:HOH:O	2.18	0.44
1:B:339:ARG:HH22	1:B:472:GLU:CG	2.30	0.44
1:A:422:ILE:HD13	1:A:465:ILE:HG13	2.00	0.44
1:B:144:VAL:HG21	1:B:227:THR:HG21	1.99	0.44
1:A:372:VAL:O	2:A:600:LYS:CG	2.65	0.43
1:B:262:ASP:HA	1:B:263:PRO:HD2	1.90	0.43
1:A:178:THR:CG2	1:A:179:THR:N	2.82	0.43
1:B:231:GLY:HA2	5:B:2034:HOH:O	2.18	0.43
1:B:28:THR:OG1	1:B:57:GLU:HG3	2.18	0.43
1:B:461:ASN:C	1:B:461:ASN:ND2	2.71	0.43
1:A:385:THR:HG21	1:A:422:ILE:HD11	1.99	0.43
1:B:215:PHE:CB	1:B:232:GLY:HA3	2.48	0.43
1:B:27:ILE:HD12	1:B:27:ILE:H	1.83	0.43
1:B:372:VAL:O	2:B:600:LYS:CG	2.67	0.43
1:A:110:ILE:HG22	1:A:111:ASP:N	2.33	0.43
1:A:99:GLU:HG3	5:A:2019:HOH:O	2.18	0.42
1:A:73:LEU:HD13	1:A:144:VAL:HA	2.01	0.42
1:A:230:ARG:NH1	1:A:230:ARG:CG	2.79	0.42
1:B:275:LEU:HD21	1:B:283:LEU:HD23	2.01	0.42
1:B:220:TRP:HD1	1:B:221:LYS:HZ2	1.66	0.42
1:A:111:ASP:HA	1:A:112:PRO:HD3	1.85	0.42
1:B:85:VAL:HG22	1:B:131:MET:HA	2.01	0.42
1:B:32:LYS:HE3	1:B:233:SER:HB2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:60:VAL:HG22	1:A:210:PRO:HG2	2.00	0.42
1:B:69:THR:HG21	1:B:101:HIS:HE1	1.85	0.42
1:B:235:LEU:HD13	1:B:295:SER:HA	2.02	0.42
1:A:275:LEU:HD21	1:A:283:LEU:HD23	2.01	0.41
1:B:32:LYS:C	1:B:32:LYS:HD3	2.42	0.41
1:A:327:MET:HE1	5:A:2044:HOH:O	2.20	0.41
1:A:80:ALA:O	1:A:130:ALA:HA	2.21	0.41
2:A:600:LYS:N	1:B:357:PHE:HB3	2.36	0.40
1:B:216:LEU:HA	1:B:226:THR:O	2.21	0.40
1:A:69:THR:HG22	5:A:2013:HOH:O	2.21	0.40
1:A:28:THR:OG1	1:A:57:GLU:HG3	2.22	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	468/510 (92%)	449 (96%)	17 (4%)	2 (0%)	43	80
1	B	468/510 (92%)	436 (93%)	26 (6%)	6 (1%)	18	51
All	All	936/1020 (92%)	885 (95%)	43 (5%)	8 (1%)	25	62

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	GLY
1	B	67	GLY
1	B	457	ALA
1	B	491	LEU
1	A	457	ALA
1	B	232	GLY
1	B	493	ILE
1	B	174	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	401/436 (92%)	375 (94%)	26 (6%)	24	56
1	B	401/436 (92%)	360 (90%)	41 (10%)	11	28
All	All	802/872 (92%)	735 (92%)	67 (8%)	16	41

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS
1	A	56	GLU
1	A	78	GLU
1	A	92	GLU
1	A	99	GLU
1	A	100	LEU
1	A	131	MET
1	A	143	LEU
1	A	181	ASP
1	A	197	LYS
1	A	198	ARG
1	A	200	TYR
1	A	226	THR
1	A	268	ARG
1	A	340	ASN
1	A	358	LEU
1	A	382	ILE
1	A	385	THR
1	A	409	GLU
1	A	420	ARG
1	A	422	ILE
1	A	425	LEU
1	A	429	VAL
1	A	434	LEU
1	A	436	LEU
1	A	466	VAL
1	B	25	LYS
1	B	27	ILE
1	B	30	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	87	ASN
1	B	90	GLU
1	B	99	GLU
1	B	114	VAL
1	B	121	GLU
1	B	131	MET
1	B	143	LEU
1	B	151	SER
1	B	168	GLN
1	B	198	ARG
1	B	215	PHE
1	B	226	THR
1	B	267	LYS
1	B	275	LEU
1	B	289	GLN
1	B	320	ILE
1	B	323	LYS
1	B	324	THR
1	B	329	LYS
1	B	338	LYS
1	B	358	LEU
1	B	360	LYS
1	B	382	ILE
1	B	390	LYS
1	B	397	ILE
1	B	403	HIS
1	B	404	VAL
1	B	415	ASN
1	B	425	LEU
1	B	429	VAL
1	B	430	GLN
1	B	434	LEU
1	B	436	LEU
1	B	459	LYS
1	B	461	ASN
1	B	466	VAL
1	B	491	LEU
1	B	493	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	289	GLN
1	B	168	GLN
1	B	431	HIS
1	B	455	GLN
1	B	461	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 ⓘ

8 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	$\# Z > 2$
4	SAM	A	1500	-	26,29,29	1.01	2 (7%)	38,42,42	2.12	6 (15%)
2	LYS	A	600	-	9,9,9	0.78	0	10,10,10	1.31	2 (20%)
2	LYS	A	601	-	9,9,9	0.64	0	10,10,10	1.53	2 (20%)
3	TAR	A	700	-	9,9,9	1.09	0	12,12,12	0.89	0
4	SAM	B	1500	-	26,29,29	1.04	2 (7%)	38,42,42	2.21	8 (21%)
2	LYS	B	600	-	9,9,9	0.84	1 (11%)	10,10,10	1.25	2 (20%)
2	LYS	B	601	-	9,9,9	0.59	0	10,10,10	1.55	3 (30%)
3	TAR	B	700	-	9,9,9	1.12	0	12,12,12	0.94	0

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
4	SAM	A	1500	-	-	0/13/33/33	0/1/3/3
2	LYS	A	600	-	-	0/9/9/9	0/0/0/0
2	LYS	A	601	-	-	0/9/9/9	0/0/0/0
3	TAR	A	700	-	-	0/12/12/12	0/0/0/0
4	SAM	B	1500	-	-	0/13/33/33	0/1/3/3
2	LYS	B	600	-	-	0/9/9/9	0/0/0/0
2	LYS	B	601	-	-	0/9/9/9	0/0/0/0
3	TAR	B	700	-	-	0/12/12/12	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1500	SAM	C2-N3	3.34	1.38	1.32
4	A	1500	SAM	C2-N3	3.33	1.38	1.32
4	B	1500	SAM	C2-N1	2.44	1.38	1.33
4	A	1500	SAM	C2-N1	2.43	1.38	1.33
2	B	600	LYS	OXT-C	-2.13	1.22	1.30

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1500	SAM	N3-C2-N1	-10.21	120.18	128.71
4	A	1500	SAM	N3-C2-N1	-10.20	120.18	128.71
4	B	1500	SAM	CG-CB-CA	3.99	118.09	112.22
4	B	1500	SAM	N3-C4-N9	3.98	132.62	125.43
4	A	1500	SAM	N3-C4-N9	3.70	132.11	125.43
2	A	601	LYS	OXT-C-O	-3.34	116.52	124.07
2	A	600	LYS	C-CA-N	-3.08	104.27	109.36
2	B	601	LYS	OXT-C-O	-3.01	117.27	124.07
2	A	601	LYS	OXT-C-CA	2.92	123.43	116.88
2	B	601	LYS	OXT-C-CA	2.72	122.99	116.88
4	A	1500	SAM	C4'-O4'-C1'	2.63	112.61	109.75
4	B	1500	SAM	C4'-O4'-C1'	2.63	112.60	109.75
4	B	1500	SAM	C5-C4-N3	-2.55	120.15	125.70
2	B	600	LYS	C-CA-N	-2.55	105.15	109.36
4	B	1500	SAM	C5'-C4'-C3'	-2.43	110.62	116.32
4	A	1500	SAM	C5-C4-N3	-2.39	120.51	125.70
4	B	1500	SAM	O4'-C1'-N9	2.38	110.65	108.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600	LYS	OXT-C-O	-2.38	118.70	124.07
2	B	601	LYS	C-CA-N	2.33	113.22	109.36
4	B	1500	SAM	C2-N3-C4	2.26	120.45	114.01
4	A	1500	SAM	C2-N3-C4	2.17	120.20	114.01
4	A	1500	SAM	C5'-C4'-C3'	-2.07	111.45	116.32
2	A	600	LYS	OXT-C-O	-2.07	119.39	124.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	470/510 (92%)	-0.08	0 100 100	46, 62, 75, 94	0
1	B	470/510 (92%)	-0.05	3 (0%) 86 91	47, 62, 75, 106	0
All	All	940/1020 (92%)	-0.07	3 (0%) 90 95	46, 62, 75, 106	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	26	GLY	3.0
1	B	220	TRP	2.4
1	B	494	GLN	2.3

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	LYS	B	601	10/10	0.39	8.37	65,66,66,66	10
2	LYS	A	601	10/10	0.49	6.99	57,57,58,58	10
2	LYS	A	600	10/10	0.23	1.41	38,52,53,53	0
2	LYS	B	600	10/10	0.22	1.30	47,54,56,56	0
4	SAM	B	1500	27/27	0.20	1.16	71,79,92,92	0
4	SAM	A	1500	27/27	0.19	0.35	69,77,90,90	0
3	TAR	A	700	10/10	0.19	-0.31	95,95,96,96	0
3	TAR	B	700	10/10	0.18	-0.31	94,95,96,96	0

6.5 Other polymers ⓘ

There are no such residues in this entry.