



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:46 AM GMT

PDB ID : 3C5W  
Title : Complex between PP2A-specific methylesterase PME-1 and PP2A core enzyme  
Authors : Xing, Y.; Li, Z.; Chen, Y.; Stock, J.; Jeffrey, P.D.; Shi, Y.  
Deposited on : 2008-02-01  
Resolution : 2.80 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

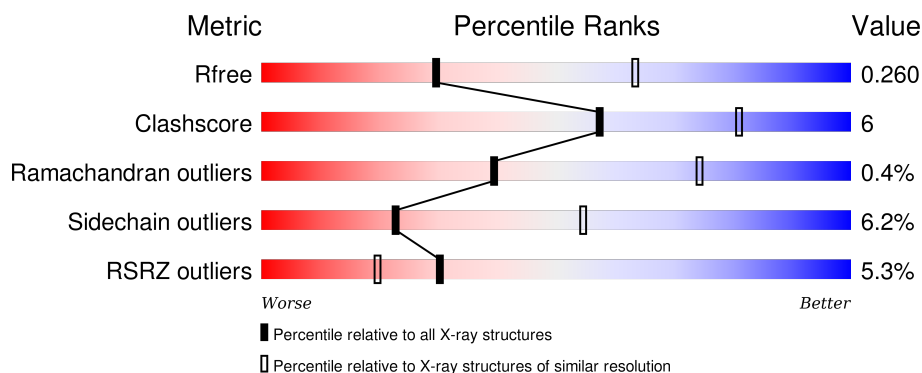
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	232	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>••</div> </div> </div>
2	C	310	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>16%</div> <div>• 5%</div> </div> </div>
3	P	310	<div> <div>8%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>• 5%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6503 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 PP2A A subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1788	1150	299	330	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLY	-	EXPRESSION TAG	UNP P30153
A	6	SER	-	EXPRESSION TAG	UNP P30153
A	7	HIS	-	EXPRESSION TAG	UNP P30153
A	8	MET	-	EXPRESSION TAG	UNP P30153

- Molecule 2 is a protein called PP2A C subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	294	Total	C	N	O	S	0	0	0
			2376	1508	402	451	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	EXPRESSION TAG	UNP P67775

- Molecule 3 is a protein called PP2A-specific methylesterase PME-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	294	Total	C	N	O	S	0	0	0
			2277	1447	394	420	16			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	35	GLY	-	EXPRESSION TAG	UNP Q9Y570

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Chain	Residue	Modelled	Actual	Comment	Reference
P	36	SER	-	EXPRESSION TAG	UNP Q9Y570
P	37	HIS	-	EXPRESSION TAG	UNP Q9Y570
P	38	MET	-	EXPRESSION TAG	UNP Q9Y570
P	156	ALA	SER	SEE REMARK 999	UNP Q9Y570
P	239	GLU	-	SEE REMARK 999	UNP Q9Y570
P	240	GLY	-	SEE REMARK 999	UNP Q9Y570
P	283	LYS	-	SEE REMARK 999	UNP Q9Y570

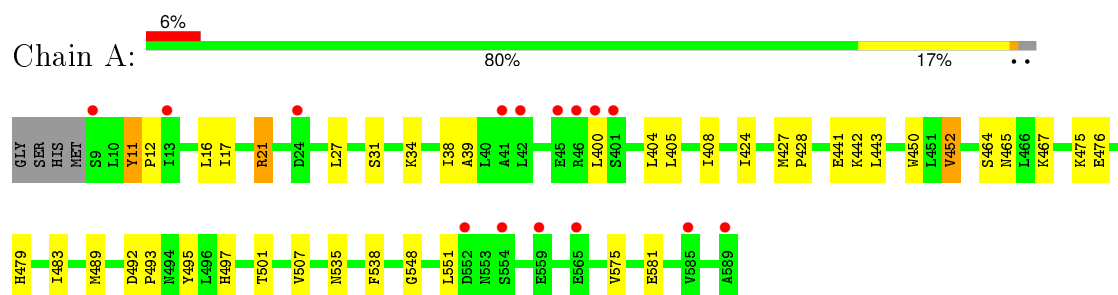
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	11	Total O 11 11	0	0
4	C	35	Total O 35 35	0	0
4	P	16	Total O 16 16	0	0

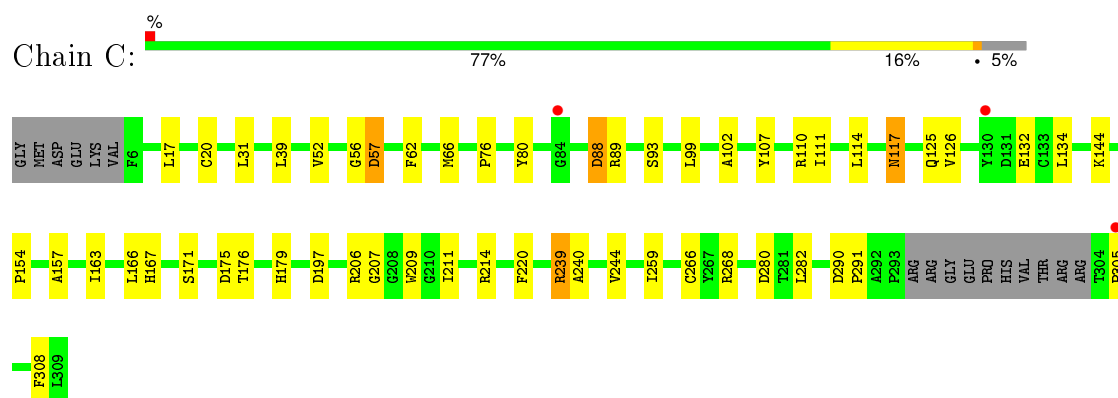
### 3 Residue-property plots [i](#)

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.

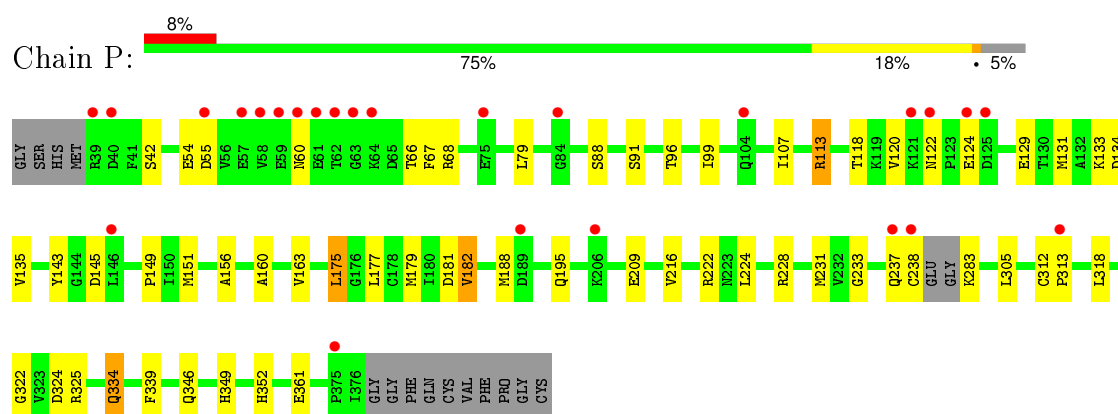
#### • Molecule 1: PP2A A subunit



#### • Molecule 2: PP2A C subunit



#### • Molecule 3: PP2A-specific methyltransferase PME-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	129.29Å 54.84Å 125.15Å 90.00° 110.87° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 29.23 – 2.78	Depositor EDS
% Data completeness (in resolution range)	98.6 (50.00-2.80) 93.7 (29.23-2.78)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.3.0038	Depositor
R, $R_{free}$	0.195 , 0.263 0.193 , 0.260	Depositor DCC
$R_{free}$ test set	1018 reflections (5.52%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.5	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 63.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 20623 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6503	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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

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	0.38	0/1817	0.53	0/2465
2	C	0.41	0/2435	0.55	0/3302
3	P	0.37	0/2326	0.54	0/3149
All	All	0.39	0/6578	0.54	0/8916

There are no bond length outliers.

There are no bond angle outliers.

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	1788	0	1865	21	0
2	C	2376	0	2270	29	0
3	P	2277	0	2280	29	0
4	A	11	0	0	0	0
4	C	35	0	0	1	0
4	P	16	0	0	0	0
All	All	6503	0	6415	77	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 (77) 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:C:57:ASP:OD1	2:C:240:ALA:HB1	1.92	0.70
3:P:96:THR:HG23	3:P:107:ILE:HG13	1.75	0.69
1:A:467:LYS:HB2	1:A:507:VAL:HG13	1.76	0.67
2:C:175:ASP:H	2:C:179:HIS:HD2	1.46	0.63
3:P:156:ALA:HA	3:P:182:VAL:HG22	1.80	0.63
3:P:120:VAL:HG12	3:P:122:ASN:H	1.64	0.62
3:P:67:PHE:O	3:P:68:ARG:HB3	2.00	0.61
1:A:11:TYR:H	1:A:12:PRO:HD3	1.64	0.61
1:A:467:LYS:HB2	1:A:507:VAL:CG1	2.31	0.59
3:P:67:PHE:HA	3:P:118:THR:HG23	1.85	0.58
2:C:176:THR:H	2:C:179:HIS:CD2	2.21	0.58
3:P:55:ASP:HB3	3:P:66:THR:CG2	2.34	0.58
3:P:149:PRO:HB3	3:P:175:LEU:HD21	1.87	0.56
2:C:39:LEU:HD22	2:C:154:PRO:HD3	1.89	0.55
3:P:216:VAL:HG21	3:P:224:LEU:HD13	1.88	0.55
2:C:80:TYR:HB2	2:C:111:ILE:HG22	1.89	0.54
1:A:11:TYR:N	1:A:12:PRO:CD	2.71	0.54
1:A:31:SER:O	1:A:34:LYS:HB3	2.08	0.54
1:A:442:LYS:HB2	1:A:443:LEU:HD12	1.90	0.53
2:C:176:THR:H	2:C:179:HIS:HD2	1.57	0.53
2:C:308:PHE:HA	3:P:349:HIS:CE1	2.43	0.53
2:C:305:PRO:HD2	3:P:325:ARG:HH12	1.74	0.53
1:A:11:TYR:N	1:A:12:PRO:HD3	2.23	0.53
3:P:238:CYS:HB2	3:P:283:LYS:HB2	1.91	0.51
2:C:93:SER:HB2	2:C:132:GLU:OE1	2.11	0.51
2:C:107:TYR:HB3	2:C:110:ARG:HB2	1.92	0.51
1:A:16:LEU:HD22	1:A:38:ILE:HD13	1.92	0.50
2:C:290:ASP:HB3	2:C:291:PRO:HD2	1.94	0.50
1:A:39:ALA:HA	1:A:400:LEU:HD11	1.93	0.50
2:C:114:LEU:HD21	2:C:157:ALA:HB2	1.93	0.50
3:P:322:GLY:O	3:P:325:ARG:HG2	2.12	0.49
3:P:324:ASP:OD1	3:P:325:ARG:HD3	2.13	0.49
1:A:479:HIS:HA	1:A:483:ILE:HD12	1.95	0.49
1:A:400:LEU:O	1:A:405:LEU:HB2	2.13	0.49
3:P:91:SER:HB3	3:P:352:HIS:HE1	1.78	0.48
2:C:111:ILE:HG23	4:C:1001:HOH:O	2.13	0.48
2:C:175:ASP:H	2:C:179:HIS:CD2	2.29	0.48
3:P:88:SER:OG	3:P:233:GLY:HA3	2.13	0.48
1:A:424:ILE:HG12	1:A:450:TRP:CE3	2.48	0.48
2:C:66:MET:HE2	2:C:66:MET:HA	1.96	0.48
3:P:131:MET:O	3:P:135:VAL:HG23	2.13	0.47
1:A:428:PRO:HD3	1:A:465:ASN:ND2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:ASN:HA	1:A:538:PHE:CE2	2.50	0.46
3:P:181:ASP:OD2	3:P:349:HIS:ND1	2.48	0.46
2:C:209:TRP:CZ3	2:C:220:PHE:HB3	2.51	0.46
1:A:405:LEU:HA	1:A:408:ILE:HD12	1.98	0.45
2:C:117:ASN:ND2	2:C:167:HIS:CE1	2.85	0.45
2:C:117:ASN:HD22	2:C:117:ASN:H	1.64	0.45
3:P:42:SER:HA	3:P:209:GLU:HG3	1.98	0.45
3:P:163:VAL:HG22	3:P:177:LEU:HD21	1.98	0.45
2:C:171:SER:HB2	2:C:197:ASP:HB2	1.98	0.44
2:C:20:CYS:HB2	2:C:62:PHE:CE2	2.52	0.44
3:P:179:MET:HB3	3:P:318:LEU:HD12	2.00	0.44
1:A:492:ASP:HA	1:A:493:PRO:HD2	1.86	0.44
3:P:224:LEU:HG	3:P:228:ARG:HD2	1.99	0.43
1:A:548:GLY:HA2	1:A:551:LEU:HD12	2.01	0.43
3:P:352:HIS:CD2	3:P:352:HIS:H	2.35	0.43
2:C:163:ILE:HD12	2:C:282:LEU:HD22	2.01	0.43
1:A:452:VAL:HG22	1:A:497:HIS:CE1	2.54	0.43
2:C:56:GLY:HA3	2:C:259:ILE:O	2.19	0.43
3:P:113:ARG:NH1	3:P:134:ASP:OD2	2.49	0.42
3:P:67:PHE:O	3:P:68:ARG:CB	2.67	0.42
2:C:117:ASN:HD22	2:C:117:ASN:N	2.18	0.42
2:C:88:ASP:OD1	2:C:89:ARG:HG2	2.19	0.42
3:P:312:CYS:HA	3:P:313:PRO:HD3	1.90	0.42
3:P:54:GLU:O	3:P:68:ARG:HA	2.19	0.42
3:P:129:GLU:CD	3:P:129:GLU:H	2.24	0.42
1:A:489:MET:HB2	1:A:501:THR:OG1	2.20	0.42
3:P:160:ALA:HA	3:P:305:LEU:HD11	2.02	0.41
1:A:17:ILE:O	1:A:21:ARG:HG3	2.20	0.41
3:P:334:GLN:HB3	3:P:339:PHE:CZ	2.56	0.41
2:C:31:LEU:HD11	2:C:102:ALA:HA	2.02	0.41
2:C:76:PRO:HG3	2:C:107:TYR:CZ	2.56	0.41
1:A:538:PHE:HB3	1:A:575:VAL:HA	2.03	0.41
2:C:166:LEU:O	2:C:239:ARG:HA	2.20	0.41
2:C:211:ILE:H	2:C:211:ILE:HG13	1.63	0.41
2:C:17:LEU:HD13	2:C:99:LEU:HA	2.03	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	226/232 (97%)	214 (95%)	11 (5%)	1 (0%)	39	74
2	C	290/310 (94%)	272 (94%)	16 (6%)	2 (1%)	26	62
3	P	290/310 (94%)	278 (96%)	12 (4%)	0	100	100
All	All	806/852 (95%)	764 (95%)	39 (5%)	3 (0%)	39	74

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	GLU
2	C	88	ASP
2	C	207	GLY

### 5.3.2 Protein sidechains [i](#)

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	199/202 (98%)	188 (94%)	11 (6%)	27	59
2	C	260/274 (95%)	246 (95%)	14 (5%)	27	60
3	P	247/258 (96%)	228 (92%)	19 (8%)	16	41
All	All	706/734 (96%)	662 (94%)	44 (6%)	23	54

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	TYR
1	A	21	ARG
1	A	27	LEU
1	A	404	LEU
1	A	427	MET
1	A	452	VAL
1	A	464	SER
1	A	475	LYS
1	A	476	GLU
1	A	495	TYR
1	A	581	GLU
2	C	52	VAL
2	C	57	ASP
2	C	117	ASN
2	C	125	GLN
2	C	126	VAL
2	C	134	LEU
2	C	144	LYS
2	C	206	ARG
2	C	214	ARG
2	C	239	ARG
2	C	244	VAL
2	C	266	CYS
2	C	268	ARG
2	C	280	ASP
3	P	60	ASN
3	P	79	LEU
3	P	99	ILE
3	P	113	ARG
3	P	124	GLU
3	P	133	LYS
3	P	143	TYR
3	P	145	ASP
3	P	151	MET
3	P	175	LEU
3	P	182	VAL
3	P	188	MET
3	P	195	GLN
3	P	222	ARG
3	P	231	MET
3	P	237	GLN
3	P	334	GLN
3	P	346	GLN

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Mol	Chain	Res	Type
3	P	361	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	444	ASN
1	A	465	ASN
1	A	506	ASN
2	C	117	ASN
2	C	125	GLN
2	C	167	HIS
2	C	179	HIS
2	C	288	GLN
3	P	48	GLN
3	P	60	ASN
3	P	164	HIS
3	P	192	ASN
3	P	220	GLN
3	P	307	ASN
3	P	336	GLN
3	P	352	HIS
3	P	370	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](#)

There are no ligands in this entry.

## 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<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	228/232 (98%)	0.47	15 (6%) 22 13	40, 45, 50, 54	0
2	C	294/310 (94%)	0.02	3 (1%) 84 77	38, 44, 50, 76	0
3	P	294/310 (94%)	0.26	25 (8%) 13 6	35, 44, 52, 58	0
All	All	816/852 (95%)	0.23	43 (5%) 30 20	35, 45, 51, 76	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	P	62	THR	5.4
1	A	554	SER	4.4
3	P	61	GLU	4.3
3	P	59	GLU	4.2
3	P	60	ASN	4.0
1	A	589	ALA	4.0
3	P	39	ARG	3.9
1	A	42	LEU	3.8
1	A	41	ALA	3.7
3	P	104	GLN	3.6
3	P	75	GLU	3.5
1	A	9	SER	3.4
3	P	238	CYS	3.2
3	P	125	ASP	3.2
1	A	401	SER	3.2
1	A	400	LEU	3.2
1	A	565	GLU	3.1
1	A	585	VAL	3.1
3	P	124	GLU	3.1
1	A	45	GLU	3.1
2	C	305	PRO	2.9
1	A	46	ARG	2.8
3	P	57	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
3	P	375	PRO	2.7
3	P	40	ASP	2.6
3	P	189	ASP	2.6
3	P	58	VAL	2.6
1	A	13	ILE	2.5
3	P	237	GLN	2.5
2	C	84	GLY	2.5
3	P	64	LYS	2.4
3	P	122	ASN	2.4
3	P	121	LYS	2.4
3	P	84	GLY	2.4
1	A	552	ASP	2.3
3	P	63	GLY	2.2
1	A	24	ASP	2.2
3	P	146	LEU	2.2
2	C	130	TYR	2.1
1	A	559	GLU	2.1
3	P	313	PRO	2.1
3	P	55	ASP	2.1
3	P	206	LYS	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.