



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:48 PM GMT

PDB ID : 4WAS  
Title : STRUCTURE OF THE ETR1P/NADP/CROTONYL-COA COMPLEX  
Authors : Quade, N.; Voegeli, B.; Rosenthal, R.; Capitani, G.; Erb, T.J.  
Deposited on : 2014-08-31  
Resolution : 1.70 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

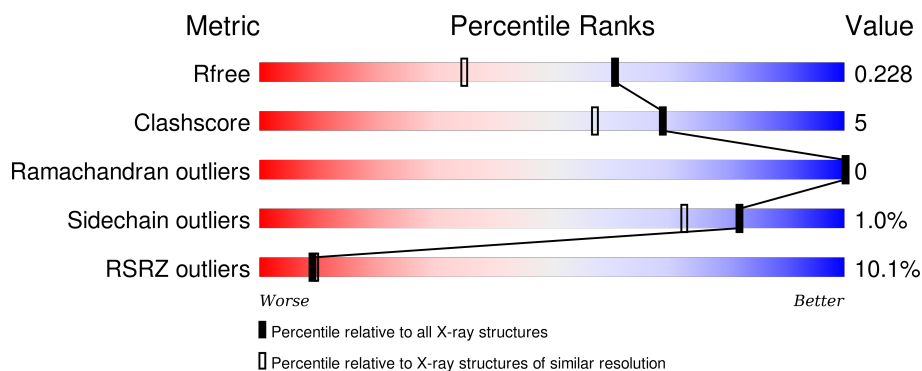
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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	364	<div> <div>8%</div> <div>90%</div> <div>10%</div> </div>
1	B	364	<div> <div>9%</div> <div>89%</div> <div>11%</div> </div>
1	C	364	<div> <div>13%</div> <div>88%</div> <div>11%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	COO	A	402	X	-	-	-
3	COO	B	402[A]	-	-	-	X
3	COO	B	402[B]	-	-	-	X
3	COO	C	402	-	-	-	X

## 2 Entry composition [i](#)

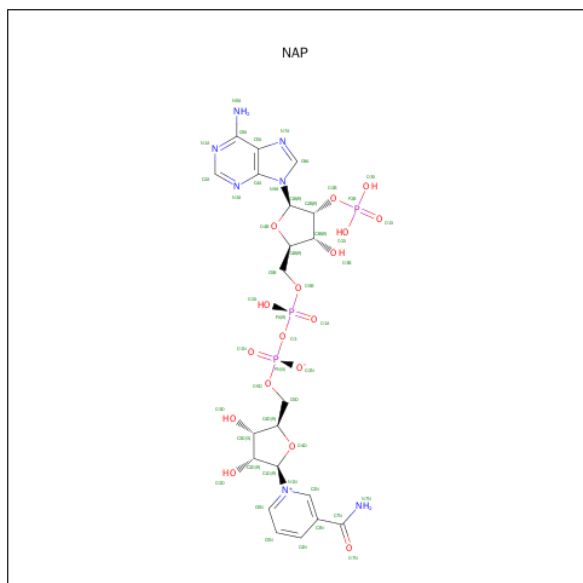
There are 4 unique types of molecules in this entry. The entry contains 10132 atoms, of which 1035 are hydrogens and 0 are deuteriums.

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 Enoyl-[acyl-carrier-protein] reductase [NADPH, B-specific] 1, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	364	Total	C	H	N	O	S	0	0	0
			3133	1768	345	466	548	6			
1	B	364	Total	C	H	N	O	S	0	2	0
			3153	1779	345	471	552	6			
1	C	364	Total	C	H	N	O	S	0	0	0
			3133	1768	345	466	548	6			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



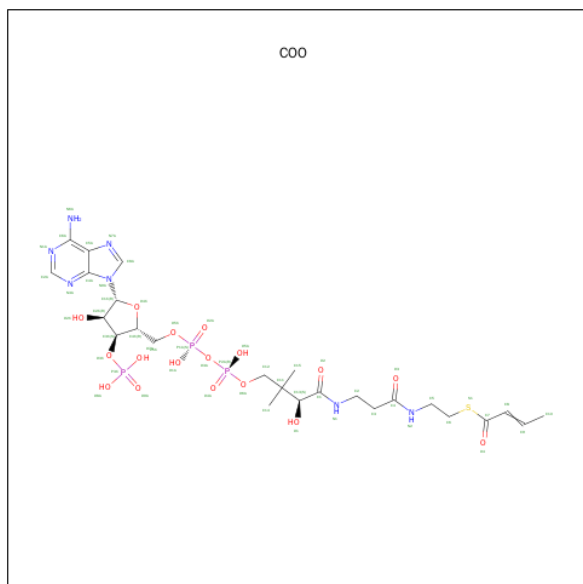
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is CROTONYL COENZYME A (three-letter code: COO) (formula:  $C_{25}H_{40}N_7O_{17}P_3S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			31	15	2	11	2	1		
3	B	1	Total	C	N	O	P	S	0	1
			43	23	3	13	2	2		
3	C	1	Total	C	N	O	S		0	0
			12	8	1	2	1			

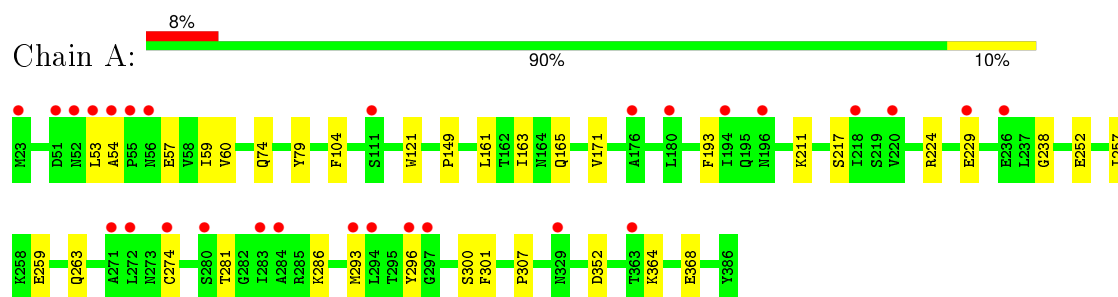
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	175	Total	O	0	0
			175	175		
4	B	147	Total	O	0	0
			147	147		
4	C	161	Total	O	0	0
			161	161		

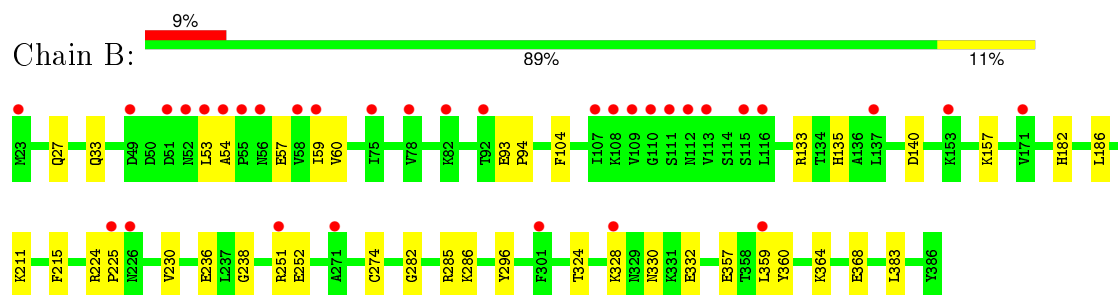
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

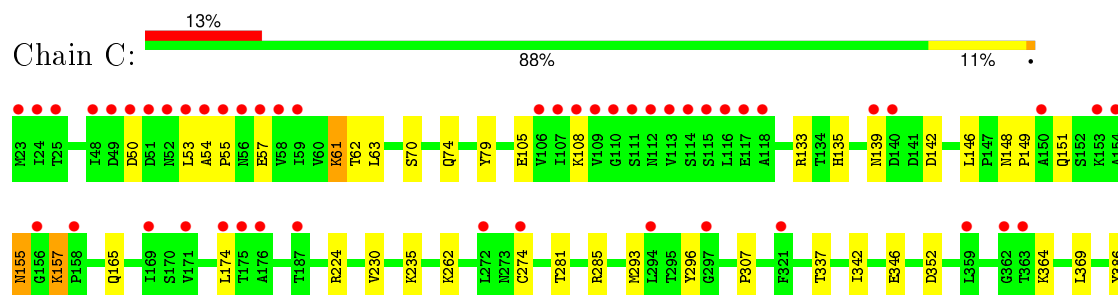
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH, B-specific] 1, mitochondrial



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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	147.92Å 106.14Å 94.41Å 90.00° 98.41° 90.00°	Depositor
Resolution (Å)	37.81 – 1.70 37.81 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (37.81-1.70) 99.1 (37.81-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.01 (at 1.70Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.188 , 0.224 0.197 , 0.228	Depositor DCC
$R_{free}$ test set	1097 reflections (0.70%)	DCC
Wilson B-factor (Å <sup>2</sup> )	36.1	Xtriage
Anisotropy	0.451	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 58.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 156706 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10132	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0/2847	0.56	0/3870
1	B	0.39	0/2867	0.53	0/3896
1	C	0.40	0/2847	0.54	1/3870 (0.0%)
All	All	0.41	0/8561	0.54	1/11636 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	293	MET	CG-SD-CE	-5.68	91.11	100.20

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	2788	345	2767	22	0
1	B	2808	345	2784	25	0
1	C	2788	345	2767	31	0
2	A	48	0	25	2	0
2	B	48	0	25	1	0
2	C	48	0	25	1	0
3	A	31	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	28	1	0
3	C	12	0	10	1	0
4	A	175	0	0	4	0
4	B	147	0	0	4	0
4	C	161	0	0	3	0
All	All	9097	1035	8456	79	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 5.

All (79) 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:C:54:ALA:HB1	1:C:55:PRO:HD2	1.59	0.84
1:B:211:LYS:HE3	1:B:238:GLY:HA2	1.61	0.80
1:B:224:ARG:HD2	1:B:230:VAL:HG21	1.68	0.76
1:C:224:ARG:HD2	1:C:230:VAL:HG21	1.67	0.75
1:B:54:ALA:HB3	1:B:57:GLU:HG3	1.66	0.75
1:B:285[A]:ARG:NH2	4:B:641:HOH:O	2.19	0.74
1:A:296:TYR:O	2:A:401:NAP:H2N	1.93	0.68
1:C:364:LYS:HG3	1:C:369:LEU:HD11	1.80	0.63
1:B:211:LYS:HE3	1:B:238:GLY:CA	2.29	0.63
1:C:296:TYR:O	2:C:401:NAP:H2N	2.04	0.58
1:B:182:HIS:ND1	4:B:585:HOH:O	2.32	0.58
1:B:296:TYR:O	2:B:401:NAP:H2N	2.04	0.57
1:B:211:LYS:NZ	1:B:236:GLU:O	2.37	0.57
1:C:174:LEU:HD22	1:C:337:THR:HG22	1.87	0.57
1:C:54:ALA:HB3	1:C:57:GLU:HG3	1.89	0.55
3:B:402[B]:COO:H103	4:B:583:HOH:O	2.06	0.55
1:A:257:ILE:HD12	1:A:286:LYS:HE3	1.88	0.55
1:B:224:ARG:HB2	1:B:225:PRO:HD2	1.88	0.54
1:C:50:ASP:HB2	1:C:108:LYS:HD2	1.91	0.53
1:C:165:GLN:HG2	1:C:352:ASP:HB3	1.91	0.52
1:C:364:LYS:HG3	1:C:369:LEU:CD1	2.39	0.51
1:A:257:ILE:CD1	1:A:286:LYS:HE3	2.41	0.50
1:C:133:ARG:HD2	1:C:135:HIS:O	2.11	0.50
1:C:54:ALA:HB3	1:C:57:GLU:CG	2.42	0.50
1:B:364:LYS:HE3	1:B:368:GLU:HB3	1.93	0.50
1:C:155:ASN:ND2	1:C:155:ASN:O	2.34	0.50
1:A:53:LEU:HD21	1:A:59:ILE:HG13	1.94	0.49
1:A:364:LYS:HE2	1:A:368:GLU:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:SER:HB3	3:C:402:COO:C9	2.43	0.48
1:B:357[A]:GLU:HA	1:B:383:LEU:O	2.14	0.48
1:A:229:GLU:HG3	4:A:649:HOH:O	2.14	0.48
1:B:54:ALA:HB3	1:B:57:GLU:CG	2.39	0.48
1:A:193:PHE:CE1	1:A:217:SER:HB3	2.49	0.47
1:C:274:CYS:HB3	1:C:296:TYR:CZ	2.50	0.46
1:B:330:ASN:OD1	1:B:332:GLU:HG2	2.15	0.46
1:A:281:THR:HG23	1:A:307:PRO:HD3	1.97	0.46
1:A:259:GLU:O	1:A:263:GLN:HG2	2.16	0.46
1:A:54:ALA:HB3	1:A:57:GLU:HG3	1.98	0.46
1:A:364:LYS:HE3	1:A:368:GLU:OE1	2.16	0.46
1:B:133:ARG:HD2	1:B:135:HIS:O	2.16	0.46
1:A:274:CYS:HB3	1:A:296:TYR:CZ	2.50	0.46
1:C:61:LYS:HE3	1:C:61:LYS:HB3	1.76	0.45
1:C:63:LEU:HD11	1:C:105:GLU:HB2	1.99	0.45
1:B:252:GLU:OE1	4:B:600:HOH:O	2.21	0.45
1:C:61:LYS:HG2	4:C:660:HOH:O	2.15	0.45
1:B:60:VAL:HB	1:B:104:PHE:HB3	1.97	0.45
1:A:74:GLN:HA	1:A:79:TYR:HB3	1.99	0.44
1:C:148:ASN:HB2	1:C:149:PRO:CD	2.46	0.44
1:B:324:THR:O	1:B:328:LYS:HB2	2.18	0.44
1:C:139:ASN:O	1:C:142:ASP:HB2	2.17	0.44
1:B:274:CYS:HB3	1:B:296:TYR:CZ	2.53	0.43
1:C:54:ALA:HB1	1:C:55:PRO:CD	2.40	0.43
1:B:140:ASP:N	1:B:140:ASP:OD1	2.51	0.43
1:B:282:GLY:O	1:B:286:LYS:HG2	2.19	0.43
1:C:157:LYS:HZ2	1:C:157:LYS:HB3	1.84	0.43
1:A:171:VAL:HG12	2:A:401:NAP:H5N	2.01	0.42
1:C:146:LEU:CD2	1:C:342:ILE:HD11	2.49	0.42
1:A:300:SER:O	1:A:301:PHE:HB2	2.19	0.42
1:C:157:LYS:HD3	1:C:346:GLU:OE1	2.20	0.42
1:A:165:GLN:HG2	1:A:352:ASP:HB3	2.01	0.42
1:A:60:VAL:HB	1:A:104:PHE:HB3	2.02	0.42
1:C:157:LYS:HG2	1:C:157:LYS:H	1.67	0.42
1:C:62:THR:O	1:C:386:TYR:HB2	2.20	0.42
1:B:27:GLN:HG3	1:B:360:TYR:OH	2.20	0.41
1:B:332:GLU:H	1:B:332:GLU:CD	2.24	0.41
1:C:148:ASN:OD1	1:C:151:GLN:HG3	2.20	0.41
1:A:121:TRP:CH2	1:A:163:ILE:HD13	2.55	0.41
1:B:53:LEU:HD21	1:B:59:ILE:HG13	2.03	0.41
1:C:281:THR:HG23	1:C:307:PRO:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:GLU:HG2	4:A:566:HOH:O	2.21	0.41
1:A:293:MET:HG2	4:A:579:HOH:O	2.21	0.41
1:C:262:LYS:HD3	4:C:587:HOH:O	2.21	0.41
1:B:93:GLU:HG3	1:B:94:PRO:HD2	2.02	0.41
1:C:74:GLN:HA	1:C:79:TYR:HB3	2.01	0.41
4:A:523:HOH:O	1:C:235:LYS:HE3	2.21	0.40
1:C:285:ARG:NH1	4:C:503:HOH:O	2.54	0.40
1:B:186:LEU:HD12	1:B:215:PHE:CD2	2.57	0.40
1:A:149:PRO:HG3	1:A:161:LEU:O	2.22	0.40
1:A:211:LYS:HB2	1:A:238:GLY:HA3	2.02	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	362/364 (100%)	354 (98%)	8 (2%)	0	100	100
1	B	364/364 (100%)	353 (97%)	11 (3%)	0	100	100
1	C	362/364 (100%)	352 (97%)	10 (3%)	0	100	100
All	All	1088/1092 (100%)	1059 (97%)	29 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	307/307 (100%)	306 (100%)	1 (0%)	94	92
1	B	309/307 (101%)	305 (99%)	4 (1%)	76	62
1	C	307/307 (100%)	303 (99%)	4 (1%)	76	62
All	All	923/921 (100%)	914 (99%)	9 (1%)	82	72

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	ARG
1	B	33	GLN
1	B	157	LYS
1	B	251	ARG
1	B	359	LEU
1	C	53	LEU
1	C	61	LYS
1	C	155	ASN
1	C	157	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

7 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	NAP	A	401	-	42,52,52	1.94	8 (19%)	54,80,80	1.88	8 (14%)
3	COO	A	402	-	23,30,55	1.75	3 (13%)	34,42,81	1.74	5 (14%)
2	NAP	B	401	-	42,52,52	2.00	11 (26%)	54,80,80	1.99	11 (20%)
3	COO	B	402[A]	-	23,30,55	1.72	3 (13%)	34,42,81	1.67	5 (14%)
3	COO	B	402[B]	-	23,30,55	1.73	3 (13%)	34,42,81	1.77	4 (11%)
2	NAP	C	401	-	42,52,52	2.01	8 (19%)	54,80,80	1.87	10 (18%)
3	COO	C	402	-	9,11,55	1.81	2 (22%)	11,12,81	3.03	4 (36%)

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	NAP	A	401	-	-	0/27/67/67	0/5/5/5
3	COO	A	402	-	1/1/7/16	0/38/39/70	0/0/0/3
2	NAP	B	401	-	-	0/27/67/67	0/5/5/5
3	COO	B	402[A]	-	-	0/38/39/70	0/0/0/3
3	COO	B	402[B]	-	-	0/38/39/70	0/0/0/3
2	NAP	C	401	-	-	0/27/67/67	0/5/5/5
3	COO	C	402	-	-	0/9/10/70	0/0/0/3

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	NAP	C3B-C4B	-2.82	1.45	1.53
2	A	401	NAP	C3B-C4B	-2.70	1.45	1.53
2	B	401	NAP	C3B-C4B	-2.69	1.45	1.53
2	A	401	NAP	C2D-C3D	-2.43	1.46	1.53
2	B	401	NAP	C2D-C3D	-2.38	1.46	1.53
2	C	401	NAP	C2D-C3D	-2.37	1.46	1.53
2	B	401	NAP	PA-O2A	-2.04	1.46	1.54
2	A	401	NAP	C6A-N6A	2.01	1.41	1.34
2	C	401	NAP	C8A-N7A	2.03	1.38	1.34
2	B	401	NAP	C5A-N7A	2.09	1.46	1.39
2	A	401	NAP	C5A-N7A	2.09	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	COO	C3-C4	2.15	1.54	1.50
2	B	401	NAP	C8A-N7A	2.16	1.38	1.34
2	B	401	NAP	C2N-C3N	2.20	1.42	1.39
3	A	402	COO	P1A-O5X	2.36	1.63	1.54
3	B	402[A]	COO	P1A-O5X	2.40	1.63	1.54
3	B	402[B]	COO	P1A-O5X	2.40	1.63	1.54
2	C	401	NAP	C6A-N6A	2.41	1.42	1.34
2	B	401	NAP	C6A-N6A	2.46	1.42	1.34
2	A	401	NAP	C6N-N1N	3.03	1.43	1.35
2	C	401	NAP	C6N-N1N	3.27	1.44	1.35
2	B	401	NAP	C6N-N1N	3.51	1.44	1.35
2	A	401	NAP	O4D-C1D	4.21	1.46	1.41
3	C	402	COO	C4-N2	4.40	1.45	1.33
2	B	401	NAP	C7N-N7N	4.60	1.42	1.33
2	A	401	NAP	C7N-N7N	4.73	1.42	1.33
2	C	401	NAP	C7N-N7N	4.85	1.42	1.33
3	B	402[B]	COO	C4-N2	4.88	1.45	1.33
3	B	402[A]	COO	C4-N2	4.89	1.45	1.33
3	B	402[A]	COO	C1-N1	4.90	1.43	1.33
3	B	402[B]	COO	C1-N1	4.90	1.43	1.33
2	B	401	NAP	O4D-C1D	4.92	1.47	1.41
3	A	402	COO	C4-N2	4.98	1.45	1.33
3	A	402	COO	C1-N1	4.98	1.44	1.33
2	C	401	NAP	O4D-C1D	5.01	1.47	1.41
2	B	401	NAP	O4B-C1B	6.13	1.49	1.41
2	C	401	NAP	O4B-C1B	6.86	1.49	1.41
2	A	401	NAP	O4B-C1B	6.95	1.50	1.41

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NAP	N3A-C2A-N1A	-8.53	122.37	128.89
2	C	401	NAP	N3A-C2A-N1A	-8.32	122.52	128.89
2	B	401	NAP	N3A-C2A-N1A	-7.81	122.91	128.89
2	B	401	NAP	C1B-N9A-C4A	-4.96	119.46	126.94
2	A	401	NAP	C4B-O4B-C1B	-4.82	104.42	109.72
2	B	401	NAP	C4B-O4B-C1B	-4.40	104.88	109.72
2	A	401	NAP	C4D-O4D-C1D	-4.17	105.14	109.72
2	C	401	NAP	C4D-O4D-C1D	-3.96	105.37	109.72
2	A	401	NAP	C1B-N9A-C4A	-3.94	121.00	126.94
2	B	401	NAP	C4A-C5A-N7A	-3.82	105.96	109.48
2	C	401	NAP	O4D-C1D-N1N	-3.82	103.94	108.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	NAP	C4B-O4B-C1B	-3.65	105.71	109.72
2	B	401	NAP	O4D-C1D-N1N	-3.57	104.20	108.13
2	B	401	NAP	O7N-C7N-N7N	-3.34	117.90	122.59
3	B	402[A]	COO	C10-C9-C8	-3.27	119.15	125.27
2	C	401	NAP	C4A-C5A-N7A	-3.26	106.48	109.48
3	A	402	COO	C6-C5-N2	-3.20	105.96	112.36
3	A	402	COO	C10-C9-C8	-3.08	119.50	125.27
2	A	401	NAP	C4A-C5A-N7A	-2.94	106.77	109.48
3	A	402	COO	O4-C7-S1	-2.75	118.91	122.37
2	C	401	NAP	C1B-N9A-C4A	-2.74	122.81	126.94
3	B	402[B]	COO	O4-C7-S1	-2.66	119.03	122.37
3	B	402[B]	COO	C10-C9-C8	-2.62	120.36	125.27
3	C	402	COO	C9-C8-C7	-2.57	118.88	123.68
2	B	401	NAP	C4D-O4D-C1D	-2.56	106.91	109.72
3	C	402	COO	O4-C7-S1	-2.40	119.36	122.37
3	B	402[A]	COO	C3-C2-N1	-2.25	106.95	111.88
3	B	402[A]	COO	O4-C7-S1	-2.11	119.72	122.37
3	B	402[A]	COO	P2A-O3A-P1A	-2.09	125.67	132.67
3	B	402[B]	COO	P2A-O3A-P1A	-2.09	125.67	132.67
2	C	401	NAP	O2X-P2B-O1X	-2.01	104.11	110.58
2	A	401	NAP	C2B-C3B-C4B	2.01	106.61	101.85
2	C	401	NAP	C3B-C2B-C1B	2.08	106.75	102.73
2	B	401	NAP	C6N-C5N-C4N	2.10	122.61	119.44
2	A	401	NAP	C2N-C3N-C4N	2.24	120.78	118.29
2	C	401	NAP	O2N-PN-O3	2.34	115.71	105.09
2	A	401	NAP	O2N-PN-O3	2.38	115.88	105.09
2	C	401	NAP	C2B-C3B-C4B	2.40	107.54	101.85
2	B	401	NAP	C2A-N1A-C6A	2.46	123.16	118.77
3	A	402	COO	O3A-P2A-O6A	2.46	109.46	102.94
2	B	401	NAP	O2B-P2B-O1X	2.57	113.52	107.11
2	B	401	NAP	O7N-C7N-C3N	3.19	123.07	119.59
3	C	402	COO	C3-C4-N2	3.35	121.29	116.19
3	B	402[A]	COO	C6-S1-C7	6.29	107.59	99.59
3	A	402	COO	C6-S1-C7	6.81	108.26	99.59
3	B	402[B]	COO	C6-S1-C7	7.45	109.07	99.59
3	C	402	COO	C6-S1-C7	7.98	109.74	99.59

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	402	COO	C13

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAP	2	0
2	B	401	NAP	1	0
3	B	402[B]	COO	1	0
2	C	401	NAP	1	0
3	C	402	COO	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	364/364 (100%)	0.38	28 (7%)	16 18	34, 43, 71, 101	0
1	B	364/364 (100%)	0.60	33 (9%)	11 13	33, 47, 91, 159	0
1	C	364/364 (100%)	0.60	49 (13%)	4 5	30, 47, 97, 129	0
All	All	1092/1092 (100%)	0.53	110 (10%)	9 9	30, 45, 89, 159	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	53	LEU	7.7
1	C	111	SER	7.7
1	C	109	VAL	7.0
1	C	53	LEU	6.9
1	C	112	ASN	6.7
1	B	54	ALA	6.4
1	C	113	VAL	6.1
1	B	52	ASN	6.1
1	B	109	VAL	5.9
1	C	55	PRO	5.4
1	A	272	LEU	5.3
1	C	56	ASN	5.1
1	B	23	MET	5.0
1	B	51	ASP	4.9
1	C	54	ALA	4.8
1	A	54	ALA	4.7
1	C	110	GLY	4.6
1	C	50	ASP	4.5
1	B	78	VAL	4.5
1	C	116	LEU	4.5
1	C	108	LYS	4.4
1	C	154	ALA	4.4
1	B	56	ASN	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	110	GLY	4.1
1	B	301	PHE	4.1
1	C	150	ALA	4.1
1	C	107	ILE	4.1
1	B	113	VAL	4.1
1	A	52	ASN	4.0
1	A	53	LEU	3.9
1	B	112	ASN	3.8
1	B	116	LEU	3.7
1	A	271	ALA	3.7
1	C	359	LEU	3.6
1	C	49	ASP	3.6
1	C	114	SER	3.6
1	C	363	THR	3.6
1	C	25	THR	3.5
1	A	51	ASP	3.5
1	B	55	PRO	3.4
1	C	58	VAL	3.4
1	B	111	SER	3.3
1	A	274	CYS	3.3
1	C	153	LYS	3.3
1	C	139	ASN	3.2
1	A	55	PRO	3.2
1	A	363	THR	3.2
1	C	51	ASP	3.1
1	A	220	VAL	3.1
1	C	117	GLU	3.0
1	C	171	VAL	3.0
1	B	171	VAL	3.0
1	C	118	ALA	3.0
1	C	156	GLY	2.9
1	A	283	ILE	2.9
1	C	115	SER	2.9
1	C	140	ASP	2.9
1	A	293	MET	2.9
1	A	236	GLU	2.8
1	B	225	PRO	2.8
1	A	23	MET	2.8
1	B	153	LYS	2.8
1	C	272	LEU	2.8
1	B	92	THR	2.7
1	C	59	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	296	TYR	2.7
1	C	24	ILE	2.7
1	A	294	LEU	2.7
1	B	75	ILE	2.7
1	A	176	ALA	2.7
1	B	251	ARG	2.6
1	C	48	ILE	2.6
1	B	328	LYS	2.5
1	B	49	ASP	2.5
1	B	137	LEU	2.5
1	A	329	ASN	2.5
1	C	297	GLY	2.5
1	A	56	ASN	2.4
1	C	106	VAL	2.4
1	A	284	ALA	2.4
1	C	158	PRO	2.4
1	C	175	THR	2.3
1	A	180	LEU	2.3
1	C	294	LEU	2.3
1	C	187	THR	2.3
1	B	226	ASN	2.3
1	C	169	ILE	2.3
1	A	218	ILE	2.2
1	B	108	LYS	2.2
1	B	107	ILE	2.2
1	A	194	ILE	2.2
1	B	82	LYS	2.2
1	C	52	ASN	2.2
1	C	174	LEU	2.2
1	C	57	GLU	2.1
1	B	115	SER	2.1
1	B	59	ILE	2.1
1	C	362	GLY	2.1
1	A	229	GLU	2.1
1	A	196	ASN	2.1
1	A	297	GLY	2.1
1	B	271	ALA	2.1
1	C	176	ALA	2.1
1	B	359	LEU	2.1
1	A	280	SER	2.1
1	A	111	SER	2.1
1	B	58	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	274	CYS	2.0
1	C	321	PHE	2.0
1	C	23	MET	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(Å <sup>2</sup> )	Q<0.9
3	COO	B	402[B]	31/53	0.58	0.33	3.62	65,78,89,94	12
3	COO	B	402[A]	31/53	0.58	0.33	3.47	70,78,89,94	12
3	COO	C	402	12/53	0.85	0.23	2.67	71,73,78,88	0
3	COO	A	402	31/53	0.81	0.18	1.87	68,72,77,86	0
2	NAP	C	401	48/48	0.96	0.13	-0.03	34,43,63,80	0
2	NAP	A	401	48/48	0.96	0.11	-0.30	33,43,53,56	0
2	NAP	B	401	48/48	0.96	0.10	-0.54	37,43,55,59	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.