



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2017 – 08:04 PM EDT

PDB ID : 2PRZ  
Title : S. cerevisiae orotate phosphoribosyltransferase complexed with OMP  
Authors : Gonzalez-Segura, L.; Hurley, T.D.; McClard, R.W.  
Deposited on : unknown  
Resolution : 1.90 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

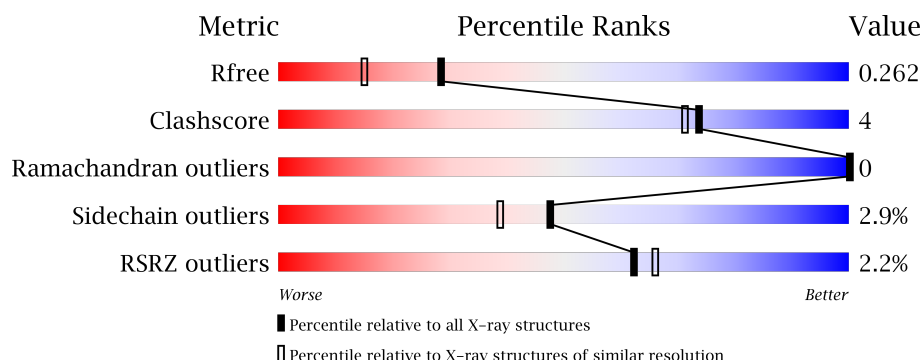
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	226	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>5%</div> </div> </div>
1	B	226	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>.</div> </div> </div>
1	C	226	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>5%</div> </div> </div>
1	D	226	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>5%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7201 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.

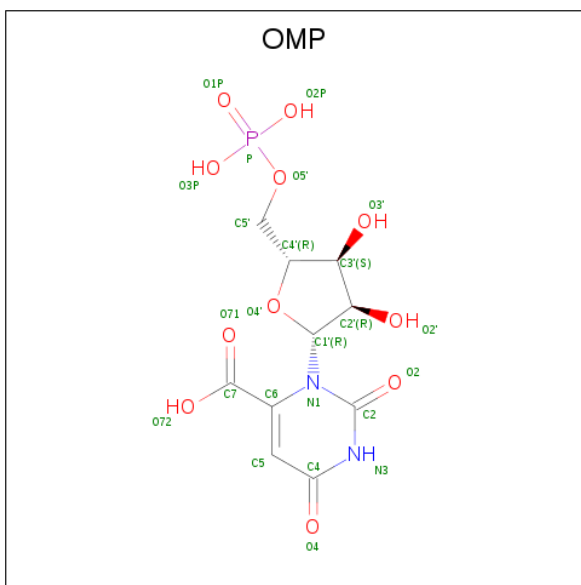
- Molecule 1 is a protein called Orotate phosphoribosyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1657	1069	270	315	3			
1	B	216	Total	C	N	O	S	0	0	0
			1669	1078	271	316	4			
1	C	215	Total	C	N	O	S	0	0	0
			1657	1069	270	315	3			
1	D	217	Total	C	N	O	S	0	0	0
			1673	1080	272	317	4			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

- Molecule 3 is OROTIDINE-5'-MONOPHOSPHATE (three-letter code: OMP) (formula: C<sub>10</sub>H<sub>13</sub>N<sub>2</sub>O<sub>11</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 24	C 10	N 2	O 11	P 1	0	0
3	B	1	Total 24	C 10	N 2	O 11	P 1	0	0
3	C	1	Total 24	C 10	N 2	O 11	P 1	0	0
3	D	1	Total 24	C 10	N 2	O 11	P 1	0	0

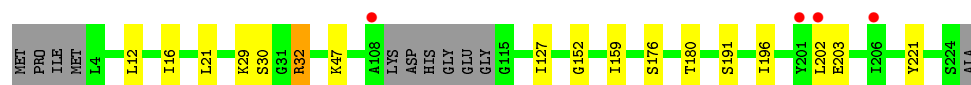
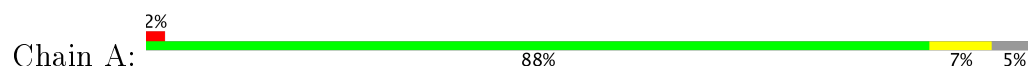
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	113	Total O 113 113	0	0
4	B	119	Total O 119 119	0	0
4	C	89	Total O 89 89	0	0
4	D	124	Total O 124 124	0	0

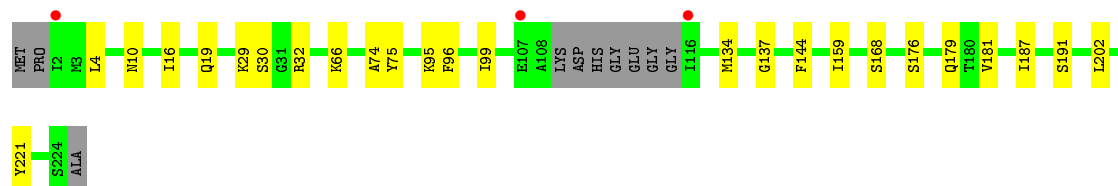
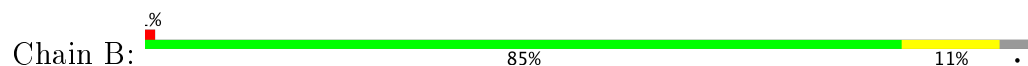
### 3 Residue-property plots [i](#)

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

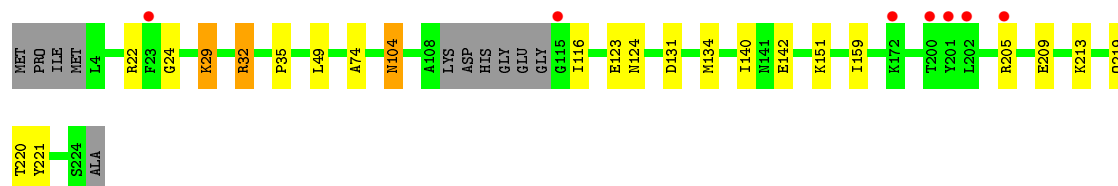
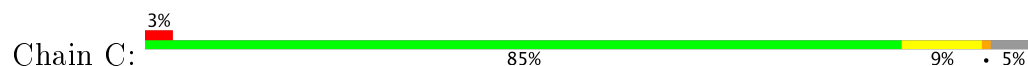
- Molecule 1: Orotate phosphoribosyltransferase 1



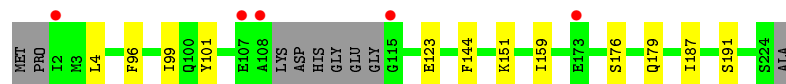
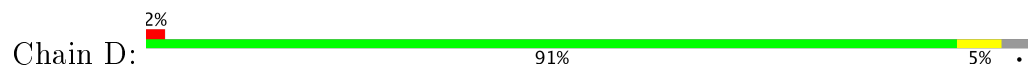
- Molecule 1: Orotate phosphoribosyltransferase 1



- Molecule 1: Orotate phosphoribosyltransferase 1



- Molecule 1: Orotate phosphoribosyltransferase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.06 Å 99.47 Å 112.00 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 46.94 – 1.90	Depositor EDS
% Data completeness (in resolution range)	95.8 (50.00-1.90) 95.8 (46.94-1.90)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.66 (at 1.90 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.229 , 0.262 0.228 , 0.262	Depositor DCC
$R_{free}$ test set	3715 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.9	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.70 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.9674e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: OMP, CL

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	0/1680	0.49	0/2265
1	B	0.39	0/1692	0.49	0/2281
1	C	0.38	0/1680	0.50	0/2265
1	D	0.40	0/1696	0.50	0/2286
All	All	0.39	0/6748	0.50	0/9097

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 [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	1657	0	1705	9	0
1	B	1669	0	1722	16	0
1	C	1657	0	1705	13	0
1	D	1673	0	1725	7	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	24	0	10	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	24	0	10	3	0
3	C	24	0	10	2	0
3	D	24	0	10	2	0
4	A	113	0	0	2	0
4	B	119	0	0	2	0
4	C	89	0	0	2	0
4	D	124	0	0	0	0
All	All	7201	0	6897	52	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 4.

All (52) 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:B:32:ARG:HG2	1:B:221:TYR:CZ	2.20	0.76
1:A:176:SER:O	1:A:180:THR:HG23	1.86	0.74
1:B:16:ILE:HD11	1:B:202:LEU:HD21	1.69	0.73
1:B:10:ASN:HB3	4:B:644:HOH:O	1.88	0.72
1:B:134:MET:HE1	1:B:181:VAL:HG21	1.78	0.65
3:A:450:OMP:H2'	3:A:450:OMP:O2	1.98	0.63
1:C:74:ALA:H	1:C:104:ASN:HD21	1.45	0.62
3:D:750:OMP:H2'	3:D:750:OMP:O2	1.99	0.62
1:B:30:SER:OG	1:B:32:ARG:HD3	2.00	0.61
1:C:123:GLU:HG2	1:C:151:LYS:HB2	1.84	0.60
1:D:123:GLU:HG3	1:D:151:LYS:HE3	1.85	0.59
3:B:550:OMP:O2	3:B:550:OMP:H2'	2.01	0.59
1:B:176:SER:H	1:B:179:GLN:NE2	2.01	0.59
1:C:32:ARG:HD2	1:C:221:TYR:CE1	2.40	0.57
1:C:104:ASN:HD22	1:C:104:ASN:H	1.53	0.57
1:A:16:ILE:HD11	1:A:202:LEU:HD22	1.86	0.56
1:A:196:ILE:HG13	4:A:547:HOH:O	2.05	0.56
3:D:750:OMP:C7	3:D:750:OMP:O4'	2.53	0.56
1:C:49:LEU:HD11	1:D:101:TYR:CD2	2.41	0.56
1:D:96:PHE:HD2	1:D:99:ILE:HD12	1.71	0.56
3:C:650:OMP:O2	3:C:650:OMP:H2'	2.04	0.56
1:A:32:ARG:HD2	1:A:221:TYR:CE1	2.42	0.54
3:C:650:OMP:O4'	3:C:650:OMP:C7	2.55	0.54
3:B:550:OMP:C7	3:B:550:OMP:O4'	2.55	0.53
1:B:134:MET:HE3	1:B:137:GLY:HA2	1.91	0.52
1:B:29:LYS:HE3	3:B:550:OMP:H4'	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:MET:HE2	1:C:140:ILE:HG13	1.91	0.51
1:C:22:ARG:HG2	4:C:679:HOH:O	2.10	0.51
1:D:96:PHE:CD2	1:D:99:ILE:HD12	2.45	0.51
3:A:450:OMP:O4'	3:A:450:OMP:C7	2.59	0.49
1:D:176:SER:H	1:D:179:GLN:NE2	2.10	0.49
1:A:30:SER:OG	1:A:32:ARG:HG3	2.13	0.49
1:B:32:ARG:HG2	1:B:221:TYR:CE1	2.47	0.49
1:B:66:LYS:HE2	1:B:95:LYS:HE3	1.95	0.48
1:D:144:PHE:HZ	1:D:187:ILE:HD11	1.78	0.48
1:A:32:ARG:HD3	4:A:543:HOH:O	2.14	0.47
1:C:134:MET:CE	1:C:140:ILE:HG13	2.44	0.47
1:B:32:ARG:HD2	4:B:659:HOH:O	2.14	0.47
1:D:159:ILE:O	1:D:191:SER:HA	2.15	0.46
1:C:74:ALA:H	1:C:104:ASN:ND2	2.12	0.46
1:C:24:GLY:O	1:C:35:PRO:HA	2.17	0.44
1:C:29:LYS:HE2	4:C:731:HOH:O	2.18	0.43
1:B:144:PHE:HZ	1:B:187:ILE:HD11	1.84	0.43
1:B:96:PHE:O	1:B:99:ILE:HG12	2.19	0.43
1:B:176:SER:H	1:B:179:GLN:HE21	1.65	0.42
1:B:74:ALA:HA	1:B:75:TYR:HA	1.82	0.41
1:A:16:ILE:CD1	1:A:202:LEU:HD22	2.50	0.41
1:C:104:ASN:ND2	1:C:104:ASN:H	2.16	0.41
1:A:159:ILE:O	1:A:191:SER:HA	2.21	0.41
1:C:131:ASP:O	1:C:159:ILE:HA	2.21	0.40
1:A:127:ILE:CD1	1:A:152:GLY:HA3	2.51	0.40
1:B:159:ILE:O	1:B:191:SER:HA	2.21	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	211/226 (93%)	208 (99%)	3 (1%)	0	100	100
1	B	212/226 (94%)	210 (99%)	2 (1%)	0	100	100
1	C	211/226 (93%)	207 (98%)	4 (2%)	0	100	100
1	D	213/226 (94%)	210 (99%)	3 (1%)	0	100	100
All	All	847/904 (94%)	835 (99%)	12 (1%)	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	177/185 (96%)	171 (97%)	6 (3%)	42	32
1	B	179/185 (97%)	176 (98%)	3 (2%)	66	62
1	C	177/185 (96%)	166 (94%)	11 (6%)	21	10
1	D	179/185 (97%)	178 (99%)	1 (1%)	89	90
All	All	712/740 (96%)	691 (97%)	21 (3%)	48	39

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	21	LEU
1	A	29	LYS
1	A	32	ARG
1	A	47	LYS
1	A	203	GLU
1	B	4	LEU
1	B	19	GLN
1	B	168	SER
1	C	29	LYS
1	C	32	ARG
1	C	104	ASN
1	C	116	ILE

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Mol	Chain	Res	Type
1	C	124	ASN
1	C	142	GLU
1	C	205	ARG
1	C	209	GLU
1	C	213	LYS
1	C	219	GLN
1	C	220	THR
1	D	4	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	100	GLN
1	B	179	GLN
1	C	104	ASN
1	C	124	ASN
1	C	141	ASN
1	C	164	GLN
1	C	219	GLN
1	D	141	ASN
1	D	179	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 ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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$
3	OMP	A	450	-	18,25,25	1.07	1 (5%)	22,38,38	2.67	4 (18%)
3	OMP	B	550	-	18,25,25	1.10	2 (11%)	22,38,38	2.74	4 (18%)
3	OMP	C	650	-	18,25,25	1.03	1 (5%)	22,38,38	2.56	4 (18%)
3	OMP	D	750	-	18,25,25	1.10	2 (11%)	22,38,38	2.67	4 (18%)

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
3	OMP	A	450	-	-	0/6/30/30	0/2/2/2
3	OMP	B	550	-	-	0/6/30/30	0/2/2/2
3	OMP	C	650	-	-	0/6/30/30	0/2/2/2
3	OMP	D	750	-	-	0/6/30/30	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	550	OMP	O4'-C1'	2.17	1.44	1.41
3	C	650	OMP	C6-N1	2.47	1.43	1.36
3	D	750	OMP	C6-N1	2.49	1.43	1.36
3	D	750	OMP	O4'-C1'	2.49	1.44	1.41
3	A	450	OMP	C6-N1	2.58	1.43	1.36
3	B	550	OMP	C6-N1	2.62	1.43	1.36

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	750	OMP	C5-C4-N3	-3.38	120.07	124.06
3	B	550	OMP	C5-C4-N3	-3.32	120.14	124.06
3	A	450	OMP	C5-C4-N3	-3.28	120.18	124.06
3	C	650	OMP	C5-C4-N3	-3.16	120.33	124.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	450	OMP	C4'-O4'-C1'	3.37	113.36	109.77
3	D	750	OMP	C4'-O4'-C1'	3.68	113.69	109.77
3	C	650	OMP	C4'-O4'-C1'	3.82	113.84	109.77
3	B	550	OMP	C4'-O4'-C1'	4.23	114.27	109.77
3	C	650	OMP	C4-C5-C6	4.52	119.65	116.73
3	B	550	OMP	C4-C5-C6	4.57	119.68	116.73
3	A	450	OMP	C4-C5-C6	4.62	119.71	116.73
3	D	750	OMP	C4-C5-C6	4.87	119.87	116.73
3	C	650	OMP	C4-N3-C2	9.48	122.27	114.13
3	D	750	OMP	C4-N3-C2	9.55	122.33	114.13
3	B	550	OMP	C4-N3-C2	10.09	122.79	114.13
3	A	450	OMP	C4-N3-C2	10.13	122.83	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	450	OMP	2	0
3	B	550	OMP	3	0
3	C	650	OMP	2	0
3	D	750	OMP	2	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	215/226 (95%)	0.11	4 (1%) 67 70	18, 28, 49, 55	0
1	B	216/226 (95%)	0.07	3 (1%) 75 78	17, 27, 38, 45	0
1	C	215/226 (95%)	0.24	7 (3%) 47 50	19, 31, 51, 61	0
1	D	217/226 (96%)	0.14	5 (2%) 61 64	17, 27, 40, 44	0
All	All	863/904 (95%)	0.14	19 (2%) 62 66	17, 28, 44, 61	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	LEU	4.2
1	C	202	LEU	3.8
1	C	201	TYR	3.7
1	D	108	ALA	3.2
1	C	115	GLY	2.8
1	A	201	TYR	2.7
1	B	107	GLU	2.7
1	D	107	GLU	2.7
1	C	205	ARG	2.6
1	B	116	ILE	2.5
1	C	172	LYS	2.5
1	D	173	GLU	2.5
1	C	200	THR	2.4
1	A	206	ILE	2.3
1	B	2	ILE	2.2
1	D	2	ILE	2.2
1	D	115	GLY	2.1
1	A	108	ALA	2.1
1	C	23	PHE	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<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
3	OMP	D	750	24/24	0.95	0.10	-0.10	23,26,28,29	0
3	OMP	A	450	24/24	0.97	0.09	-0.23	20,23,25,27	0
3	OMP	C	650	24/24	0.97	0.09	-0.62	23,26,27,27	0
3	OMP	B	550	24/24	0.97	0.08	-0.88	22,23,27,29	0
2	CL	C	2	1/1	0.99	0.05	-	36,36,36,36	0
2	CL	B	225	1/1	0.97	0.04	-	38,38,38,38	0
2	CL	A	1	1/1	0.99	0.04	-	34,34,34,34	0
2	CL	D	225	1/1	0.94	0.07	-	40,40,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.