



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:28 AM GMT

PDB ID : 2QWR  
Title : Crystal structure of disulfide-bond-crosslinked complex of bovine hsc70 (1-394aa)R171C and bovine Auxilin (810-910aa)D876C in the AMPPNP intact form  
Authors : Jiang, J.; Maes, E.G.; Wang, L.; Taylor, A.B.; Hinck, A.P.; Lafer, E.M.; Sousa, R.  
Deposited on : 2007-08-10  
Resolution : 2.21 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](mailto: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.

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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

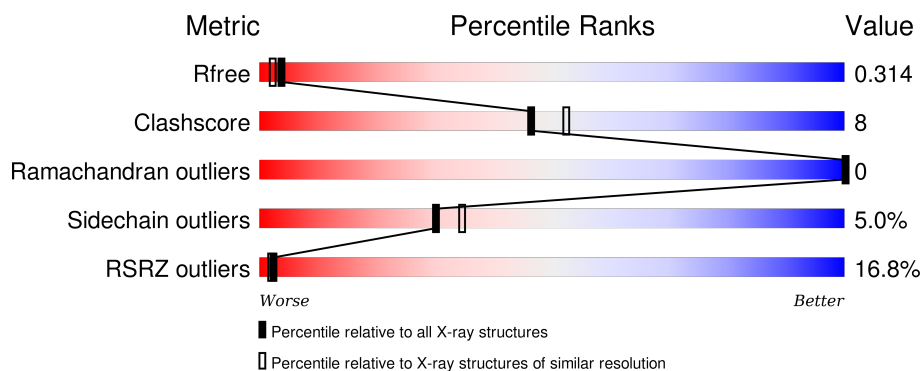
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.21 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	4405 (2.24-2.20)
Clashscore	102246	5146 (2.24-2.20)
Ramachandran outliers	100387	5065 (2.24-2.20)
Sidechain outliers	100360	5066 (2.24-2.20)
RSRZ outliers	91569	4414 (2.24-2.20)

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  $\geq 3$ , 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	394	
2	B	92	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3863 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 Heat shock cognate 71 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	0	0
			2959	1856	517	577	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	CYS	ARG	ENGINEERED	UNP P19120

- Molecule 2 is a protein called Putative tyrosine-protein phosphatase auxilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	92	Total	C	N	O	S	0	0	0
			754	488	126	135	5			

There is a discrepancy between the modelled and reference sequences:

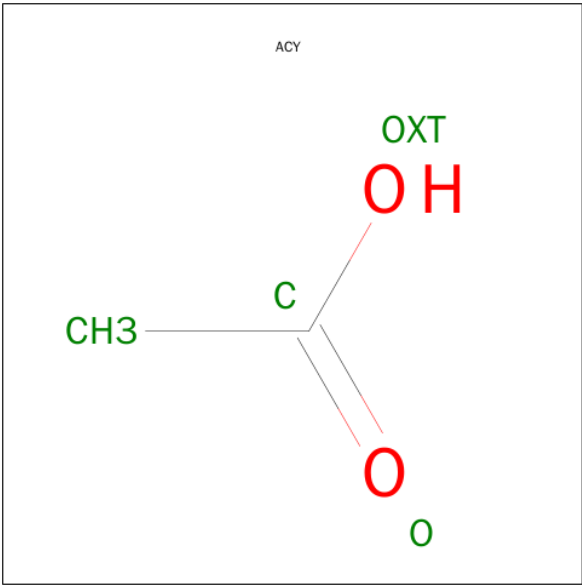
Chain	Residue	Modelled	Actual	Comment	Reference
B	876	CYS	ASP	ENGINEERED	UNP Q27974

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			3	2	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			5	3	2		

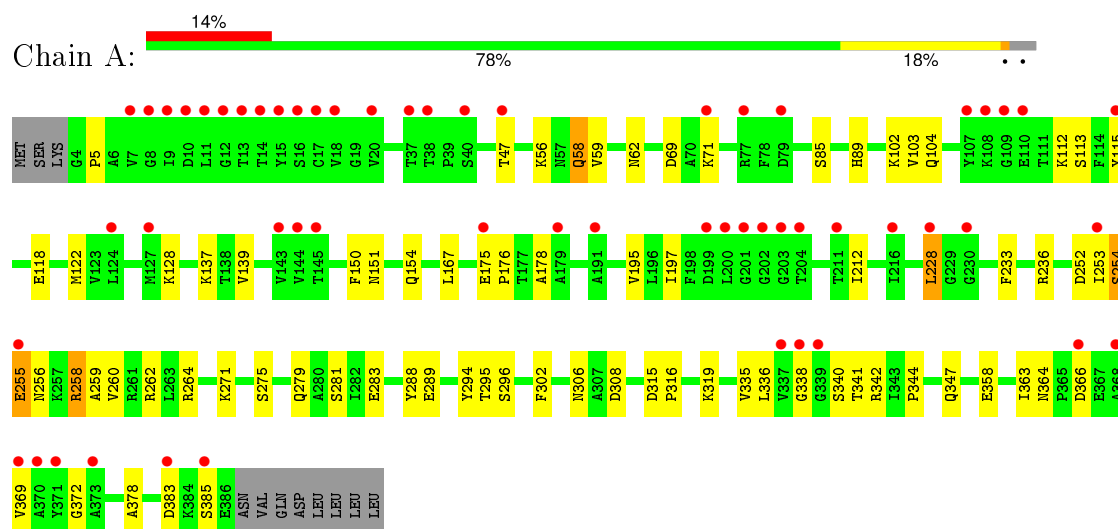
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	98	Total	O	0	0
			98	98		
6	B	7	Total	O	0	0
			7	7		

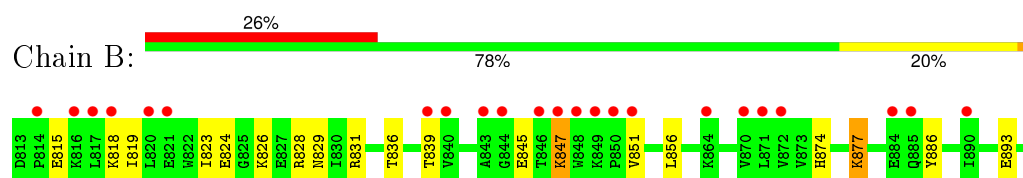
### 3 Residue-property plots [i](#)

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: Heat shock cognate 71 kDa protein



- Molecule 2: Putative tyrosine-protein phosphatase auxilin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	38.80 Å 56.49 Å 225.88 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.67 – 2.21 31.67 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.7 (31.67-2.21) 99.7 (31.67-2.21)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.56 (at 2.20 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.230 , 0.294 0.281 , 0.314	Depositor DCC
$R_{free}$ test set	1308 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.4	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 33.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 25852 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3863	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	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.*

<sup>1</sup> Intensities estimated from amplitudes.

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ACY, ANP

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	0.69	1/3005 (0.0%)	0.74	2/4058 (0.0%)
2	B	0.49	0/773	0.57	0/1046
All	All	0.66	1/3778 (0.0%)	0.71	2/5104 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	340	SER	CB-OG	5.01	1.48	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	ASP	CB-CG-OD1	6.14	123.83	118.30
1	A	228	LEU	CA-CB-CG	5.84	128.73	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2959	0	2955	44	0
2	B	754	0	760	13	0
3	A	31	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	3	0	0	0	0
5	A	11	0	13	1	0
6	A	98	0	0	3	0
6	B	7	0	0	0	0
All	All	3863	0	3741	57	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 8.

All (57) 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:256:ASN:O	1:A:260:VAL:HG23	1.82	0.79
1:A:233:PHE:HA	1:A:306:ASN:HD21	1.47	0.78
1:A:151:ASN:H	1:A:154:GLN:HE21	1.34	0.75
1:A:255:GLU:HA	1:A:255:GLU:OE1	1.89	0.73
2:B:823:ILE:HG12	2:B:893:GLU:HG2	1.73	0.71
1:A:233:PHE:HA	1:A:306:ASN:ND2	2.10	0.66
1:A:128:LYS:HE2	1:A:139:VAL:O	1.96	0.65
1:A:58:GLN:HE22	1:A:62:ASN:HD22	1.43	0.65
1:A:358:GLU:HG3	6:A:3213:HOH:O	1.99	0.62
1:A:151:ASN:H	1:A:154:GLN:NE2	1.98	0.60
2:B:828:ARG:HG2	2:B:897:ALA:HA	1.83	0.59
1:A:258:ARG:O	1:A:262:ARG:HG3	2.03	0.58
1:A:256:ASN:HB3	1:A:259:ALA:HB3	1.85	0.56
1:A:56:LYS:O	1:A:59:VAL:HG12	2.06	0.55
2:B:874:HIS:HB3	2:B:877:LYS:HD3	1.89	0.55
1:A:176:PRO:HB2	1:A:197:ILE:HG13	1.89	0.55
1:A:283:GLU:HG2	1:A:294:TYR:CD1	2.41	0.55
2:B:877:LYS:CD	2:B:877:LYS:H	2.22	0.53
1:A:197:ILE:HD13	1:A:335:VAL:HB	1.92	0.52
2:B:877:LYS:N	2:B:877:LYS:CD	2.73	0.51
1:A:315:ASP:HB2	1:A:316:PRO:HD3	1.92	0.50
1:A:175:GLU:HG2	1:A:369:VAL:HG11	1.93	0.50
1:A:112:LYS:HE2	6:A:3230:HOH:O	2.11	0.50
2:B:831:ARG:HG2	2:B:856:LEU:HB3	1.95	0.49
1:A:118:GLU:O	1:A:122:MET:HG3	2.13	0.49
1:A:236:ARG:HH22	1:A:308:ASP:CG	2.17	0.48
1:A:252:ASP:OD1	1:A:254:SER:HB2	2.13	0.48
1:A:255:GLU:CA	1:A:255:GLU:OE1	2.62	0.48
1:A:338:GLY:HA2	3:A:487:ANP:O1A	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:877:LYS:HD2	2:B:877:LYS:N	2.30	0.47
1:A:178:ALA:O	1:A:372:GLY:HA3	2.15	0.47
2:B:847:LYS:NZ	2:B:847:LYS:HA	2.31	0.46
1:A:363:ILE:O	1:A:364:ASN:C	2.55	0.46
1:A:195:VAL:HG21	1:A:212:ILE:HD11	1.99	0.45
6:A:3202:HOH:O	2:B:877:LYS:HE3	2.17	0.45
1:A:102:LYS:HE3	1:A:115:TYR:CZ	2.52	0.45
1:A:128:LYS:HG3	1:A:167:LEU:HD21	2.00	0.44
2:B:877:LYS:H	2:B:877:LYS:HD3	1.83	0.43
2:B:826:LYS:HE3	2:B:836:THR:HG21	2.01	0.43
1:A:366:ASP:OD1	1:A:366:ASP:N	2.47	0.43
1:A:253:ILE:HG22	1:A:288:TYR:CG	2.53	0.43
1:A:71:LYS:HG2	5:A:3147:GOL:H32	2.00	0.43
1:A:150:PHE:CD2	1:A:154:GLN:HB3	2.54	0.42
1:A:271:LYS:HG3	1:A:302:PHE:CZ	2.54	0.42
1:A:336:LEU:HD22	1:A:341:THR:HB	2.01	0.42
1:A:275:SER:HA	1:A:344:PRO:HD3	2.02	0.41
1:A:103:VAL:O	1:A:113:SER:HA	2.19	0.41
2:B:818:LYS:NZ	2:B:839:THR:O	2.48	0.41
1:A:195:VAL:HG21	1:A:212:ILE:CD1	2.51	0.41
1:A:295:THR:OG1	1:A:296:SER:N	2.53	0.41
1:A:5:PRO:HD3	1:A:137:LYS:HE3	2.02	0.41
1:A:336:LEU:HD11	1:A:347:GLN:HG2	2.03	0.40
1:A:264:ARG:HD2	1:A:264:ARG:HH11	1.72	0.40
2:B:819:ILE:CD1	2:B:886:TYR:HB3	2.52	0.40
1:A:288:TYR:O	1:A:289:GLU:C	2.59	0.40
1:A:378:ALA:HB1	1:A:383:ASP:HB2	2.02	0.40
1:A:342:ARG:HH11	1:A:342:ARG:HD3	1.75	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	381/394 (97%)	364 (96%)	17 (4%)	0	100	100
2	B	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
All	All	471/486 (97%)	449 (95%)	22 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	317/328 (97%)	304 (96%)	13 (4%)	37	45
2	B	81/81 (100%)	74 (91%)	7 (9%)	13	12
All	All	398/409 (97%)	378 (95%)	20 (5%)	30	34

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	THR
1	A	58	GLN
1	A	85	SER
1	A	89	HIS
1	A	104	GLN
1	A	228	LEU
1	A	254	SER
1	A	255	GLU
1	A	258	ARG
1	A	279	GLN
1	A	281	SER
1	A	319	LYS
1	A	385	SER
2	B	815	GLU
2	B	824	GLU
2	B	829	ASN
2	B	845	GLU
2	B	847	LYS

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Mol	Chain	Res	Type
2	B	851	VAL
2	B	877	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	58	GLN
1	A	104	GLN
1	A	154	GLN
1	A	306	ASN
1	A	351	GLN
1	A	376	GLN
2	B	829	ASN
2	B	874	HIS
2	B	895	ASN

### 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](#)

4 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	ACY	A	1022	-	2,2,3	1.15	0	1,1,3	0.07	0
5	GOL	A	3147	-	5,5,5	0.39	0	5,5,5	0.81	0
5	GOL	A	3148	-	4,4,5	0.58	0	2,4,5	0.74	0
3	ANP	A	487	-	27,33,33	2.28	5 (18%)	30,52,52	3.37	12 (40%)

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	ACY	A	1022	-	-	0/0/0/0	0/0/0/0
5	GOL	A	3147	-	-	0/4/4/4	0/0/0/0
5	GOL	A	3148	-	-	0/2/2/4	0/0/0/0
3	ANP	A	487	-	-	0/12/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	487	ANP	PG-O3G	2.07	1.62	1.56
3	A	487	ANP	O4'-C1'	3.44	1.45	1.41
3	A	487	ANP	PG-N3B	3.68	1.73	1.63
3	A	487	ANP	PB-O1B	4.56	1.51	1.46
3	A	487	ANP	PG-O1G	8.52	1.55	1.46

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	487	ANP	N3-C2-N1	-11.63	119.99	128.89
3	A	487	ANP	O1B-PB-N3B	-6.96	101.22	111.90
3	A	487	ANP	O2G-PG-O1G	-5.04	100.09	113.49
3	A	487	ANP	C2'-C1'-N9	-4.59	107.27	114.29
3	A	487	ANP	C4'-O4'-C1'	-3.01	106.41	109.72
3	A	487	ANP	C4-C5-N7	-2.84	106.87	109.48
3	A	487	ANP	C1'-N9-C4	-2.21	123.61	126.94
3	A	487	ANP	O2A-PA-O3A	2.51	116.46	105.09
3	A	487	ANP	O3A-PB-N3B	2.55	113.46	106.44
3	A	487	ANP	O4'-C1'-N9	3.39	115.19	108.10
3	A	487	ANP	O2B-PB-O1B	3.45	117.21	110.00
3	A	487	ANP	O3G-PG-O2G	5.41	123.61	107.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3147	GOL	1	0
3	A	487	ANP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	383/394 (97%)	0.98	56 (14%)	3 3	30, 45, 51, 76	0
2	B	92/92 (100%)	1.27	24 (26%)	1 1	41, 46, 54, 61	0
All	All	475/486 (97%)	1.04	80 (16%)	2 2	30, 45, 52, 76	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	814	PRO	5.1
1	A	202	GLY	4.7
1	A	12	GLY	4.1
1	A	14	THR	4.1
2	B	851	VAL	4.0
1	A	11	LEU	3.9
1	A	370	ALA	3.7
1	A	16	SER	3.7
2	B	820	LEU	3.6
1	A	145	THR	3.6
2	B	818	LYS	3.6
1	A	200	LEU	3.6
1	A	47	THR	3.6
1	A	13	THR	3.5
1	A	15	TYR	3.5
1	A	203	GLY	3.4
1	A	255	GLU	3.4
1	A	9	ILE	3.4
1	A	385	SER	3.4
1	A	339	GLY	3.3
1	A	201	GLY	3.2
1	A	338	GLY	3.2
2	B	848	TRP	3.2
1	A	7	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	17	CYS	3.1
1	A	18	VAL	3.0
1	A	143	VAL	3.0
1	A	109	GLY	3.0
1	A	228	LEU	3.0
2	B	821	GLU	3.0
1	A	107	TYR	3.0
1	A	10	ASP	2.9
2	B	840	VAL	2.9
2	B	850	PRO	2.8
2	B	871	LEU	2.8
1	A	38	THR	2.8
1	A	124	LEU	2.7
2	B	846	THR	2.7
1	A	8	GLY	2.7
1	A	179	ALA	2.6
1	A	373	ALA	2.6
1	A	204	THR	2.6
1	A	369	VAL	2.6
2	B	843	ALA	2.6
1	A	144	VAL	2.6
1	A	127	MET	2.6
1	A	37	THR	2.5
1	A	368	ALA	2.5
1	A	108	LYS	2.5
1	A	191	ALA	2.5
2	B	816	LYS	2.4
1	A	110	GLU	2.4
1	A	199	ASP	2.4
2	B	885	GLN	2.3
2	B	884	GLU	2.3
1	A	40	SER	2.3
1	A	253	ILE	2.3
1	A	71	LYS	2.3
2	B	864	LYS	2.3
1	A	20	VAL	2.3
2	B	872	VAL	2.3
2	B	847	LYS	2.3
1	A	77	ARG	2.3
2	B	870	VAL	2.2
2	B	904	GLN	2.2
1	A	79	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	337	VAL	2.2
2	B	817	LEU	2.2
1	A	383	ASP	2.2
1	A	230	GLY	2.1
1	A	115	TYR	2.1
1	A	175	GLU	2.1
2	B	844	GLY	2.1
2	B	890	ILE	2.1
1	A	366	ASP	2.1
1	A	371	TYR	2.1
2	B	839	THR	2.0
2	B	849	LYS	2.0
1	A	211	THR	2.0
1	A	216	ILE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	ACY	A	1022	3/4	0.92	0.21	0.90	45,45,46,47	0
5	GOL	A	3148	5/6	0.84	0.28	0.53	45,47,48,50	0
5	GOL	A	3147	6/6	0.88	0.26	0.47	46,48,49,53	0
3	ANP	A	487	31/31	0.89	0.24	-0.65	24,28,43,48	0

## 6.5 Other polymers

There are no such residues in this entry.