



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:56 PM GMT

PDB ID : 4QFS
Title : Structure of AMPK in complex with Br2-A769662core activator and STAU-ROSPORINE inhibitor
Authors : Calabrese, M.F.; Kurumbail, R.G.
Deposited on : 2014-05-21
Resolution : 3.55 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

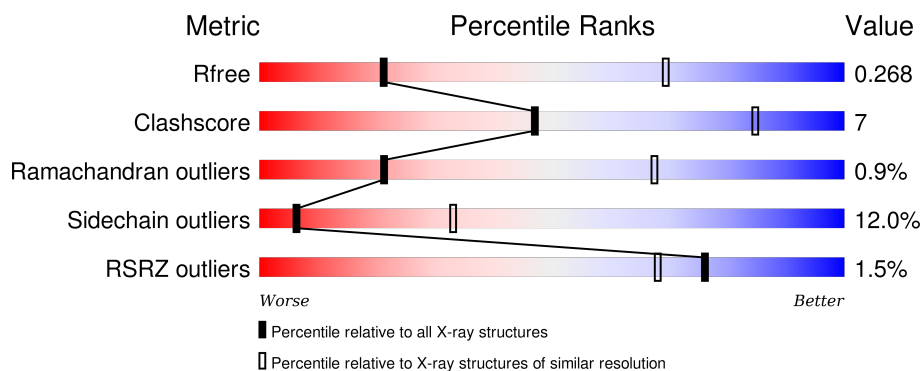
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.55 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	1240 (3.72-3.40)
Clashscore	102246	1057 (3.70-3.42)
Ramachandran outliers	100387	1017 (3.70-3.42)
Sidechain outliers	100360	1017 (3.70-3.42)
RSRZ outliers	91569	1247 (3.72-3.40)

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	503	<div> <div></div> <div>52% 18% • 28%</div> </div>
2	B	204	<div> <div></div> <div>53% 22% • 23%</div> </div>
3	C	330	<div> <div></div> <div>68% 12% • 19%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	CL	A	605	-	-	-	X
6	CL	B	301	-	-	-	X
8	SO4	C	403	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6128 atoms, of which 26 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 5'-AMP-activated protein kinase catalytic subunit alpha-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	P	S	0	0	0
			2854	1826	493	516	1	18			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P54645
A	517	ALA	-	SEE REMARK 999	UNP P54645
A	518	SER	-	SEE REMARK 999	UNP P54645
A	519	GLY	-	SEE REMARK 999	UNP P54645
A	520	GLY	-	SEE REMARK 999	UNP P54645
A	521	PRO	-	SEE REMARK 999	UNP P54645
A	522	GLY	-	SEE REMARK 999	UNP P54645
A	523	GLY	-	SEE REMARK 999	UNP P54645
A	524	SER	-	SEE REMARK 999	UNP P54645

- Molecule 2 is a protein called 5'-AMP-activated protein kinase subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	158	Total	C	N	O	S	0	0	0
			1214	790	203	218	3			

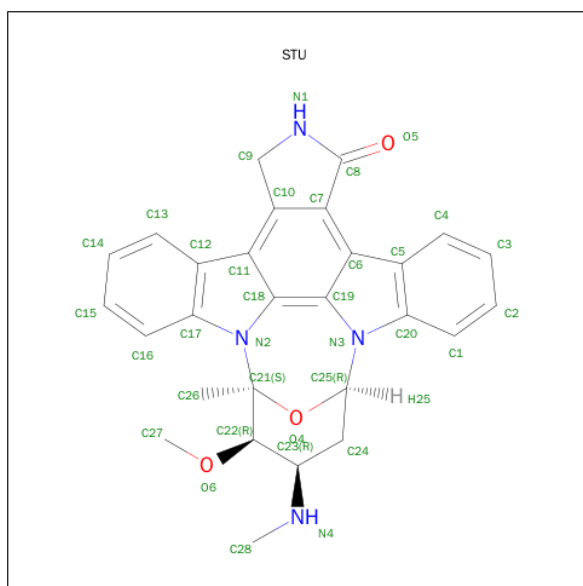
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MET	-	EXPRESSION TAG	UNP P80386
B	108	ASP	SER	ENGINEERED MUTATION	UNP P80386

- Molecule 3 is a protein called 5'-AMP-activated protein kinase subunit gamma-1.

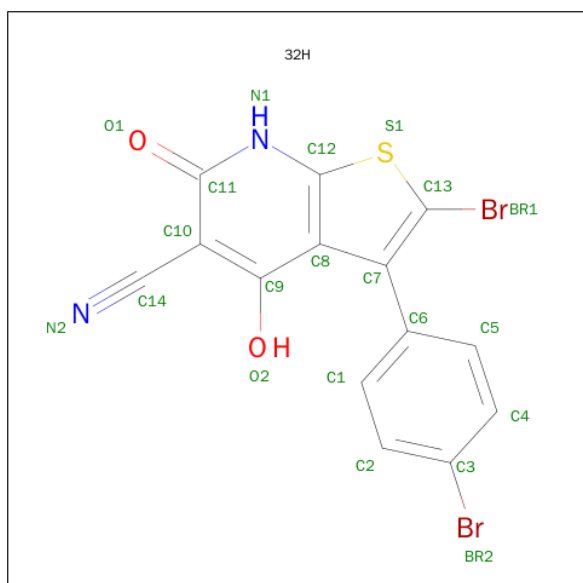
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	267	Total	C	N	O	S	0	0	0
			1940	1249	322	363	6			

- Molecule 4 is STAUROSPORINE (three-letter code: STU) (formula: $C_{28}H_{26}N_4O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	0	0
			61	28	26	4	3		

- Molecule 5 is 2-BROMO-3-(4-BROMOPHENYL)-4-HYDROXY-6-OXO-6,7-DIHYDROTHIENO[2,3-B]PYRIDINE-5-CARBONITRILE (three-letter code: 32H) (formula: $C_{14}H_6Br_2N_2O_2S$).

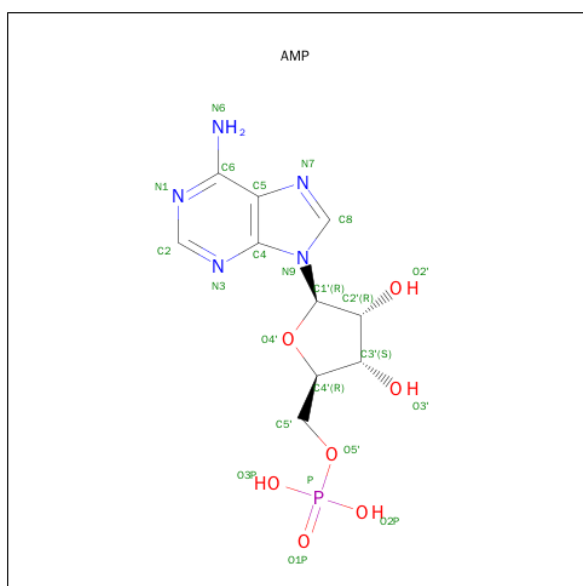


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	Br	C	N	O	S	
			21	2	14	2	2	1	

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

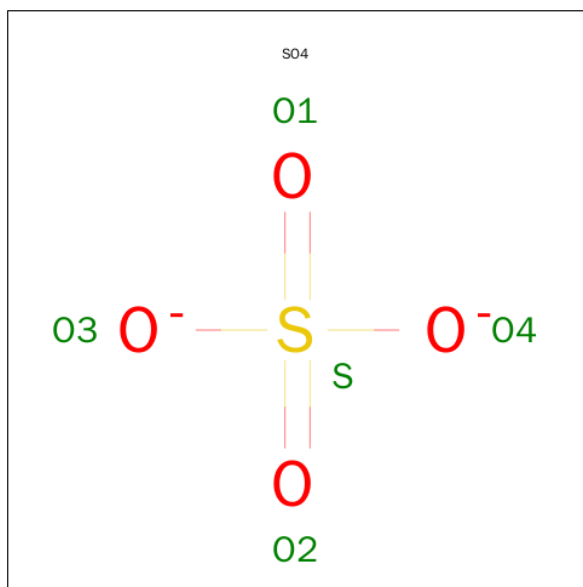
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	4	Total	Cl	0	0
			4	4		

- Molecule 7 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



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

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

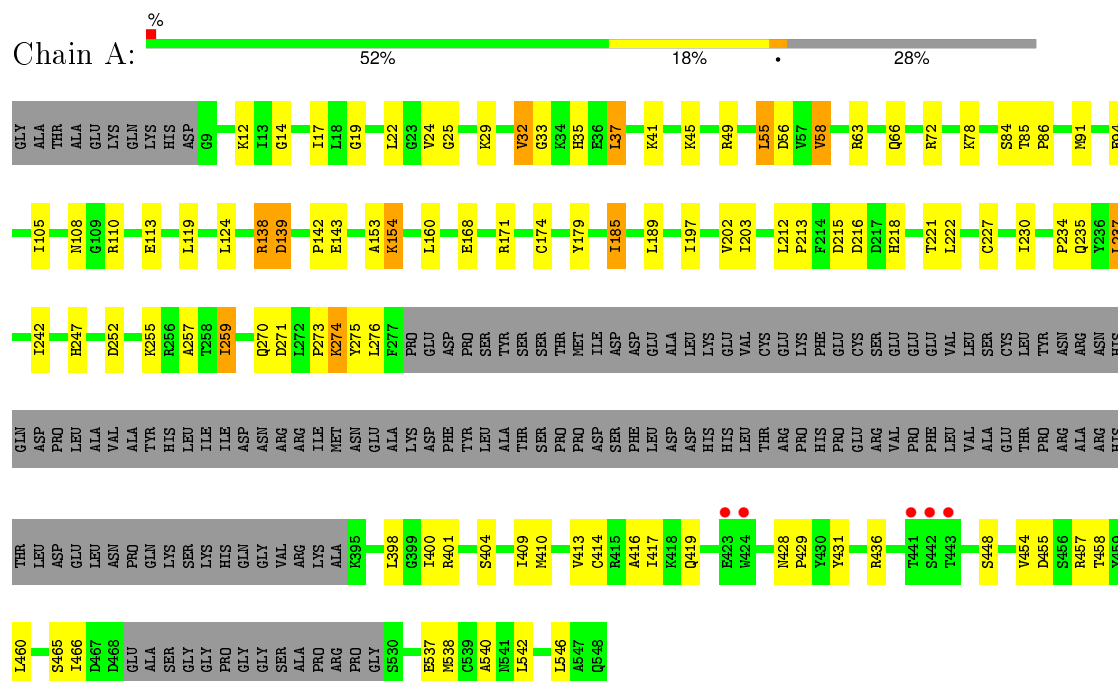


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		

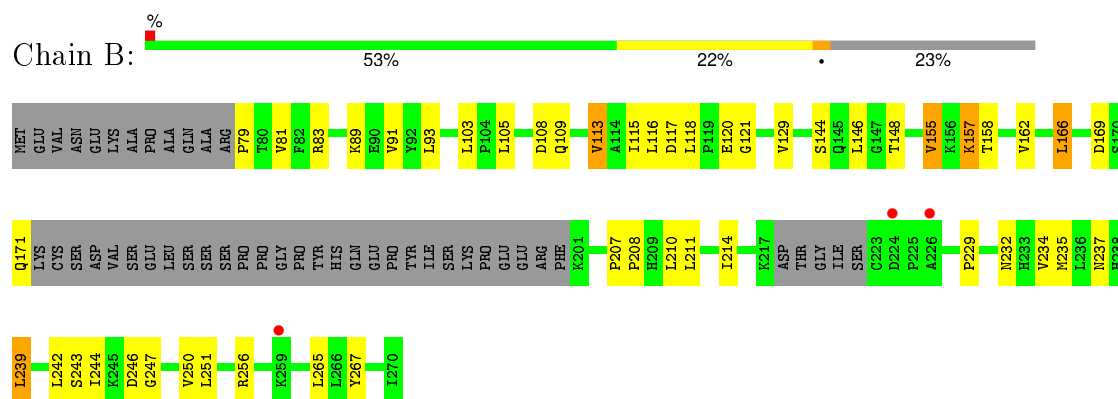
3 Residue-property plots

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: 5'-AMP-activated protein kinase catalytic subunit alpha-1

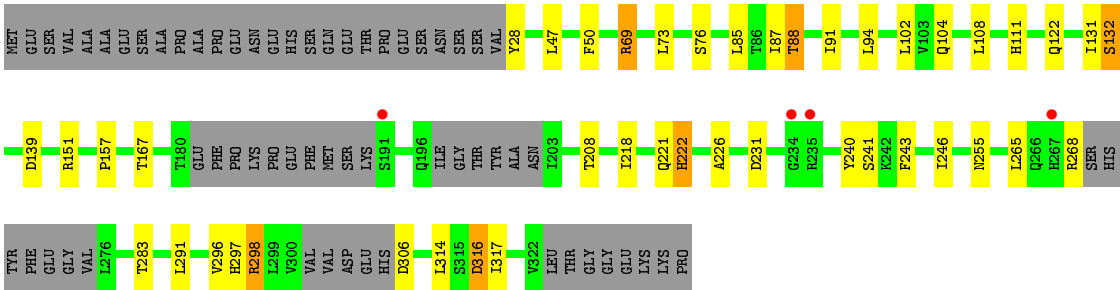


- Molecule 2: 5'-AMP-activated protein kinase subunit beta-1



- Molecule 3: 5'-AMP-activated protein kinase subunit gamma-1





4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.88Å 123.88Å 401.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.59 – 3.55 29.59 – 3.55	Depositor EDS
% Data completeness (in resolution range)	90.5 (29.59-3.55) 90.0 (29.59-3.55)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 3.55Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.226 , 0.269 0.221 , 0.268	Depositor DCC
R_{free} test set	1048 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	76.6	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 100.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 20843 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6128	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CL, TPO, 32H, STU, SO4, AMP

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	0.50	0/2905	0.76	2/3933 (0.1%)
2	B	0.49	0/1248	0.73	0/1711
3	C	0.47	0/1976	0.68	0/2710
All	All	0.49	0/6129	0.73	2/8354 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	GLY	N-CA-C	-6.69	96.37	113.10
1	A	55	LEU	N-CA-C	-5.21	96.92	111.00

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	2854	0	2797	53	0
2	B	1214	0	1170	23	0
3	C	1940	0	1775	16	0
4	A	35	26	26	4	0
5	A	21	0	5	3	0
6	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	C	23	0	12	1	0
8	C	10	0	0	0	0
All	All	6102	26	5785	89	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 (89) 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:A:455:ASP:HB2	1:A:458:THR:HG22	1.58	0.84
4:A:601:STU:H16	4:A:601:STU:H261	1.60	0.80
2:B:79:PRO:HA	2:B:117:ASP:HA	1.68	0.74
1:A:185:ILE:HD11	1:A:227:CYS:SG	2.31	0.71
3:C:87:ILE:HG23	3:C:246:ILE:HG23	1.72	0.71
1:A:252:ASP:HB3	1:A:255:LYS:HB2	1.75	0.69
5:A:602:32H:H1	2:B:108:ASP:HB2	1.74	0.69
1:A:273:PRO:HD2	1:A:276:LEU:HD12	1.75	0.68
1:A:179:TYR:HA	1:A:202:VAL:HG21	1.80	0.63
1:A:465:SER:HB3	2:B:237:ASN:HB3	1.81	0.61
1:A:49:ARG:HH21	1:A:86:PRO:HA	1.65	0.60
1:A:160:LEU:HD13	1:A:174:CYS:HB2	1.84	0.60
1:A:12:LYS:HG2	1:A:17:ILE:HG22	1.83	0.59
1:A:237:LEU:HB3	1:A:242:ILE:HD11	1.85	0.59
1:A:35:HIS:HE1	1:A:37:LEU:HD12	1.69	0.58
1:A:398:LEU:HD22	2:B:210:LEU:HB3	1.87	0.56
2:B:83:ARG:HG3	2:B:113:VAL:HG22	1.87	0.56
1:A:218:HIS:HD2	1:A:221:THR:HG23	1.71	0.56
1:A:448:SER:HB3	1:A:466:ILE:HD11	1.88	0.55
1:A:413:VAL:O	1:A:417:ILE:HG13	2.06	0.54
3:C:87:ILE:HD12	3:C:246:ILE:HG21	1.90	0.53
2:B:208:PRO:HA	2:B:211:LEU:HD12	1.91	0.52
1:A:428:ASN:HB3	1:A:429:PRO:HD2	1.90	0.52
1:A:22:LEU:HD21	1:A:32:VAL:HG13	1.91	0.52
2:B:120:GLU:HA	2:B:155:VAL:HG13	1.92	0.51
2:B:144:SER:HB3	2:B:148:THR:HB	1.92	0.51
3:C:240:TYR:HD1	3:C:265:LEU:HG	1.75	0.51
1:A:58:VAL:HG23	2:B:166:LEU:HD12	1.92	0.51
1:A:212:LEU:HB2	1:A:215:ASP:HB2	1.94	0.50
1:A:436:ARG:HD3	1:A:538:MET:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:TYR:HE1	1:A:448:SER:HB2	1.77	0.50
1:A:404:SER:HB2	1:A:409:ILE:HG13	1.94	0.50
2:B:91:VAL:HG22	2:B:129:VAL:HG13	1.94	0.50
1:A:414:CYS:C	1:A:416:ALA:H	2.15	0.49
1:A:274:LYS:HD2	1:A:275:TYR:H	1.76	0.49
1:A:455:ASP:HB3	1:A:457:ARG:H	1.78	0.49
1:A:179:TYR:HD2	1:A:202:VAL:HG23	1.78	0.49
1:A:540:ALA:HB2	2:B:251:LEU:HD11	1.96	0.48
2:B:121:GLY:H	2:B:155:VAL:HG13	1.78	0.48
1:A:138:ARG:O	1:A:139:ASP:HB3	2.13	0.48
1:A:197:ILE:HD11	1:A:259:ILE:HG12	1.96	0.47
1:A:105:ILE:O	1:A:108:ASN:O	2.31	0.47
2:B:267:TYR:HB2	3:C:50:PHE:HD1	1.79	0.47
1:A:45:LYS:HB3	1:A:91:MET:HB2	1.96	0.47
4:A:601:STU:C16	4:A:601:STU:H261	2.30	0.47
1:A:202:VAL:HG12	1:A:213:PRO:HG2	1.97	0.47
1:A:189:LEU:HB2	2:B:207:PRO:HG3	1.97	0.47
5:A:602:32H:C5	2:B:113:VAL:HG21	2.46	0.46
2:B:239:LEU:HD11	2:B:251:LEU:HD22	1.98	0.46
3:C:291:LEU:HD23	3:C:296:VAL:HG23	1.97	0.46
2:B:91:VAL:HG13	2:B:129:VAL:HG22	1.99	0.45
1:A:142:PRO:HD2	1:A:179:TYR:CZ	2.51	0.45
2:B:93:LEU:HB2	2:B:105:LEU:HD21	1.98	0.45
3:C:132:SER:OG	3:C:157:PRO:HD3	2.16	0.45
2:B:242:LEU:HB2	2:B:250:VAL:HB	1.99	0.44
3:C:73:LEU:HD21	3:C:85:LEU:HB2	1.98	0.44
1:A:247:HIS:CG	1:A:257:ALA:HB2	2.52	0.44
1:A:85:THR:HB	1:A:86:PRO:HD2	1.98	0.44
1:A:428:ASN:HB2	1:A:431:TYR:HB3	2.00	0.44
1:A:138:ARG:O	1:A:139:ASP:CB	2.66	0.44
1:A:153:ALA:O	1:A:154:LYS:HD2	2.18	0.43
1:A:398:LEU:O	1:A:460:LEU:HD11	2.19	0.43
1:A:218:HIS:CD2	1:A:221:THR:HG23	2.50	0.43
3:C:316:ASP:OD1	7:C:401:AMP:H3'	2.18	0.43
3:C:226:ALA:HA	3:C:241:SER:HA	2.00	0.43
1:A:142:PRO:HD2	1:A:179:TYR:CE2	2.53	0.43
1:A:78:LYS:H	1:A:94:GLU:HG2	1.83	0.42
5:A:602:32H:BR1	5:A:602:32H:C1	3.23	0.42
1:A:160:LEU:HD23	1:A:160:LEU:HA	1.73	0.42
3:C:131:ILE:HG13	3:C:132:SER:H	1.85	0.42
3:C:314:LEU:HA	3:C:317:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:SER:HB2	2:B:162:VAL:HG22	2.00	0.42
1:A:401:ARG:HG2	1:A:401:ARG:H	1.73	0.42
3:C:243:PHE:O	3:C:246:ILE:HG13	2.18	0.42
3:C:69:ARG:HG2	3:C:87:ILE:HD11	2.01	0.42
2:B:157:LYS:HE2	2:B:157:LYS:H	1.84	0.42
1:A:410:MET:O	1:A:413:VAL:HG22	2.19	0.42
3:C:218:ILE:O	3:C:222:HIS:HB2	2.20	0.42
1:A:19:GLY:HA3	1:A:32:VAL:HG23	2.01	0.42
1:A:142:PRO:HD3	1:A:203:ILE:HG12	2.02	0.42
3:C:297:HIS:HB3	3:C:298:ARG:CZ	2.49	0.42
1:A:33:GLY:O	1:A:41:LYS:HA	2.21	0.41
1:A:143:GLU:HB3	4:A:601:STU:H281	2.03	0.41
4:A:601:STU:C26	4:A:601:STU:C16	2.95	0.41
3:C:88:THR:HA	3:C:91:ILE:HD12	2.03	0.41
1:A:234:PRO:HD2	1:A:237:LEU:HD22	2.02	0.41
1:A:63:ARG:O	1:A:66:GLN:HB2	2.21	0.41
2:B:81:VAL:HG22	2:B:115:ILE:HG12	2.04	0.40
2:B:214:ILE:HB	2:B:229:PRO:HD2	2.02	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	355/503 (71%)	333 (94%)	20 (6%)	2 (1%)	30	74
2	B	152/204 (74%)	137 (90%)	12 (8%)	3 (2%)	9	53
3	C	257/330 (78%)	242 (94%)	13 (5%)	2 (1%)	24	69
All	All	764/1037 (74%)	712 (93%)	45 (6%)	7 (1%)	21	67

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	GLY
1	A	139	ASP
3	C	122	GLN
3	C	231	ASP
2	B	246	ASP
2	B	247	GLY
2	B	244	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	306/448 (68%)	274 (90%)	32 (10%)	8	41
2	B	130/185 (70%)	110 (85%)	20 (15%)	3	23
3	C	189/299 (63%)	166 (88%)	23 (12%)	6	32
All	All	625/932 (67%)	550 (88%)	75 (12%)	6	33

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	VAL
1	A	29	LYS
1	A	32	VAL
1	A	37	LEU
1	A	55	LEU
1	A	56	ASP
1	A	58	VAL
1	A	72	ARG
1	A	110	ARG
1	A	113	GLU
1	A	119	LEU
1	A	124	LEU
1	A	138	ARG
1	A	154	LYS
1	A	168	GLU
1	A	171	ARG

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Mol	Chain	Res	Type
1	A	185	ILE
1	A	216	ASP
1	A	222	LEU
1	A	230	ILE
1	A	235	GLN
1	A	237	LEU
1	A	259	ILE
1	A	270	GLN
1	A	271	ASP
1	A	274	LYS
1	A	400	ILE
1	A	419	GLN
1	A	454	VAL
1	A	537	GLU
1	A	542	LEU
1	A	546	LEU
2	B	89	LYS
2	B	103	LEU
2	B	109	GLN
2	B	113	VAL
2	B	116	LEU
2	B	118	LEU
2	B	146	LEU
2	B	155	VAL
2	B	157	LYS
2	B	158	THR
2	B	166	LEU
2	B	169	ASP
2	B	171	GLN
2	B	232	ASN
2	B	234	VAL
2	B	235	MET
2	B	239	LEU
2	B	243	SER
2	B	256	ARG
2	B	265	LEU
3	C	28	TYR
3	C	47	LEU
3	C	69	ARG
3	C	76	SER
3	C	88	THR
3	C	94	LEU

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Mol	Chain	Res	Type
3	C	102	LEU
3	C	104	GLN
3	C	108	LEU
3	C	111	HIS
3	C	132	SER
3	C	139	ASP
3	C	151	ARG
3	C	167	THR
3	C	208	THR
3	C	221	GLN
3	C	222	HIS
3	C	255	ASN
3	C	268	ARG
3	C	283	THR
3	C	298	ARG
3	C	306	ASP
3	C	316	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	218	HIS
2	B	110	ASN
2	B	216	ASN
2	B	232	ASN
3	C	104	GLN
3	C	247	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	TPO	A	172	1	8,10,11	1.20	1 (12%)	7,14,16	1.85	2 (28%)

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
1	TPO	A	172	1	-	0/8/11/13	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	172	TPO	P-OG1	-2.52	1.52	1.60

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TPO	O-C-CA	-2.13	119.82	125.44
1	A	172	TPO	O3P-P-O2P	2.90	118.42	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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
4	STU	A	601	-	27,42,42	2.31	9 (33%)	23,68,68	1.81	7 (30%)
5	32H	A	602	-	19,23,23	1.01	2 (10%)	17,34,34	3.31	2 (11%)
7	AMP	C	401	-	20,25,25	0.53	0	22,38,38	0.60	0
8	SO4	C	402	-	4,4,4	0.31	0	6,6,6	0.24	0
8	SO4	C	403	-	4,4,4	0.30	0	6,6,6	0.17	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	STU	A	601	-	-	0/4/42/42	0/0/8/8
5	32H	A	602	-	-	0/5/6/6	0/3/3/3
7	AMP	C	401	-	-	0/6/26/26	0/3/3/3
8	SO4	C	402	-	-	0/0/0/0	0/0/0/0
8	SO4	C	403	-	-	0/0/0/0	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	602	32H	C7-C8	2.05	1.45	1.42
5	A	602	32H	C11-N1	2.77	1.38	1.33
4	A	601	STU	O5-C8	2.81	1.29	1.23
4	A	601	STU	C7-C10	2.83	1.46	1.40
4	A	601	STU	C6-C19	3.12	1.46	1.42
4	A	601	STU	C19-C18	3.29	1.49	1.41
4	A	601	STU	C7-C6	3.67	1.49	1.43
4	A	601	STU	C11-C18	3.96	1.47	1.42
4	A	601	STU	C5-C20	4.51	1.48	1.41
4	A	601	STU	C10-C11	4.52	1.49	1.42
4	A	601	STU	C12-C17	4.58	1.48	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	32H	C10-C11-N1	-12.66	114.60	124.19
4	A	601	STU	C1-C20-C5	-2.84	116.64	120.73
4	A	601	STU	C16-C17-C12	-2.69	116.86	120.73
4	A	601	STU	O5-C8-C7	-2.21	124.93	128.62
4	A	601	STU	C1-C20-N3	2.06	134.66	132.18
4	A	601	STU	C13-C12-C17	2.68	122.78	119.39
4	A	601	STU	C4-C5-C20	2.93	123.09	119.39
4	A	601	STU	C16-C17-N2	4.52	137.74	132.22
5	A	602	32H	C7-C8-C12	4.80	111.36	107.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	STU	4	0
5	A	602	32H	3	0
7	C	401	AMP	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 [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(Å ²)	Q<0.9
1	A	361/503 (71%)	-0.39	5 (1%) 78 69	44, 72, 170, 275	0
2	B	158/204 (77%)	-0.18	3 (1%) 70 61	54, 85, 123, 137	0
3	C	267/330 (80%)	-0.18	4 (1%) 76 68	63, 114, 234, 265	0
All	All	786/1037 (75%)	-0.27	12 (1%) 76 68	44, 90, 230, 275	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	442	SER	3.7
1	A	441	THR	2.7
3	C	191	SER	2.7
3	C	267	HIS	2.7
3	C	235	ARG	2.5
3	C	234	GLY	2.3
1	A	443	THR	2.3
2	B	226	ALA	2.2
2	B	224	ASP	2.1
1	A	424	TRP	2.1
2	B	259	LYS	2.0
1	A	423	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(\AA^2)	Q<0.9
1	TPO	A	172	11/12	0.95	0.17	-	73,75,79,81	0

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(\AA^2)	Q<0.9
6	CL	B	301	1/1	0.89	0.56	9.94	89,89,89,89	0
8	SO4	C	403	5/5	0.78	0.39	2.36	142,142,142,143	0
6	CL	A	605	1/1	0.97	0.28	2.01	50,50,50,50	0
8	SO4	C	402	5/5	0.76	0.32	0.96	143,144,145,145	0
4	STU	A	601	35/35	0.95	0.25	0.89	52,59,65,67	0
7	AMP	C	401	23/23	0.88	0.27	0.65	134,145,184,206	0
5	32H	A	602	21/21	0.94	0.22	-0.12	91,99,111,168	0
6	CL	A	603	1/1	0.95	0.14	-	69,69,69,69	0
6	CL	A	604	1/1	0.82	0.12	-	117,117,117,117	0
6	CL	A	606	1/1	0.83	0.12	-	56,56,56,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.