



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:17 AM GMT

PDB ID : 3DWL
Title : Crystal Structure of Fission Yeast Arp2/3 Complex Lacking the Arp2 Subunit
Authors : Nolen, B.J.; Pollard, T.D.
Deposited on : 2008-07-22
Resolution : 3.78 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

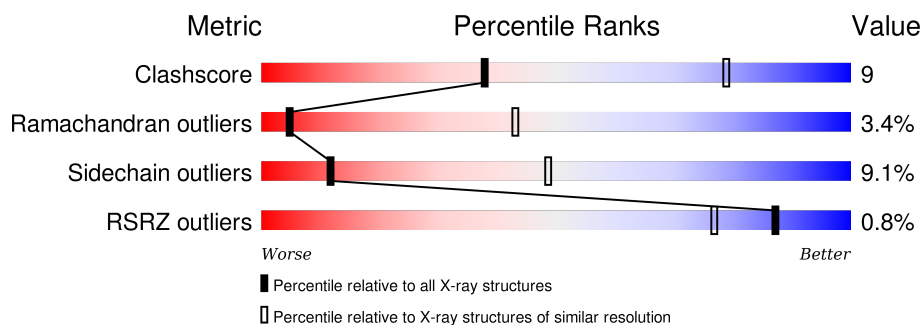
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.78 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	1412 (4.06-3.50)
Ramachandran outliers	100387	1351 (4.06-3.50)
Sidechain outliers	100360	1347 (4.06-3.50)
RSRZ outliers	91569	1281 (4.06-3.50)

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 $\leq 5\%$. 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	427	
1	B	427	
2	C	377	
2	H	377	
3	D	317	
3	I	317	
4	E	174	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	J	174	<div><div></div><div>28%8%64%</div></div>
5	F	168	<div>%<div><div></div><div>75%21%..</div></div></div>
5	K	168	<div>2%<div><div></div><div>73%23%..</div></div></div>
6	G	152	<div><div></div><div>56%18%.25%</div></div>
6	L	152	<div>%<div><div></div><div>55%20%.25%</div></div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18705 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 Actin-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	1	0	0
			2555	1617	432	496	10			
1	B	355	Total	C	N	O	S	1	0	0
			2556	1617	432	497	10			

- Molecule 2 is a protein called Actin-related protein 2/3 complex subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	336	Total	C	N	O	S	0	0	0
			2252	1413	402	432	5			
2	H	337	Total	C	N	O	S	0	0	0
			2262	1418	403	436	5			

- Molecule 3 is a protein called Actin-related protein 2/3 complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	272	Total	C	N	O	S	0	0	0
			2028	1302	350	368	8			
3	I	272	Total	C	N	O	S	0	0	0
			2028	1302	350	368	8			

- Molecule 4 is a protein called Actin-related protein 2/3 complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	63	Total	C	N	O	S	0	0	0
			397	249	71	73	4			
4	J	63	Total	C	N	O	S	0	0	0
			397	249	71	73	4			

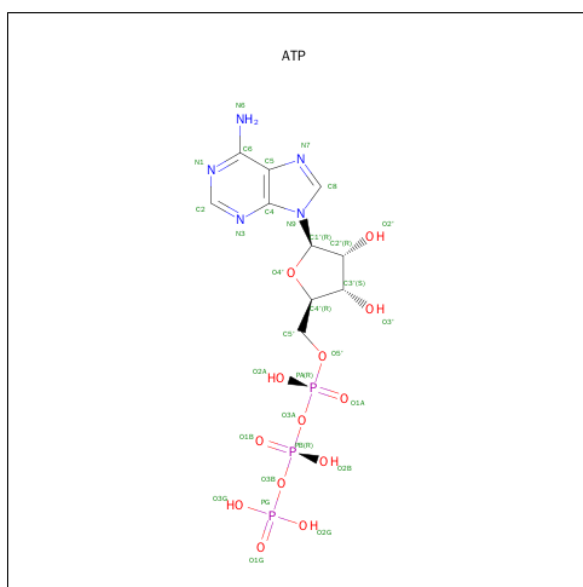
- Molecule 5 is a protein called Actin-related protein 2/3 complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	166	Total	C	N	O	S	1	0	0
			1294	825	215	247	7			
5	K	166	Total	C	N	O	S	1	0	0
			1294	825	215	247	7			

- Molecule 6 is a protein called Actin-related protein 2/3 complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	114	Total	C	N	O	S	0	0	0
			790	497	136	155	2			
6	L	114	Total	C	N	O	S	0	0	0
			790	497	136	155	2			

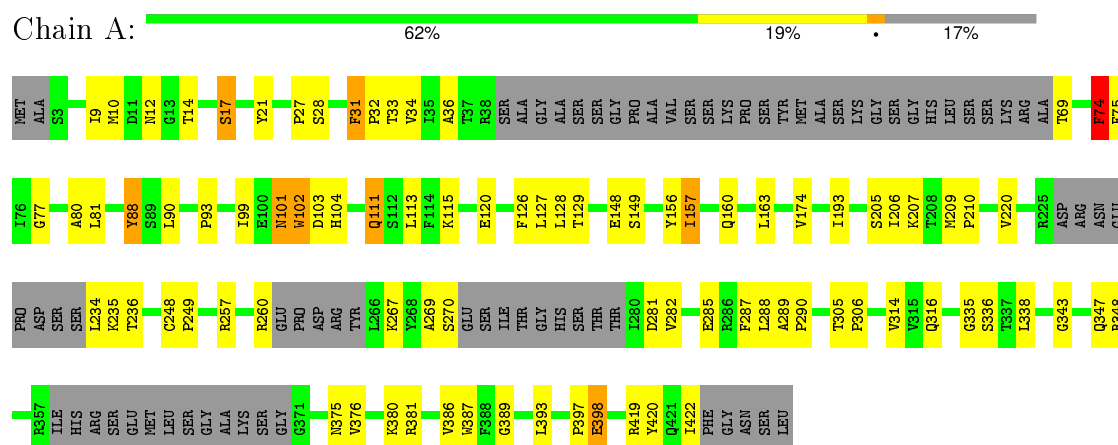
- Molecule 7 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



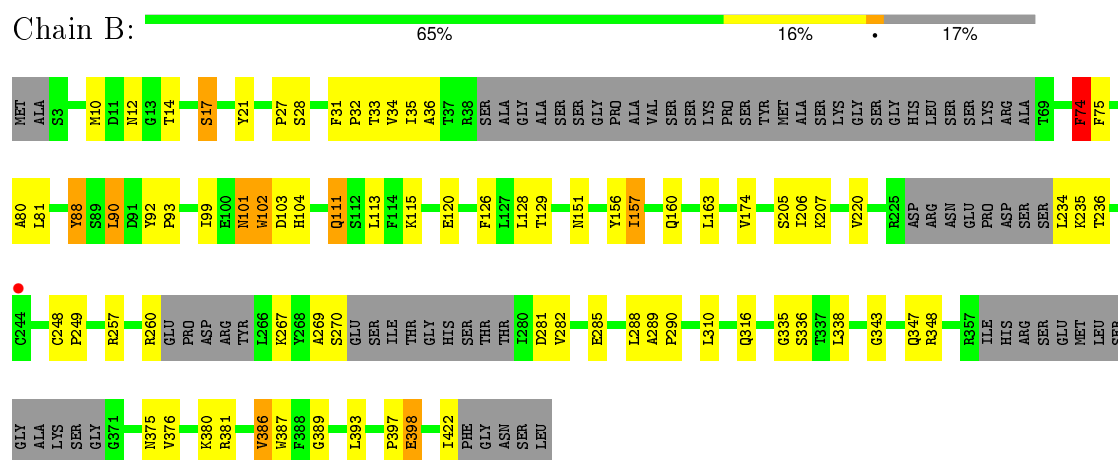
3 Residue-property plots

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.

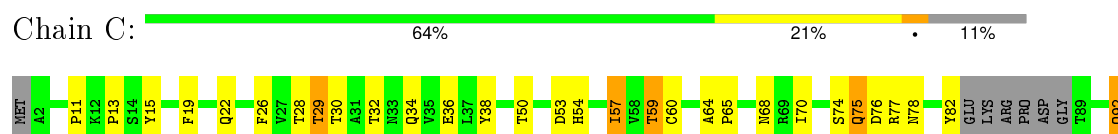
• Molecule 1: Actin-related protein 3

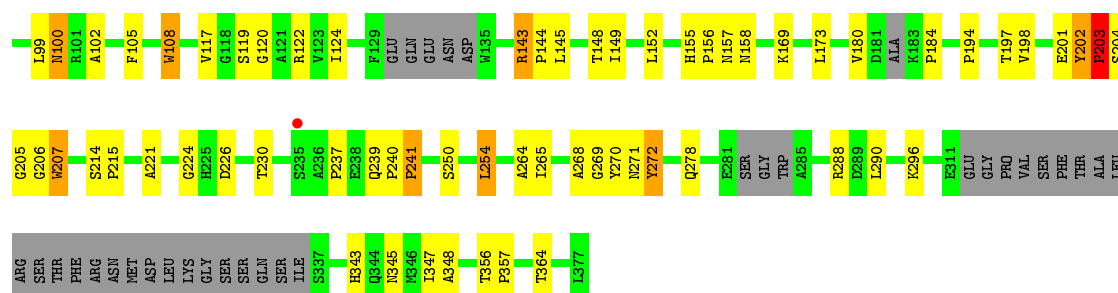


• Molecule 1: Actin-related protein 3

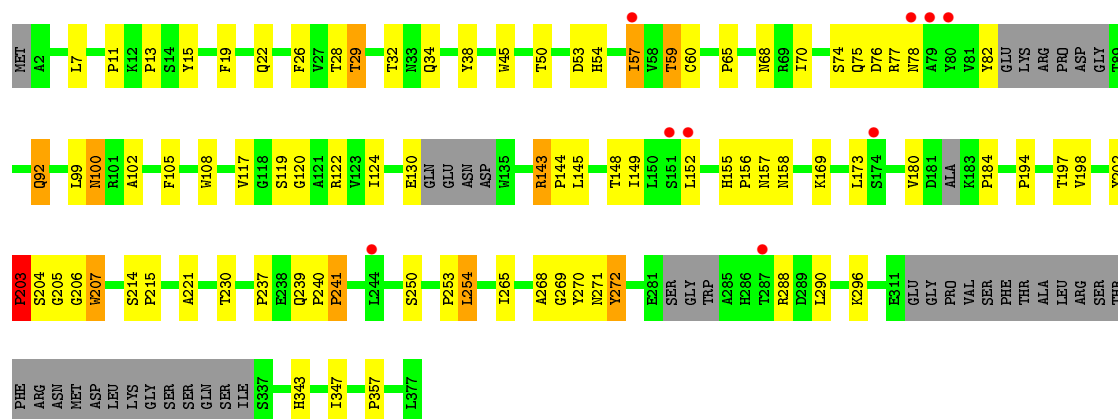


• Molecule 2: Actin-related protein 2/3 complex subunit 1

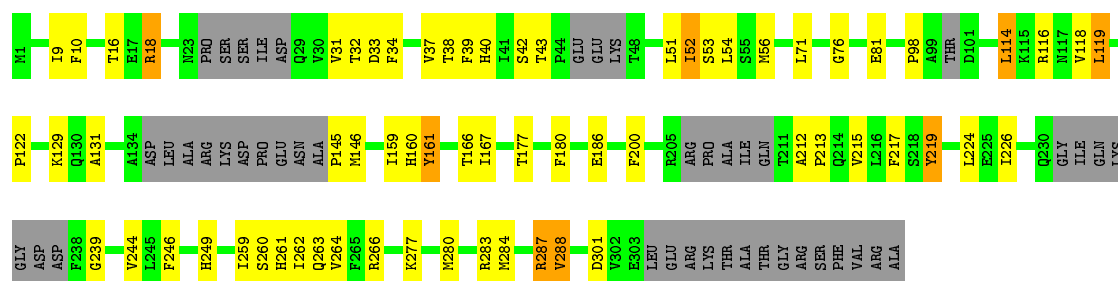




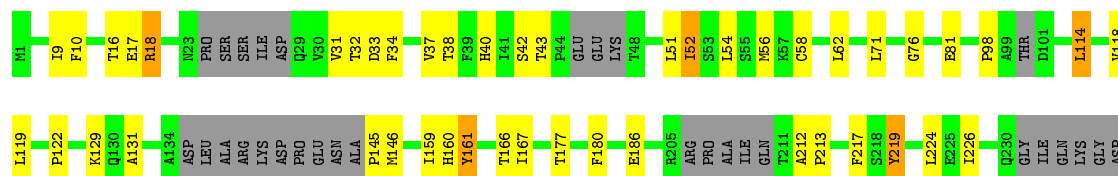
• Molecule 2: Actin-related protein 2/3 complex subunit 1

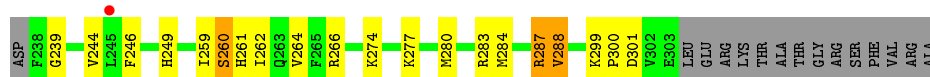


• Molecule 3: Actin-related protein 2/3 complex subunit 2

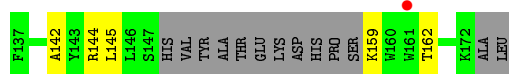
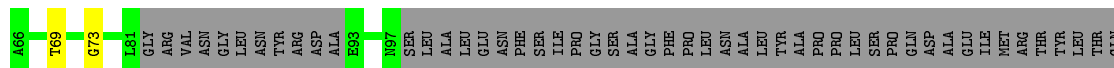
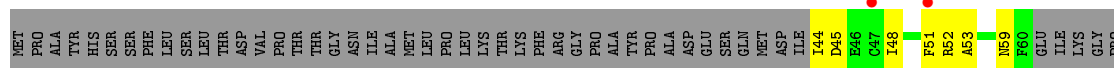


• Molecule 3: Actin-related protein 2/3 complex subunit 2

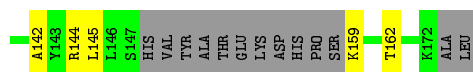
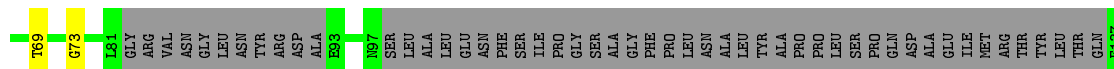
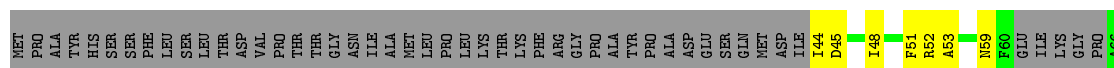




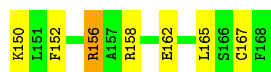
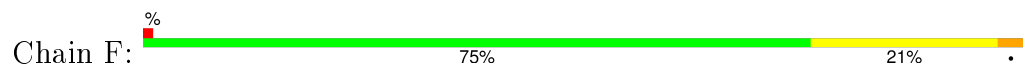
- Molecule 4: Actin-related protein 2/3 complex subunit 3



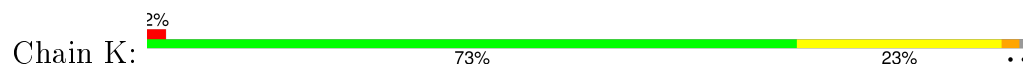
- Molecule 4: Actin-related protein 2/3 complex subunit 3



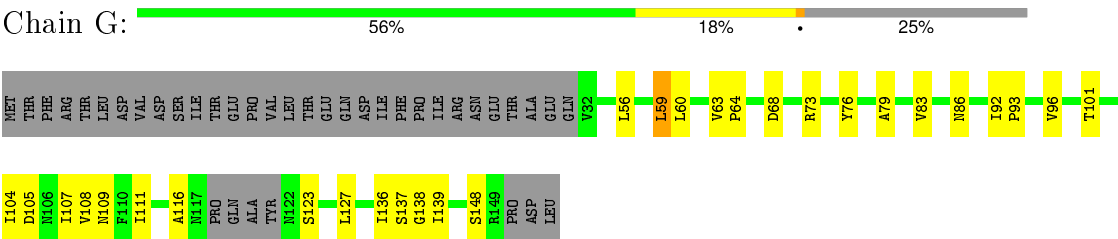
- Molecule 5: Actin-related protein 2/3 complex subunit 4



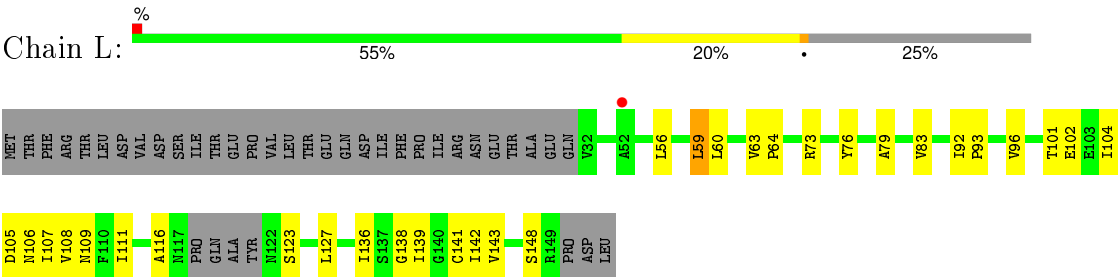
- Molecule 5: Actin-related protein 2/3 complex subunit 4



● Molecule 6: Actin-related protein 2/3 complex subunit 5



● Molecule 6: Actin-related protein 2/3 complex subunit 5



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 2 2	Depositor
Cell constants a, b, c, α , β , γ	218.97Å 218.97Å 315.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.00 – 3.78 49.05 – 3.79	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.00-3.78) 85.8 (49.05-3.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 3.77Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.324 , 0.344 0.297 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	87.8	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 106.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	1 of 75459 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	18705	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% 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

5.1 Standard geometry

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

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	0.44	1/2610 (0.0%)	0.56	2/3567 (0.1%)
1	B	0.41	1/2611 (0.0%)	0.56	2/3569 (0.1%)
2	C	0.37	0/2300	0.61	8/3170 (0.3%)
2	H	0.37	1/2310 (0.0%)	0.61	8/3184 (0.3%)
3	D	0.39	0/2072	0.56	3/2816 (0.1%)
3	I	0.39	0/2072	0.56	3/2816 (0.1%)
4	E	0.35	0/399	0.45	0/540
4	J	0.39	0/399	0.45	0/540
5	F	0.37	0/1314	0.54	0/1777
5	K	0.43	1/1314 (0.1%)	0.54	1/1777 (0.1%)
6	G	0.38	0/799	0.53	0/1097
6	L	0.35	0/799	0.51	0/1097
All	All	0.40	4/18999 (0.0%)	0.56	27/25950 (0.1%)

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
1	A	0	1
1	B	0	1
5	F	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	88	TYR	C-O	12.02	1.46	1.23
5	K	167	CYS	C-O	-9.32	1.05	1.23
1	B	88	TYR	C-O	8.89	1.40	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	130	GLU	C-O	5.62	1.34	1.23

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	TYR	CA-C-O	-12.76	93.31	120.10
1	B	88	TYR	O-C-N	-12.05	103.42	122.70
1	B	88	TYR	CA-C-O	-8.63	101.97	120.10
1	A	88	TYR	O-C-N	-8.15	109.67	122.70
2	C	241	PRO	N-CA-CB	6.19	110.72	103.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	88	TYR	Mainchain
1	B	88	TYR	Mainchain
5	F	167	CYS	Mainchain

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	2555	0	2244	47	0
1	B	2556	0	2244	44	0
2	C	2252	0	1845	43	0
2	H	2262	0	1851	38	0
3	D	2028	0	1774	39	0
3	I	2028	0	1774	42	0
4	E	397	0	275	4	0
4	J	397	0	275	4	0
5	F	1294	0	1260	27	0
5	K	1294	0	1260	27	0
6	G	790	0	717	17	0
6	L	790	0	717	19	0
7	A	31	0	12	0	0
7	B	31	0	12	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18705	0	16260	322	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 9.

The worst 5 of 322 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)
3:D:177:THR:HG22	3:D:244:VAL:HG12	1.58	0.86
1:B:21:TYR:CE1	3:I:32:THR:HG22	2.13	0.83
3:I:177:THR:HG22	3:I:244:VAL:HG12	1.59	0.83
1:B:31:PHE:HB2	1:B:32:PRO:HD2	1.61	0.82
3:D:18:ARG:CG	3:D:18:ARG:HH11	1.94	0.81

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	343/427 (80%)	299 (87%)	36 (10%)	8 (2%)	8	51
1	B	343/427 (80%)	300 (88%)	37 (11%)	6 (2%)	11	56
2	C	324/377 (86%)	245 (76%)	56 (17%)	23 (7%)	1	23
2	H	325/377 (86%)	245 (75%)	59 (18%)	21 (6%)	1	26
3	D	258/317 (81%)	215 (83%)	35 (14%)	8 (3%)	5	45
3	I	258/317 (81%)	217 (84%)	33 (13%)	8 (3%)	5	45
4	E	53/174 (30%)	40 (76%)	11 (21%)	2 (4%)	4	39
4	J	53/174 (30%)	40 (76%)	11 (21%)	2 (4%)	4	39
5	F	164/168 (98%)	144 (88%)	18 (11%)	2 (1%)	16	63

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	K	164/168 (98%)	143 (87%)	19 (12%)	2 (1%)	16	63
6	G	110/152 (72%)	97 (88%)	11 (10%)	2 (2%)	11	55
6	L	110/152 (72%)	97 (88%)	11 (10%)	2 (2%)	11	55
All	All	2505/3230 (78%)	2082 (83%)	337 (14%)	86 (3%)	5	43

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	TRP
1	A	206	ILE
2	C	54	HIS
2	C	108	TRP
2	C	143	ARG

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	240/364 (66%)	214 (89%)	26 (11%)	8	40
1	B	240/364 (66%)	215 (90%)	25 (10%)	9	42
2	C	181/317 (57%)	163 (90%)	18 (10%)	10	44
2	H	182/317 (57%)	165 (91%)	17 (9%)	11	47
3	D	185/287 (64%)	169 (91%)	16 (9%)	13	52
3	I	185/287 (64%)	169 (91%)	16 (9%)	13	52
4	E	23/150 (15%)	19 (83%)	4 (17%)	2	18
4	J	23/150 (15%)	19 (83%)	4 (17%)	2	18
5	F	140/157 (89%)	131 (94%)	9 (6%)	22	63
5	K	140/157 (89%)	132 (94%)	8 (6%)	25	67
6	G	74/134 (55%)	67 (90%)	7 (10%)	11	46
6	L	74/134 (55%)	70 (95%)	4 (5%)	27	68
All	All	1687/2818 (60%)	1533 (91%)	154 (9%)	12	48

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	101	PHE
1	B	102	TRP
5	K	22	LEU
5	F	156	ARG
6	G	136	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	101	ASN
1	B	151	ASN
3	I	253	GLN
1	B	111	GLN
1	B	192	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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
7	ATP	A	428	-	24,33,33	0.93	1 (4%)	31,52,52	2.01	7 (22%)
7	ATP	B	428	-	24,33,33	1.00	1 (4%)	31,52,52	1.94	5 (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
7	ATP	A	428	-	-	0/18/38/38	0/3/3/3
7	ATP	B	428	-	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	428	ATP	C5-C4	3.09	1.47	1.40
7	B	428	ATP	C5-C4	3.21	1.47	1.40

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	428	ATP	N3-C2-N1	-6.86	123.64	128.89
7	A	428	ATP	N3-C2-N1	-6.67	123.79	128.89
7	A	428	ATP	PA-O3A-PB	-4.63	119.73	132.73
7	B	428	ATP	PA-O3A-PB	-3.94	121.68	132.73
7	B	428	ATP	PB-O3B-PG	-3.78	120.00	132.67

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, 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	355/427 (83%)	-0.21	0 100 100	65, 74, 88, 94	1 (0%)
1	B	355/427 (83%)	-0.20	1 (0%) 94 89	65, 74, 88, 94	1 (0%)
2	C	336/377 (89%)	-0.25	1 (0%) 94 89	65, 76, 86, 95	0
2	H	337/377 (89%)	0.06	9 (2%) 58 42	65, 76, 86, 95	0
3	D	272/317 (85%)	-0.27	0 100 100	65, 72, 86, 96	0
3	I	272/317 (85%)	-0.27	1 (0%) 93 87	65, 72, 86, 96	0
4	E	63/174 (36%)	0.04	3 (4%) 34 22	66, 73, 83, 84	0
4	J	63/174 (36%)	-0.36	0 100 100	66, 73, 83, 84	0
5	F	166/168 (98%)	-0.12	1 (0%) 90 82	65, 74, 84, 99	1 (0%)
5	K	166/168 (98%)	0.09	3 (1%) 71 56	65, 74, 84, 99	1 (0%)
6	G	114/152 (75%)	-0.27	0 100 100	66, 73, 82, 84	0
6	L	114/152 (75%)	-0.01	1 (0%) 85 74	66, 73, 82, 84	0
All	All	2613/3230 (80%)	-0.16	20 (0%) 87 77	65, 74, 86, 99	4 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	287	THR	3.4
4	E	161	TRP	3.1
5	K	42	ARG	2.7
2	H	174	SER	2.6
2	H	151	SER	2.6

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 [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
7	ATP	B	428	31/31	0.89	0.27	0.21	102,102,108,108	0
7	ATP	A	428	31/31	0.90	0.21	-0.22	97,98,106,106	0

6.5 Other polymers [i](#)

There are no such residues in this entry.