Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:45 AM GMT

PDB ID	:	2Y8L
Title	:	Structure of an active form of mammalian AMPK in complex with two ADP
Authors	:	Xiao, B.; Sanders, M.J.; Underwood, E.; Heath, R.; Mayer, F.; Carmena, D.; Jing, C.; Walker, P.A.; Eccleston, J.F.; Haire, L.F.; Saiu, P.; Howell, S.A.; Aasland, R.; Martin, S.R.; Carling, D.; Gamblin, S.J.
Deposited on	:	2011-02-07
Resolution	:	2.50 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

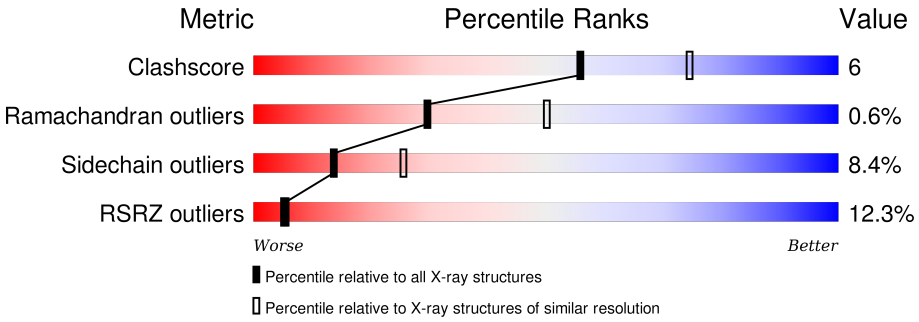
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 <=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	173	5%, 46%, 12%, 40%
2	B	87	21%, 66%, 10%, 21%
3	E	330	10%, 75%, 16%, 8%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4045 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 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	104	855	539	152	157	7	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	378	MET	-	EXPRESSION TAG	UNP P54645
A	379	SER	-	EXPRESSION TAG	UNP P54645
A	380	HIS	-	EXPRESSION TAG	UNP P54645
A	381	HIS	-	EXPRESSION TAG	UNP P54645
A	382	HIS	-	EXPRESSION TAG	UNP P54645
A	383	HIS	-	EXPRESSION TAG	UNP P54645
A	384	HIS	-	EXPRESSION TAG	UNP P54645
A	385	HIS	-	EXPRESSION TAG	UNP P54645
A	386	SER	-	EXPRESSION TAG	UNP P54645
A	387	GLY	-	EXPRESSION TAG	UNP P54645
A	388	LEU	-	EXPRESSION TAG	UNP P54645
A	389	VAL	-	EXPRESSION TAG	UNP P54645
A	390	PRO	-	EXPRESSION TAG	UNP P54645
A	391	ARG	-	EXPRESSION TAG	UNP P54645
A	392	GLY	-	EXPRESSION TAG	UNP P54645
A	393	SER	-	CLONING ARTIFACT	UNP P54645
A	394	MET	-	CLONING ARTIFACT	UNP P54645
A	395	ALA	-	CLONING ARTIFACT	UNP P54645
A	545	ASN	-	CLONING ARTIFACT	UNP P54645
A	546	SER	-	CLONING ARTIFACT	UNP P54645
A	547	CYS	-	CLONING ARTIFACT	UNP P54645
A	548	THR	-	CLONING ARTIFACT	UNP P54645
A	549	VAL	-	CLONING ARTIFACT	UNP P54645
A	550	ASN	-	CLONING ARTIFACT	UNP P54645

- Molecule 2 is a protein called 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-

2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	69	Total	C	N	O	S	0	0	0
			570	374	97	96	3			

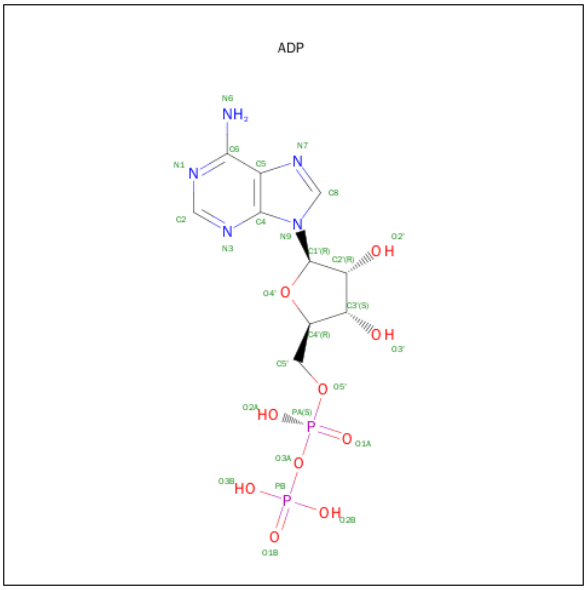
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	186	MET	-	CLONING ARTIFACT	UNP O43741

- Molecule 3 is a protein called 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1.

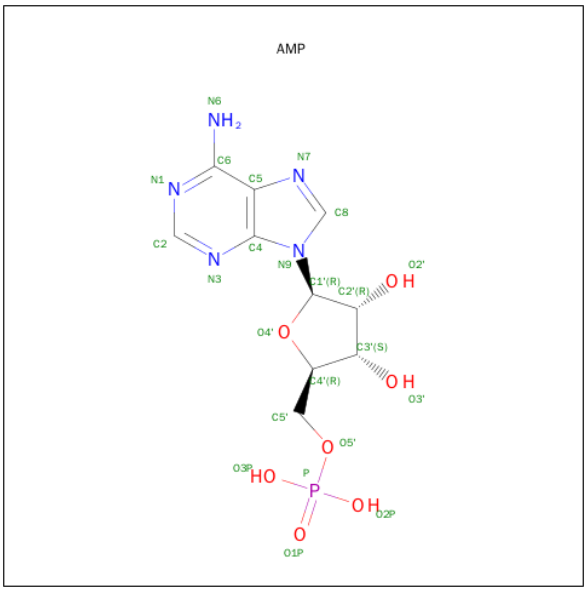
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	305	Total	C	N	O	S	0	0	1
			2442	1584	408	443	7			

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



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

- Molecule 6 is water.

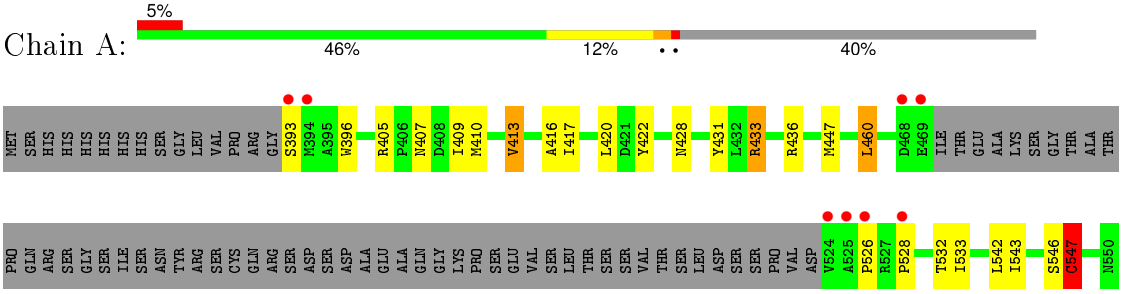
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	23	Total	O	0	0
			23	23		
6	B	17	Total	O	0	0
			17	17		
6	E	61	Total	O	0	0
			61	61		

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.

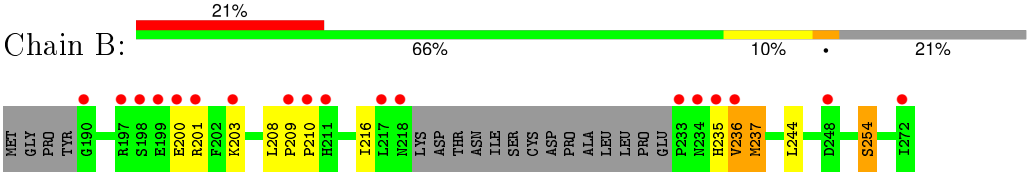
• Molecule 1: 5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-1

Chain A:



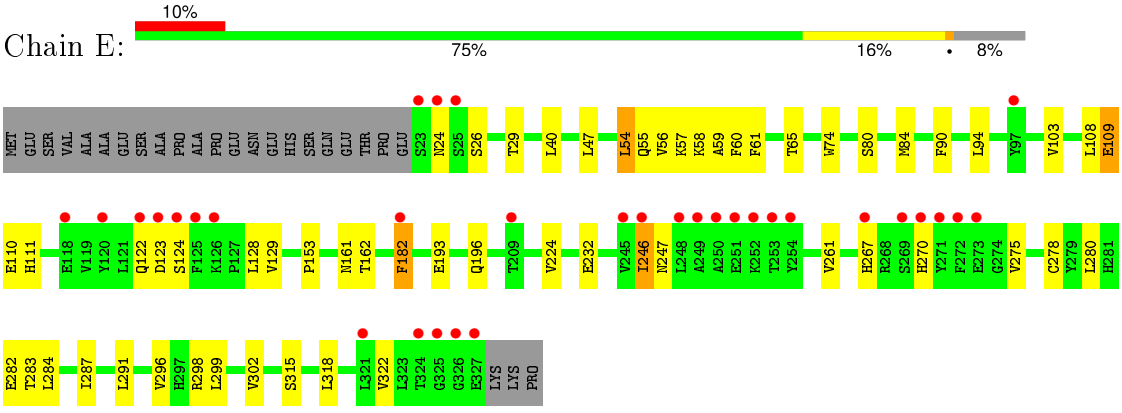
• Molecule 2: 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT BETA-2

Chain B:



• Molecule 3: 5'-AMP-ACTIVATED PROTEIN KINASE SUBUNIT GAMMA-1

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	48.57Å 121.46Å 125.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.42 – 2.50 19.93 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (87.42-2.50) 98.0 (19.93-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.73 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.228 , 0.253 0.224 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	50.8	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 44.1	EDS
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 25984 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4045	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: AMP, ADP

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	0.49	1/873 (0.1%)	0.66	1/1178 (0.1%)
2	B	0.45	0/585	0.67	0/789
3	E	0.51	0/2494	0.65	0/3386
All	All	0.50	1/3952 (0.0%)	0.65	1/5353 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
3	E	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	547	CYS	CB-SG	-5.04	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	460	LEU	CA-CB-CG	6.86	131.08	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	209	PRO	Peptide
3	E	182	PHE	Peptide

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	855	0	845	24	0
2	B	570	0	595	9	0
3	E	2442	0	2506	25	0
4	E	54	0	24	0	0
5	E	23	0	12	0	0
6	A	23	0	0	0	0
6	B	17	0	0	0	0
6	E	61	0	0	0	0
All	All	4045	0	3982	49	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 6.

All (49) 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)
2:B:208:LEU:O	2:B:210:PRO:HD3	1.44	1.14
1:A:416:ALA:HB2	1:A:546:SER:HB3	1.70	0.72
3:E:84:MET:HE3	3:E:153:PRO:HG3	1.77	0.65
2:B:208:LEU:O	2:B:210:PRO:CD	2.36	0.65
1:A:543:ILE:O	1:A:547:CYS:HB2	1.98	0.64
1:A:428:ASN:HB2	1:A:431:TYR:HB3	1.79	0.63
1:A:447:MET:HE3	1:A:542:LEU:HD12	1.80	0.62
2:B:200:GLU:HG3	2:B:203:LYS:HB2	1.83	0.61
3:E:108:LEU:O	3:E:111:HIS:HB2	2.03	0.59
3:E:282:GLU:HB2	3:E:287:ILE:HD11	1.85	0.59
1:A:417:ILE:HG23	1:A:422:TYR:HB2	1.85	0.57
1:A:532:THR:H	3:E:161:ASN:HD21	1.53	0.57
3:E:55:GLN:HB2	3:E:58:LYS:HD2	1.88	0.56
1:A:431:TYR:OH	1:A:433:ARG:NH1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:MET:CE	1:A:542:LEU:HD12	2.37	0.54
1:A:393:SER:N	3:E:65:THR:HG22	2.23	0.54
3:E:57:LYS:HD2	3:E:109:GLU:HG3	1.89	0.53
1:A:409:ILE:O	1:A:413:VAL:HG13	2.08	0.53
3:E:193:GLU:OE1	3:E:280:LEU:HD22	2.08	0.53
3:E:56:VAL:HG13	3:E:60:PHE:CE2	2.44	0.53
3:E:109:GLU:HA	3:E:109:GLU:OE1	2.09	0.53
3:E:60:PHE:CE1	3:E:90:PHE:HB2	2.44	0.52
3:E:84:MET:CE	3:E:153:PRO:HG3	2.40	0.51
1:A:526:PRO:HG3	3:E:128:LEU:HD23	1.93	0.50
2:B:235:HIS:O	2:B:237:MET:HG2	2.10	0.50
1:A:396:TRP:CZ3	2:B:254:SER:HB2	2.47	0.50
1:A:532:THR:H	3:E:161:ASN:ND2	2.10	0.49
1:A:396:TRP:HB2	2:B:216:ILE:HB	1.93	0.49
1:A:405:ARG:HB3	1:A:407:ASN:OD1	2.13	0.48
3:E:47:LEU:HD21	3:E:162:THR:HB	1.97	0.47
3:E:246:ILE:H	3:E:246:ILE:HG13	1.61	0.47
3:E:283:THR:O	3:E:287:ILE:HD12	2.15	0.46
1:A:422:TYR:CE1	1:A:436:ARG:HG3	2.50	0.46
1:A:416:ALA:CB	1:A:546:SER:HB3	2.42	0.46
1:A:528:PRO:HA	3:E:80:SER:HB3	1.98	0.46
1:A:417:ILE:HG13	1:A:542:LEU:HD21	1.99	0.45
1:A:410:MET:CE	1:A:410:MET:HA	2.46	0.45
3:E:84:MET:HE3	3:E:128:LEU:HD11	1.99	0.44
3:E:54:LEU:HD13	3:E:59:ALA:HB2	2.00	0.43
1:A:543:ILE:O	1:A:547:CYS:CB	2.66	0.42
2:B:236:VAL:HG13	2:B:236:VAL:O	2.18	0.42
3:E:278:CYS:HB3	3:E:299:LEU:HD13	2.02	0.41
3:E:56:VAL:HG13	3:E:60:PHE:HE2	1.85	0.41
2:B:235:HIS:O	2:B:237:MET:N	2.54	0.41
1:A:533:ILE:HG21	3:E:74:TRP:CD2	2.55	0.41
3:E:61:PHE:O	3:E:65:THR:OG1	2.30	0.41
1:A:407:ASN:OD1	1:A:407:ASN:N	2.53	0.40
3:E:108:LEU:HA	3:E:111:HIS:ND1	2.37	0.40
1:A:393:SER:HB2	2:B:244:LEU:HD21	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	100/173 (58%)	98 (98%)	2 (2%)	0	100	100
2	B	65/87 (75%)	57 (88%)	7 (11%)	1 (2%)	13	22
3	E	303/330 (92%)	287 (95%)	14 (5%)	2 (1%)	26	46
All	All	468/590 (79%)	442 (94%)	23 (5%)	3 (1%)	30	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	236	VAL
3	E	122	GLN
3	E	182	PHE

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	97/157 (62%)	92 (95%)	5 (5%)	29	51
2	B	65/81 (80%)	62 (95%)	3 (5%)	33	57
3	E	277/299 (93%)	248 (90%)	29 (10%)	8	16
All	All	439/537 (82%)	402 (92%)	37 (8%)	14	25

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	413	VAL
1	A	420	LEU
1	A	433	ARG
1	A	460	LEU
1	A	547	CYS
2	B	201	ARG
2	B	237	MET
2	B	254	SER
3	E	24	ASN
3	E	26	SER
3	E	29	THR
3	E	40	LEU
3	E	54	LEU
3	E	94	LEU
3	E	103	VAL
3	E	109	GLU
3	E	110	GLU
3	E	123	ASP
3	E	124	SER
3	E	129	VAL
3	E	196	GLN
3	E	224	VAL
3	E	232	GLU
3	E	246	ILE
3	E	247	ASN
3	E	261	VAL
3	E	267	HIS
3	E	270	HIS
3	E	275	VAL
3	E	284	LEU
3	E	291	LEU
3	E	296	VAL
3	E	298	ARG
3	E	302	VAL
3	E	315	SER
3	E	318	LEU
3	E	322	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	397	HIS
3	E	24	ASN

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Mol	Chain	Res	Type
3	E	122	GLN
3	E	147	ASN
3	E	161	ASN
3	E	168	HIS
3	E	222	HIS
3	E	266	GLN

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

3 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	ADP	E	1327	-	22,29,29	1.10	2 (9%)	27,45,45	2.06	5 (18%)
4	ADP	E	1328	-	22,29,29	0.99	1 (4%)	27,45,45	2.05	5 (18%)
5	AMP	E	1329	-	20,25,25	1.01	1 (5%)	22,38,38	2.18	5 (22%)

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	ADP	E	1327	-	-	0/12/32/32	0/3/3/3
4	ADP	E	1328	-	-	0/12/32/32	0/3/3/3
5	AMP	E	1329	-	-	0/6/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1327	ADP	O4'-C1'	2.15	1.43	1.41
4	E	1327	ADP	C5-C4	3.05	1.47	1.40
4	E	1328	ADP	C5-C4	3.14	1.47	1.40
5	E	1329	AMP	C5-C4	3.24	1.47	1.40

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	E	1328	ADP	N3-C2-N1	-8.17	122.64	128.89
4	E	1327	ADP	N3-C2-N1	-8.16	122.65	128.89
5	E	1329	AMP	N3-C2-N1	-8.03	122.75	128.89
4	E	1328	ADP	C2'-C1'-N9	-2.88	109.89	114.29
5	E	1329	AMP	C4-C5-N7	-2.84	106.86	109.48
4	E	1327	ADP	C2'-C1'-N9	-2.83	109.97	114.29
4	E	1327	ADP	C4-C5-N7	-2.81	106.90	109.48
5	E	1329	AMP	O5'-P-O1P	-2.64	100.43	107.14
4	E	1328	ADP	PA-O3A-PB	-2.46	124.42	132.67
4	E	1328	ADP	C4-C5-N7	-2.38	107.29	109.48
5	E	1329	AMP	O3P-P-O2P	2.11	115.41	107.38
4	E	1328	ADP	C2-N1-C6	2.11	122.54	118.77
4	E	1327	ADP	O3B-PB-O1B	2.28	117.91	110.58
5	E	1329	AMP	C4'-O4'-C1'	2.28	112.23	109.72
4	E	1327	ADP	O3B-PB-O2B	2.65	117.47	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 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, 95^{th} 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	104/173 (60%)	0.44	8 (7%) 16 18	30, 54, 91, 111	0
2	B	69/87 (79%)	1.27	18 (26%) 1 1	32, 80, 102, 119	0
3	E	305/330 (92%)	0.45	33 (10%) 8 8	28, 50, 111, 199	0
All	All	478/590 (81%)	0.57	59 (12%) 5 5	28, 53, 105, 199	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	271	TYR	11.1
3	E	270	HIS	8.1
3	E	182	PHE	8.1
3	E	23	SER	7.1
3	E	125	PHE	7.0
3	E	253	THR	6.5
1	A	393	SER	6.4
1	A	394	MET	6.4
3	E	326	GLY	6.1
3	E	24	ASN	6.1
3	E	123	ASP	6.1
2	B	190	GLY	6.1
2	B	200	GLU	5.9
3	E	269	SER	5.7
2	B	235	HIS	5.5
3	E	25	SER	5.1
3	E	324	THR	4.9
2	B	209	PRO	4.9
2	B	217	LEU	4.9
1	A	525	ALA	4.8
2	B	210	PRO	4.6
3	E	245	VAL	4.5
2	B	201	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
3	E	250	ALA	4.4
3	E	252	LYS	4.3
2	B	218	ASN	4.2
3	E	267	HIS	4.2
1	A	468	ASP	4.1
2	B	234	ASN	4.0
3	E	124	SER	3.9
3	E	325	GLY	3.8
3	E	272	PHE	3.8
1	A	524	VAL	3.5
2	B	233	PRO	3.5
1	A	526	PRO	3.4
2	B	272	ILE	3.3
3	E	254	TYR	3.3
1	A	469	GLU	3.2
3	E	122	GLN	3.1
2	B	248	ASP	3.0
3	E	249	ALA	3.0
2	B	211	HIS	2.9
3	E	248	LEU	2.9
2	B	198	SER	2.8
3	E	120	TYR	2.8
2	B	199	GLU	2.7
2	B	197	ARG	2.7
3	E	327	GLU	2.7
2	B	203	LYS	2.6
1	A	528	PRO	2.6
2	B	236	VAL	2.5
3	E	251	GLU	2.4
3	E	273	GLU	2.4
3	E	321	LEU	2.3
3	E	118	GLU	2.3
3	E	126	LYS	2.3
3	E	246	ILE	2.2
3	E	97	TYR	2.1
3	E	209	THR	2.1

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, 95^{th} 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
5	AMP	E	1329	23/23	0.95	0.12	-0.71	37,44,47,49	0
4	ADP	E	1327	27/27	0.98	0.11	-0.90	39,43,47,51	0
4	ADP	E	1328	27/27	0.92	0.12	-0.95	52,62,71,73	0

6.5 Other polymers (i)

There are no such residues in this entry.