



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 14, 2017 – 02:49 PM EDT

PDB ID : 2OQ2  
Title : Crystal structure of yeast PAPS reductase with PAP, a product complex  
Authors : Yu, Z.; Fisher, A.J.  
Deposited on : unknown  
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030345

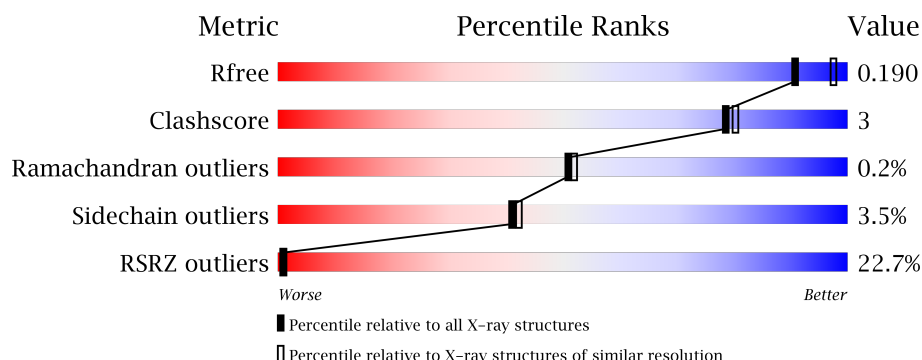
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	261	<div> <div>12%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>• •</div> </div> </div>
1	B	261	<div> <div>23%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>• •</div> </div> </div>
1	C	261	<div> <div>23%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>• •</div> </div> </div>
1	D	261	<div> <div>30%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition [i](#)

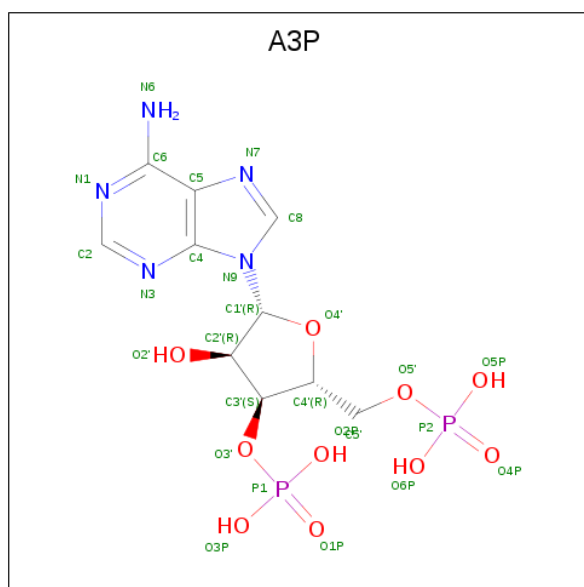
There are 3 unique types of molecules in this entry. The entry contains 8616 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Phosphoadenosine phosphosulfate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			2053	1321	341	386	5			
1	B	252	Total	C	N	O	S	0	0	0
			2036	1313	339	379	5			
1	C	257	Total	C	N	O	S	0	0	0
			2108	1354	351	398	5			
1	D	246	Total	C	N	O	S	0	0	0
			1978	1270	329	374	5			

- Molecule 2 is ADENOSINE-3'-5'-DIPHOSPHATE (three-letter code: A3P) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



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

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

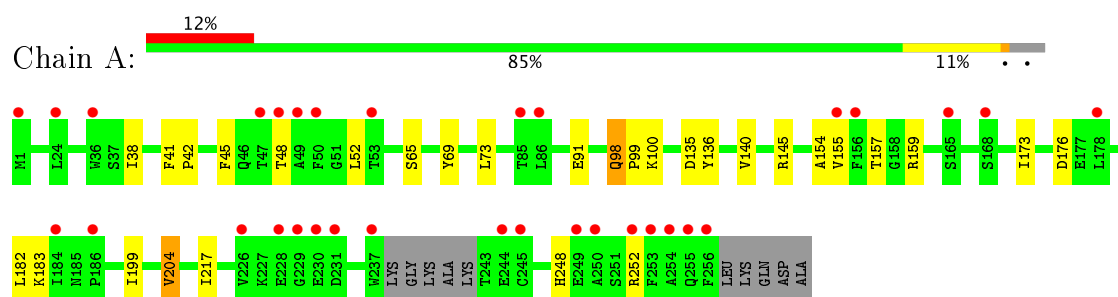
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	95	Total	O	0	0
			95	95		
3	B	41	Total	O	0	0
			41	41		
3	C	145	Total	O	0	0
			145	145		
3	D	52	Total	O	0	0
			52	52		

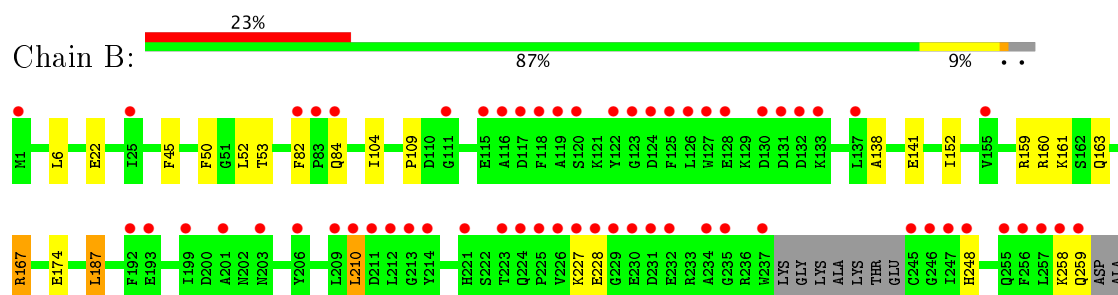
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

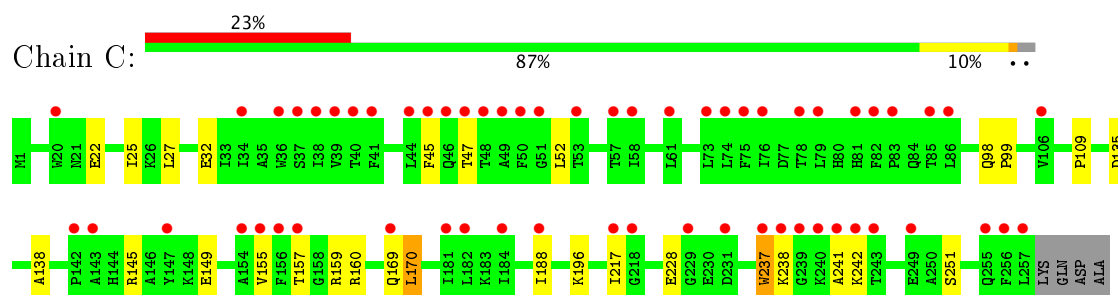
- Molecule 1: Phosphoadenosine phosphosulfate reductase



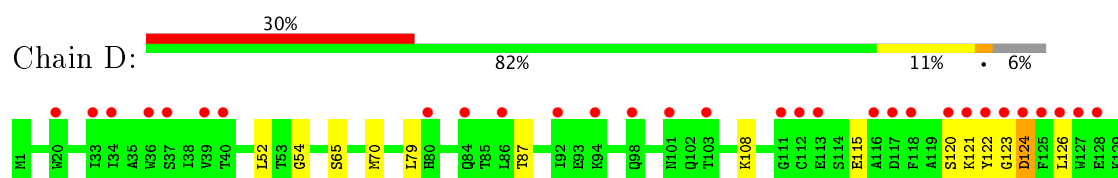
- Molecule 1: Phosphoadenosine phosphosulfate reductase

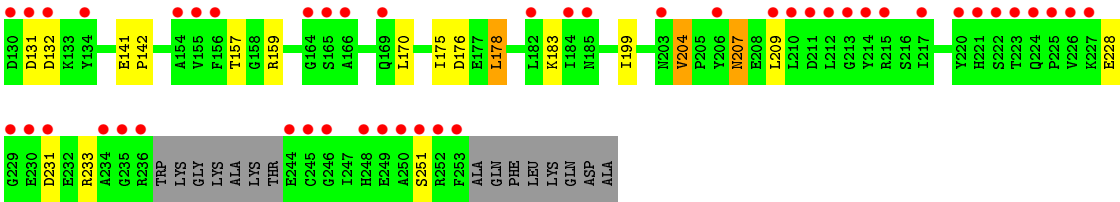


- Molecule 1: Phosphoadenosine phosphosulfate reductase



- Molecule 1: Phosphoadenosine phosphosulfate reductase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.42Å 63.08Å 323.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10 37.31 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.00-2.10) 91.4 (37.31-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.193 , 0.246 0.196 , 0.190	Depositor DCC
$R_{free}$ test set	2762 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.1	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	8616	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: A3P

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	0.42	0/2106	0.53	0/2856
1	B	0.38	0/2089	0.51	1/2838 (0.0%)
1	C	0.48	0/2162	0.58	1/2930 (0.0%)
1	D	0.61	4/2028 (0.2%)	0.56	0/2756
All	All	0.48	4/8385 (0.0%)	0.55	2/11380 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	228	GLU	CD-OE2	13.42	1.40	1.25
1	D	120	SER	CB-OG	9.11	1.54	1.42
1	D	228	GLU	CD-OE1	7.11	1.33	1.25
1	D	87	THR	C-O	5.04	1.32	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	170	LEU	CA-CB-CG	5.31	127.51	115.30
1	B	187	LEU	CA-CB-CG	5.04	126.89	115.30

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	2053	0	1977	16	0
1	B	2036	0	1949	12	0
1	C	2108	0	2049	14	0
1	D	1978	0	1879	12	0
2	A	27	0	11	0	0
2	B	27	0	11	0	0
2	C	27	0	11	0	0
2	D	27	0	11	1	0
3	A	95	0	0	2	0
3	B	41	0	0	2	0
3	C	145	0	0	3	0
3	D	52	0	0	0	0
All	All	8616	0	7898	54	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 3.

All (54) 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:176:ASP:HB2	1:A:183:LYS:HE3	1.70	0.74
1:B:82:PHE:HB3	1:B:84:GLN:HE21	1.58	0.68
1:D:176:ASP:HB2	1:D:183:LYS:HE2	1.76	0.66
1:D:207:ASN:HD22	1:D:209:LEU:H	1.49	0.61
1:D:141:GLU:HB3	1:D:142:PRO:HD3	1.82	0.60
1:C:238:LYS:HB2	3:C:1064:HOH:O	2.02	0.59
1:D:123:GLY:HA3	1:D:124:ASP:CB	2.33	0.59
1:D:159:ARG:HB3	1:D:170:LEU:HD11	1.83	0.58
1:C:159:ARG:HB3	1:C:170:LEU:HD11	1.87	0.57
1:A:157:THR:OG1	1:A:159:ARG:HD3	2.09	0.53
1:B:22:GLU:HG3	3:B:1021:HOH:O	2.08	0.53
1:B:141:GLU:HG2	3:B:1023:HOH:O	2.10	0.52
1:D:65:SER:HB3	1:D:70:MET:HG2	1.90	0.52
1:A:38:ILE:HG23	1:A:69:TYR:CE1	2.45	0.51
1:A:48:THR:HG22	1:A:73:LEU:HD11	1.91	0.51
1:A:159:ARG:HD2	1:A:248:HIS:CE1	2.46	0.50
1:D:178:LEU:HD12	1:D:251:SER:HA	1.93	0.50
1:C:237:TRP:CE2	1:C:242:LYS:HA	2.49	0.48
1:C:45:PHE:O	1:C:155:VAL:HA	2.13	0.48
1:D:121:LYS:HD3	1:D:122:TYR:CZ	2.49	0.48
1:B:109:PRO:HG3	1:B:138:ALA:HA	1.96	0.48
1:B:159:ARG:NH1	1:B:174:GLU:OE1	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:THR:CG2	1:A:73:LEU:HD11	2.44	0.47
1:C:27:LEU:HD13	1:C:32:GLU:HB3	1.96	0.47
1:A:217:ILE:HD12	3:A:1053:HOH:O	2.15	0.47
1:D:54:GLY:HA3	2:D:999:A3P:O3P	2.15	0.47
1:C:228:GLU:OE2	1:C:228:GLU:N	2.48	0.46
1:B:53:THR:HG23	1:B:187:LEU:HD12	1.96	0.46
1:C:109:PRO:HG3	1:C:138:ALA:HA	1.96	0.46
1:A:98:GLN:HB3	1:A:99:PRO:HD3	1.96	0.46
1:A:45:PHE:O	1:A:155:VAL:HA	2.16	0.46
1:C:22:GLU:O	1:C:25:ILE:HG22	2.17	0.45
1:A:52:LEU:HG	1:A:199:ILE:HG13	1.99	0.45
1:C:145:ARG:O	1:C:149:GLU:HG3	2.16	0.45
1:D:79:LEU:HD21	1:D:108:LYS:HD3	1.99	0.44
1:A:136:TYR:HA	1:A:140:VAL:HB	1.99	0.44
1:A:145:ARG:NH2	3:A:1087:HOH:O	2.46	0.44
1:B:160:ARG:HB2	1:B:163:GLN:HG3	2.01	0.43
1:C:98:GLN:HB3	1:C:99:PRO:HD3	2.00	0.43
1:D:199:ILE:HA	1:D:204:VAL:HG13	2.00	0.43
1:A:41:PHE:HA	1:A:42:PRO:HD2	1.95	0.43
1:A:199:ILE:HA	1:A:204:VAL:HG13	2.00	0.43
1:C:47:THR:HG21	3:C:1068:HOH:O	2.19	0.42
1:A:65:SER:OG	1:A:100:LYS:HE2	2.20	0.42
1:B:161:LYS:HA	1:B:167:ARG:O	2.20	0.42
1:B:50:PHE:HZ	1:B:104:ILE:HD13	1.84	0.41
1:C:160:ARG:HA	1:C:188:ILE:HA	2.02	0.41
1:D:65:SER:CB	1:D:70:MET:HG2	2.50	0.41
1:B:52:LEU:HD13	1:B:210:LEU:HD13	2.02	0.41
1:B:45:PHE:CD1	1:B:152:ILE:HG12	2.56	0.41
1:C:237:TRP:HB3	1:C:241:ALA:H	1.85	0.41
1:B:227:LYS:HB3	1:B:228:GLU:H	1.76	0.40
1:A:154:ALA:HA	1:A:182:LEU:O	2.21	0.40
1:C:217:ILE:HD12	3:C:1087:HOH:O	2.20	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	247/261 (95%)	244 (99%)	3 (1%)	0	100	100
1	B	248/261 (95%)	234 (94%)	13 (5%)	1 (0%)	38	35
1	C	255/261 (98%)	248 (97%)	7 (3%)	0	100	100
1	D	242/261 (93%)	237 (98%)	4 (2%)	1 (0%)	38	35
All	All	992/1044 (95%)	963 (97%)	27 (3%)	2 (0%)	51	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	124	ASP
1	B	258	LYS

### 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	219/233 (94%)	213 (97%)	6 (3%)	50	54
1	B	214/233 (92%)	209 (98%)	5 (2%)	56	60
1	C	227/233 (97%)	220 (97%)	7 (3%)	45	48
1	D	208/233 (89%)	196 (94%)	12 (6%)	23	20
All	All	868/932 (93%)	838 (96%)	30 (4%)	41	42

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	GLU
1	A	98	GLN
1	A	135	ASP
1	A	173	ILE

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Mol	Chain	Res	Type
1	A	204	VAL
1	A	252	ARG
1	B	6	LEU
1	B	167	ARG
1	B	210	LEU
1	B	248	HIS
1	B	259	GLN
1	C	52	LEU
1	C	135	ASP
1	C	157	THR
1	C	169	GLN
1	C	196	LYS
1	C	237	TRP
1	C	251	SER
1	D	52	LEU
1	D	115	GLU
1	D	126	LEU
1	D	131	ASP
1	D	132	ASP
1	D	157	THR
1	D	175	ILE
1	D	178	LEU
1	D	204	VAL
1	D	207	ASN
1	D	231	ASP
1	D	233	ARG

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	98	GLN
1	B	84	GLN
1	C	46	GLN
1	C	169	GLN
1	C	248	HIS
1	D	207	ASN

### 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 ⓘ

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$
2	A3P	A	999	-	26,29,29	1.07	1 (3%)	31,45,45	1.56	2 (6%)
2	A3P	B	999	-	26,29,29	1.08	1 (3%)	31,45,45	1.62	3 (9%)
2	A3P	C	999	-	26,29,29	1.03	2 (7%)	31,45,45	1.56	4 (12%)
2	A3P	D	999	-	26,29,29	1.06	1 (3%)	31,45,45	1.64	4 (12%)

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
2	A3P	A	999	-	-	0/11/31/31	0/3/3/3
2	A3P	B	999	-	-	0/11/31/31	0/3/3/3
2	A3P	C	999	-	-	0/11/31/31	0/3/3/3
2	A3P	D	999	-	-	0/11/31/31	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	999	A3P	C2-N3	2.26	1.35	1.32
2	C	999	A3P	C5-C4	3.15	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	999	A3P	C5-C4	3.16	1.47	1.40
2	B	999	A3P	C5-C4	3.27	1.47	1.40
2	D	999	A3P	C5-C4	3.33	1.48	1.40

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	A3P	N3-C2-N1	-6.70	123.02	128.86
2	D	999	A3P	N3-C2-N1	-6.66	123.06	128.86
2	A	999	A3P	N3-C2-N1	-6.48	123.22	128.86
2	C	999	A3P	N3-C2-N1	-6.35	123.33	128.86
2	D	999	A3P	C4-C5-N7	-2.87	106.64	109.41
2	B	999	A3P	C4-C5-N7	-2.55	106.95	109.41
2	D	999	A3P	O5P-P2-O5'	-2.31	100.59	106.73
2	C	999	A3P	C2-N1-C6	2.01	122.28	118.77
2	A	999	A3P	C2-N1-C6	2.04	122.34	118.77
2	B	999	A3P	O6P-P2-O5P	2.05	115.89	107.61
2	C	999	A3P	O6P-P2-O5P	2.11	116.12	107.61
2	C	999	A3P	N6-C6-N1	2.11	122.96	118.77
2	D	999	A3P	O6P-P2-O5P	2.49	117.66	107.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	999	A3P	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	251/261 (96%)	0.75	32 (12%) 4 5	31, 36, 43, 50	0
1	B	252/261 (96%)	1.27	60 (23%) 1 1	31, 36, 39, 53	0
1	C	257/261 (98%)	1.23	59 (22%) 1 1	29, 36, 42, 54	0
1	D	246/261 (94%)	1.61	77 (31%) 0 0	31, 37, 42, 50	0
All	All	1006/1044 (96%)	1.21	228 (22%) 1 1	29, 36, 42, 54	0

All (228) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	TRP	10.3
1	B	229	GLY	9.7
1	D	253	PHE	8.9
1	D	245	CYS	8.3
1	B	125	PHE	8.2
1	D	226	VAL	6.9
1	D	214	TYR	6.6
1	A	256	PHE	6.6
1	C	240	LYS	5.9
1	B	256	PHE	5.8
1	B	127	TRP	5.8
1	D	98	GLN	5.7
1	D	212	LEU	5.7
1	A	237	TRP	5.7
1	D	125	PHE	5.6
1	C	255	GLN	5.6
1	B	234	ALA	5.5
1	D	220	TYR	5.5
1	D	166	ALA	5.4
1	A	253	PHE	5.3
1	D	222	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	124	ASP	5.1
1	B	259	GLN	5.0
1	C	243	THR	5.0
1	B	228	GLU	4.8
1	C	257	LEU	4.7
1	D	231	ASP	4.7
1	D	127	TRP	4.7
1	B	226	VAL	4.6
1	D	101	ASN	4.6
1	A	255	GLN	4.6
1	B	119	ALA	4.6
1	D	210	LEU	4.5
1	C	155	VAL	4.5
1	B	231	ASP	4.5
1	B	235	GLY	4.5
1	A	178	LEU	4.4
1	C	48	THR	4.4
1	C	256	PHE	4.4
1	C	237	TRP	4.4
1	B	258	LYS	4.4
1	D	225	PRO	4.3
1	C	242	LYS	4.3
1	B	245	CYS	4.3
1	C	49	ALA	4.2
1	B	227	LYS	4.2
1	C	76	ILE	4.2
1	B	224	GLN	4.2
1	D	131	ASP	4.1
1	C	75	PHE	4.1
1	B	122	TYR	4.0
1	B	192	PHE	4.0
1	D	224	GLN	4.0
1	D	223	THR	4.0
1	B	126	LEU	4.0
1	B	214	TYR	4.0
1	B	213	GLY	4.0
1	B	248	HIS	4.0
1	B	255	GLN	3.9
1	A	254	ALA	3.9
1	C	85	THR	3.9
1	D	111	GLY	3.9
1	D	184	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	257	LEU	3.8
1	B	120	SER	3.8
1	D	118	PHE	3.8
1	B	116	ALA	3.8
1	C	86	LEU	3.7
1	B	246	GLY	3.7
1	C	74	LEU	3.7
1	C	47	THR	3.7
1	C	36	TRP	3.7
1	D	130	ASP	3.7
1	C	34	ILE	3.7
1	B	118	PHE	3.6
1	C	41	PHE	3.5
1	B	211	ASP	3.5
1	D	36	TRP	3.5
1	B	83	PRO	3.4
1	D	132	ASP	3.4
1	C	156	PHE	3.4
1	C	182	LEU	3.4
1	D	164	GLY	3.4
1	D	156	PHE	3.4
1	B	206	TYR	3.4
1	D	206	TYR	3.3
1	D	122	TYR	3.3
1	D	113	GLU	3.3
1	D	33	ILE	3.3
1	B	132	ASP	3.3
1	D	248	HIS	3.3
1	D	120	SER	3.2
1	B	210	LEU	3.2
1	C	51	GLY	3.2
1	D	126	LEU	3.2
1	B	117	ASP	3.2
1	C	44	LEU	3.2
1	C	40	THR	3.2
1	C	169	GLN	3.2
1	C	231	ASP	3.2
1	D	203	ASN	3.1
1	C	82	PHE	3.1
1	D	169	GLN	3.1
1	A	168	SER	3.1
1	B	123	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	230	GLU	3.1
1	B	212	LEU	3.1
1	D	165	SER	3.1
1	C	154	ALA	3.0
1	C	229	GLY	3.0
1	A	230	GLU	3.0
1	C	157	THR	3.0
1	D	251	SER	3.0
1	D	124	ASP	3.0
1	D	229	GLY	3.0
1	D	34	ILE	3.0
1	D	20	TRP	3.0
1	A	231	ASP	3.0
1	B	130	ASP	3.0
1	B	232	GLU	3.0
1	B	1	MET	3.0
1	A	229	GLY	3.0
1	D	182	LEU	2.9
1	D	213	GLY	2.9
1	B	223	THR	2.9
1	D	217	ILE	2.9
1	D	123	GLY	2.9
1	B	247	ILE	2.9
1	C	20	TRP	2.9
1	C	184	ILE	2.8
1	A	252	ARG	2.8
1	C	81	HIS	2.8
1	D	86	LEU	2.8
1	B	128	GLU	2.8
1	C	147	TYR	2.8
1	D	227	LYS	2.8
1	C	181	ILE	2.8
1	D	37	SER	2.8
1	A	249	GLU	2.8
1	D	40	THR	2.8
1	A	156	PHE	2.8
1	C	50	PHE	2.8
1	D	236	ARG	2.8
1	C	218	GLY	2.7
1	B	111	GLY	2.7
1	B	203	ASN	2.7
1	D	134	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	57	THR	2.7
1	C	38	ILE	2.7
1	B	82	PHE	2.7
1	C	83	PRO	2.6
1	C	45	PHE	2.6
1	C	143	ALA	2.6
1	C	106	VAL	2.6
1	D	154	ALA	2.6
1	B	225	PRO	2.6
1	A	85	THR	2.6
1	C	37	SER	2.6
1	D	244	GLU	2.6
1	C	39	VAL	2.6
1	A	250	ALA	2.6
1	D	234	ALA	2.6
1	D	92	ILE	2.6
1	C	249	GLU	2.6
1	C	238	LYS	2.6
1	B	221	HIS	2.5
1	D	215	ARG	2.5
1	D	235	GLY	2.5
1	D	80	HIS	2.5
1	C	239	GLY	2.5
1	B	131	ASP	2.5
1	D	155	VAL	2.4
1	D	252	ARG	2.4
1	D	249	GLU	2.4
1	B	199	ILE	2.4
1	A	48	THR	2.4
1	A	226	VAL	2.4
1	D	230	GLU	2.4
1	B	201	ALA	2.4
1	A	36	TRP	2.4
1	C	217	ILE	2.4
1	B	137	LEU	2.4
1	A	50	PHE	2.4
1	A	228	GLU	2.4
1	A	47	THR	2.4
1	A	24	LEU	2.3
1	D	211	ASP	2.3
1	C	188	ILE	2.3
1	A	86	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	53	THR	2.3
1	D	112	CYS	2.3
1	A	244	GLU	2.3
1	B	115	GLU	2.3
1	B	155	VAL	2.3
1	D	221	HIS	2.3
1	A	165	SER	2.3
1	D	246	GLY	2.3
1	D	185	ASN	2.3
1	C	61	LEU	2.3
1	C	241	ALA	2.3
1	C	73	LEU	2.2
1	A	155	VAL	2.2
1	D	39	VAL	2.2
1	A	1	MET	2.2
1	A	184	ILE	2.2
1	D	116	ALA	2.2
1	C	79	LEU	2.2
1	D	117	ASP	2.2
1	D	84	GLN	2.2
1	B	84	GLN	2.2
1	A	49	ALA	2.1
1	D	103	THR	2.1
1	D	128	GLU	2.1
1	A	245	CYS	2.1
1	C	142	PRO	2.1
1	C	58	ILE	2.1
1	D	94	LYS	2.1
1	D	121	LYS	2.1
1	C	78	THR	2.1
1	C	46	GLN	2.1
1	B	25	ILE	2.1
1	B	209	LEU	2.1
1	A	53	THR	2.0
1	A	186	PRO	2.0
1	D	209	LEU	2.0
1	B	133	LYS	2.0
1	B	193	GLU	2.0
1	D	250	ALA	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
2	A3P	D	999	27/27	0.90	0.16	-0.72	30,35,43,44	0
2	A3P	B	999	27/27	0.94	0.14	-0.86	36,40,41,42	0
2	A3P	C	999	27/27	0.97	0.18	-1.05	19,21,27,29	0
2	A3P	A	999	27/27	0.97	0.13	-1.23	26,27,35,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.