



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:40 AM GMT

PDB ID : 3O4R  
Title : Crystal Structure of Human Dehydrogenase/Reductase(SDR family) member 4 (DHRS4)  
Authors : Ugochukwu, E.; Bhatia, C.; Krojer, T.; Vollmar, M.; Yue, W.W.; Bountra, C.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; von Delft, F.; Oppermann, U.; Structural Genomics Consortium (SGC)  
Deposited on : 2010-07-27  
Resolution : 1.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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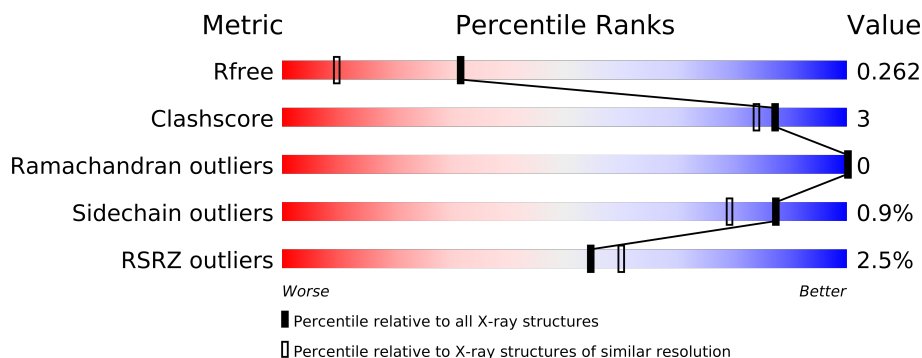
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	2456 (1.70-1.70)
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	261	
1	B	261	
1	C	261	
1	D	261	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	EDO	A	703	-	X
3	EDO	B	702	-	X
3	EDO	B	704	-	X
3	EDO	D	701	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	EPE	A	705	-	X
5	GOL	B	707	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8296 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

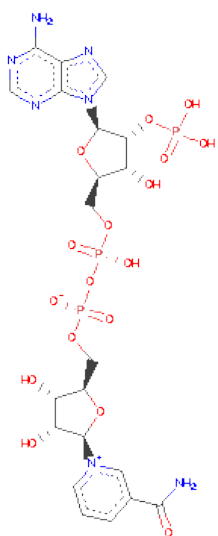
- Molecule 1 is a protein called Dehydrogenase/reductaseSDR family member 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	2	0
			1871	1173	324	363	11			
1	B	252	Total	C	N	O	S	0	5	0
			1878	1181	322	364	11			
1	C	253	Total	C	N	O	S	0	0	0
			1850	1163	319	358	10			
1	D	251	Total	C	N	O	S	0	1	0
			1856	1168	321	356	11			

There are 4 discrepancies between the modelled and reference sequences:

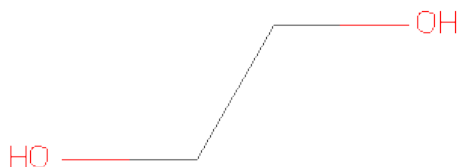
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	SER	-	EXPRESSION TAG	UNP Q9BTZ2
B	18	SER	-	EXPRESSION TAG	UNP Q9BTZ2
C	18	SER	-	EXPRESSION TAG	UNP Q9BTZ2
D	18	SER	-	EXPRESSION TAG	UNP Q9BTZ2

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (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>).



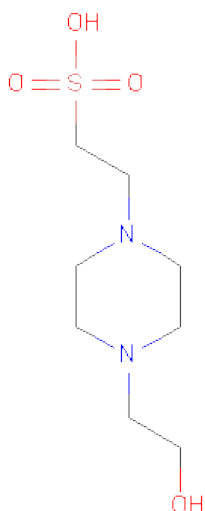
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINEETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	8	2	4	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	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

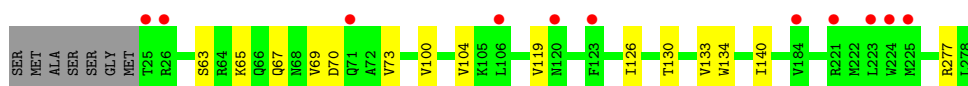
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	152	Total	O	0	0
			152	152		
6	B	177	Total	O	0	0
			177	177		
6	C	123	Total	O	0	0
			123	123		
6	D	154	Total	O	0	0
			154	154		

### 3 Residue-property plots

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: Dehydrogenase/reductaseSDR family member 4

Chain A: 



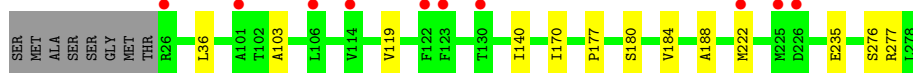
- Molecule 1: Dehydrogenase/reductaseSDR family member 4

Chain B: 



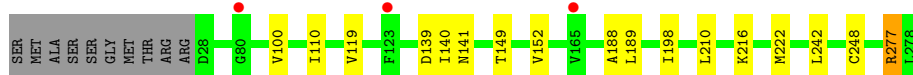
- Molecule 1: Dehydrogenase/reductaseSDR family member 4

Chain C: 



- Molecule 1: Dehydrogenase/reductaseSDR family member 4

Chain D: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.07Å 132.20Å 133.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.29 – 1.70 29.29 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.6 (29.29-1.70) 98.7 (29.29-1.70)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.210 , 0.250 0.223 , 0.262	Depositor DCC
$R_{free}$ test set	5822 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.6	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 37.1	EDS
Estimated twinning fraction	0.001 for -h,l,k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 116275 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8296	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.52	0/1902	0.61	0/2580
1	B	0.49	0/1919	0.60	0/2603
1	C	0.48	0/1876	0.58	0/2547
1	D	0.51	0/1885	0.61	0/2555
All	All	0.50	0/7582	0.60	0/10285

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1871	0	1895	14	0
1	B	1878	0	1911	8	0
1	C	1850	0	1865	8	0
1	D	1856	0	1894	12	0
2	A	48	0	25	1	0
2	B	48	0	25	0	0
2	C	48	0	25	0	0
2	D	48	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	6	0	0
3	B	8	0	12	0	0
3	D	4	0	6	0	0
4	A	15	0	17	0	0
5	B	6	0	8	0	0
5	C	6	0	8	0	0
6	A	152	0	0	7	0
6	B	177	0	0	2	0
6	C	123	0	0	2	0
6	D	154	0	0	2	0
All	All	8296	0	7722	39	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (39) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:119:VAL:HG23	6:B:303:HOH:O	1.60	1.02
1:B:119:VAL:CG2	6:B:303:HOH:O	2.12	0.97
1:A:67:GLN:O	6:A:593:HOH:O	1.92	0.87
1:A:119:VAL:HG23	6:A:373:HOH:O	1.80	0.80
1:A:119:VAL:O	6:A:373:HOH:O	2.12	0.68
1:C:119:VAL:HG23	6:C:425:HOH:O	1.93	0.67
1:A:70:ASP:N	6:A:593:HOH:O	2.31	0.63
1:A:119:VAL:CG2	6:A:373:HOH:O	2.43	0.62
1:D:100:VAL:HG13	1:D:110:ILE:CD1	2.31	0.60
1:A:126:ILE:HD11	1:A:134:TRP:HZ2	1.68	0.57
1:A:100:VAL:O	1:A:104:VAL:HG23	2.05	0.57
1:C:188:ALA:HB2	1:D:188:ALA:HB2	1.86	0.56
1:C:177:PRO:HD3	1:D:198:ILE:HG21	1.95	0.49
1:A:69:VAL:O	1:A:73:VAL:HG23	2.14	0.48
1:A:63:SER:OG	2:A:601:NAP:O2X	2.25	0.48
1:C:119:VAL:HG13	1:C:140:ILE:HB	1.96	0.48
1:D:100:VAL:HG13	1:D:110:ILE:HD11	1.97	0.47
1:A:119:VAL:HG13	1:A:140:ILE:HB	1.97	0.47
1:B:180[B]:SER:OG	1:B:181:PRO:HD3	2.15	0.46
1:C:119:VAL:CG2	6:C:425:HOH:O	2.58	0.46
1:B:100:VAL:HG13	1:B:110:ILE:CD1	2.46	0.46
1:C:170:ILE:HD11	1:C:276:SER:HB3	1.98	0.46
1:D:119:VAL:HG13	1:D:140:ILE:HB	1.97	0.46
1:B:194:LYS:NZ	1:D:277:ARG:O	2.47	0.45
1:B:100:VAL:HG13	1:B:110:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:180:SER:O	1:C:184:VAL:HG23	2.17	0.44
1:D:149:THR:O	1:D:152:VAL:HG22	2.18	0.43
1:D:216:LYS:HG2	1:D:242:LEU:HD23	2.00	0.43
1:D:139:ASP:HB2	6:D:319:HOH:O	2.19	0.42
1:D:210:LEU:HD21	1:D:248:CYS:HB3	2.01	0.42
1:A:70:ASP:HB2	6:A:593:HOH:O	2.20	0.42
1:B:144:ALA:HB3	1:B:145:PRO:HD3	2.02	0.42
1:A:126:ILE:HD11	1:A:134:TRP:CZ2	2.53	0.42
1:D:222[B]:MET:HE3	6:D:611:HOH:O	2.19	0.42
1:A:130:THR:OG1	1:A:133:VAL:HG23	2.21	0.41
1:D:141:ASN:O	1:D:189:LEU:HD21	2.21	0.40
1:B:76:LEU:HD12	1:B:83:VAL:HG11	2.03	0.40
1:A:67:GLN:C	6:A:593:HOH:O	2.49	0.40
1:C:36:LEU:HD21	1:C:103:ALA:HB2	2.04	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	254/261 (97%)	248 (98%)	6 (2%)	0	100	100
1	B	255/261 (98%)	250 (98%)	5 (2%)	0	100	100
1	C	251/261 (96%)	247 (98%)	4 (2%)	0	100	100
1	D	250/261 (96%)	246 (98%)	4 (2%)	0	100	100
All	All	1010/1044 (97%)	991 (98%)	19 (2%)	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	200/212 (94%)	198 (99%)	2 (1%)	85	76
1	B	203/212 (96%)	202 (100%)	1 (0%)	94	89
1	C	196/212 (92%)	193 (98%)	3 (2%)	76	60
1	D	199/212 (94%)	198 (100%)	1 (0%)	94	89
All	All	798/848 (94%)	791 (99%)	7 (1%)	87	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LYS
1	A	277	ARG
1	B	277	ARG
1	C	222	MET
1	C	235	GLU
1	C	277	ARG
1	D	277	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	71	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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

11 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	601	-	52,52,52	1.02	2 (3%)	80,80,80	1.72	14 (17%)
3	EDO	A	703	-	3,3,3	0.51	0	2,2,2	0.42	0
4	EPE	A	705	-	15,15,15	0.80	1 (6%)	20,20,20	2.14	8 (40%)
2	NAP	B	602	-	52,52,52	1.03	2 (3%)	80,80,80	1.60	15 (18%)
3	EDO	B	702	-	3,3,3	0.56	0	2,2,2	0.18	0
3	EDO	B	704	-	3,3,3	0.56	0	2,2,2	0.32	0
5	GOL	B	707	-	5,5,5	0.34	0	5,5,5	0.43	0
2	NAP	C	604	-	52,52,52	1.01	2 (3%)	80,80,80	1.78	14 (17%)
5	GOL	C	706	-	5,5,5	0.29	0	5,5,5	0.35	0
2	NAP	D	603	-	52,52,52	1.12	4 (7%)	80,80,80	1.76	16 (20%)
3	EDO	D	701	-	3,3,3	0.54	0	2,2,2	0.31	0

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	601	-	-	0/35/67/67	0/3/5/5
3	EDO	A	703	-	-	0/1/1/1	0/0/0/0
4	EPE	A	705	-	-	0/9/19/19	0/1/1/1
2	NAP	B	602	-	-	0/35/67/67	0/3/5/5
3	EDO	B	702	-	-	0/1/1/1	0/0/0/0
3	EDO	B	704	-	-	0/1/1/1	0/0/0/0
5	GOL	B	707	-	-	0/4/4/4	0/0/0/0
2	NAP	C	604	-	-	0/35/67/67	0/3/5/5
5	GOL	C	706	-	-	0/4/4/4	0/0/0/0
2	NAP	D	603	-	-	0/35/67/67	0/3/5/5
3	EDO	D	701	-	-	0/1/1/1	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	603	NAP	O7N-C7N	4.68	1.35	1.24
2	A	601	NAP	O7N-C7N	4.38	1.34	1.24
2	B	602	NAP	O7N-C7N	4.11	1.33	1.24
2	C	604	NAP	O7N-C7N	3.63	1.32	1.24
2	C	604	NAP	C4A-N9A	-3.23	1.33	1.37
2	D	603	NAP	C4A-N9A	-3.10	1.33	1.37
2	B	602	NAP	C4A-N9A	-3.01	1.33	1.37
4	A	705	EPE	C10-S	2.82	1.81	1.77
2	A	601	NAP	C4A-N9A	-2.69	1.33	1.37
2	D	603	NAP	C8A-N7A	2.49	1.39	1.34
2	D	603	NAP	C8A-N9A	-2.10	1.33	1.36

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	603	NAP	N3A-C2A-N1A	-10.23	120.16	128.71
2	C	604	NAP	N3A-C2A-N1A	-9.83	120.49	128.71
2	A	601	NAP	N3A-C2A-N1A	-7.61	122.34	128.71
2	B	602	NAP	N3A-C2A-N1A	-7.41	122.51	128.71
2	A	601	NAP	O4D-C1D-N1N	4.99	113.06	107.95
4	A	705	EPE	C6-C5-N4	4.88	120.23	110.61
2	C	604	NAP	O4B-C1B-C2B	-4.35	102.88	106.95
2	A	601	NAP	N3A-C4A-N9A	4.27	133.15	125.43
2	A	601	NAP	O4B-C1B-C2B	-3.88	103.32	106.95
4	A	705	EPE	O3S-S-C10	3.85	110.81	105.93
2	A	601	NAP	C4A-C5A-N7A	-3.82	106.25	109.52
2	D	603	NAP	N3A-C4A-N9A	3.73	132.17	125.43
2	C	604	NAP	N3A-C4A-N9A	3.65	132.02	125.43
2	B	602	NAP	N3A-C4A-N9A	3.39	131.55	125.43
2	D	603	NAP	C8A-N9A-C4A	3.39	109.48	106.90
2	B	602	NAP	O4D-C1D-N1N	3.35	111.38	107.95
2	A	601	NAP	C5A-C4A-N3A	-3.28	118.55	125.70
2	C	604	NAP	C3N-C7N-N7N	3.24	121.45	117.77
4	A	705	EPE	C5-N4-C3	3.21	116.84	108.86
4	A	705	EPE	O2S-S-C10	3.16	109.52	106.81
2	C	604	NAP	O4B-C1B-N9A	-2.95	105.69	108.44
2	A	601	NAP	O4B-C1B-N9A	-2.94	105.71	108.44
2	D	603	NAP	O4D-C1D-N1N	2.87	110.89	107.95
2	A	601	NAP	O2X-P2B-O2B	-2.83	98.93	107.09
2	B	602	NAP	C5D-C4D-C3D	-2.80	104.00	115.21
2	B	602	NAP	O4B-C1B-C2B	-2.78	104.35	106.95
2	C	604	NAP	O2X-P2B-O2B	-2.75	99.16	107.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	604	NAP	O3X-P2B-O2X	2.71	118.16	107.61
2	C	604	NAP	C5A-C4A-N3A	-2.64	119.94	125.70
2	C	604	NAP	C4A-C5A-N7A	-2.61	107.28	109.52
4	A	705	EPE	C5-C6-N1	2.61	115.76	110.61
2	D	603	NAP	O7N-C7N-C3N	2.60	122.51	119.58
2	A	601	NAP	O3X-P2B-O2X	2.57	117.63	107.61
2	B	602	NAP	C4D-O4D-C1D	-2.56	106.97	109.75
2	B	602	NAP	O4B-C1B-N9A	-2.52	106.10	108.44
2	D	603	NAP	O2A-PA-O3	2.51	117.07	105.14
4	A	705	EPE	C2-C3-N4	2.51	115.57	110.61
2	B	602	NAP	O7N-C7N-C3N	2.46	122.34	119.58
2	B	602	NAP	O2X-P2B-O1X	2.43	118.39	110.44
2	D	603	NAP	C5A-C4A-N3A	-2.42	120.42	125.70
4	A	705	EPE	C9-N1-C6	2.42	117.57	111.32
2	B	602	NAP	C5A-C4A-N3A	-2.39	120.49	125.70
2	D	603	NAP	O4B-C1B-N9A	-2.36	106.24	108.44
2	D	603	NAP	C2A-N3A-C4A	2.36	120.72	114.01
2	D	603	NAP	O2N-PN-O5D	2.35	117.89	108.19
2	A	601	NAP	N7A-C8A-N9A	-2.25	107.98	114.36
2	B	602	NAP	C4A-C5A-N7A	-2.24	107.60	109.52
2	C	604	NAP	C2A-N3A-C4A	2.22	120.33	114.01
2	A	601	NAP	C2A-N3A-C4A	2.21	120.31	114.01
2	C	604	NAP	O7N-C7N-N7N	-2.20	119.42	122.59
2	D	603	NAP	C1B-N9A-C4A	-2.17	122.89	126.64
2	B	602	NAP	O2N-PN-O5D	-2.16	99.25	108.19
2	B	602	NAP	O2D-C2D-C1D	2.15	117.75	111.23
4	A	705	EPE	O1S-S-C10	2.13	108.64	106.81
2	C	604	NAP	O4D-C1D-N1N	2.11	110.11	107.95
2	C	604	NAP	O2N-PN-O5D	-2.10	99.51	108.19
2	A	601	NAP	O5D-PN-O1N	-2.09	99.76	108.61
2	D	603	NAP	C4D-O4D-C1D	-2.08	107.50	109.75
2	A	601	NAP	C8A-N9A-C4A	2.07	108.48	106.90
2	D	603	NAP	C3B-C2B-C1B	-2.06	98.73	102.73
2	D	603	NAP	O4D-C1D-C2D	-2.05	103.64	106.77
2	C	604	NAP	C2B-C1B-N9A	2.04	121.47	113.74
2	D	603	NAP	N7A-C8A-N9A	-2.04	108.59	114.36
2	A	601	NAP	C4D-O4D-C1D	-2.02	107.55	109.75
2	B	602	NAP	C2D-C3D-C4D	-2.02	98.62	102.65
2	B	602	NAP	C1B-N9A-C4A	-2.01	123.16	126.64
2	D	603	NAP	O2X-P2B-O1X	2.01	117.00	110.44

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

## 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	254/261 (97%)	0.23	11 (4%) 34 38	20, 31, 47, 66	0
1	B	252/261 (96%)	0.07	2 (0%) 83 88	19, 31, 45, 63	0
1	C	253/261 (96%)	0.31	10 (3%) 36 41	21, 32, 49, 70	0
1	D	251/261 (96%)	0.06	3 (1%) 75 82	21, 31, 44, 52	0
All	All	1010/1044 (96%)	0.17	26 (2%) 54 58	19, 31, 46, 70	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	225	MET	4.8
1	A	25	THR	4.2
1	C	122	PHE	3.7
1	A	225	MET	3.2
1	C	123	PHE	3.1
1	C	226	ASP	3.1
1	C	222	MET	2.9
1	D	80	GLY	2.8
1	B	166	ILE	2.8
1	C	130	THR	2.8
1	A	26	ARG	2.5
1	A	123	PHE	2.5
1	A	224	TRP	2.4
1	B	167	VAL	2.4
1	A	106	LEU	2.4
1	C	101	ALA	2.4
1	D	123	PHE	2.3
1	C	106	LEU	2.3
1	A	120	ASN	2.3
1	C	26	ARG	2.3
1	A	223	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	184	VAL	2.1
1	C	114	VAL	2.1
1	A	71[A]	GLN	2.1
1	D	165	VAL	2.1
1	A	221	ARG	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	EPE	A	705	15/15	0.28	8.72	70,90,95,95	0
3	EDO	B	702	4/4	0.19	8.22	52,56,56,56	0
3	EDO	A	703	4/4	0.15	3.78	49,51,54,58	0
5	GOL	B	707	6/6	0.12	3.14	57,61,62,62	0
3	EDO	D	701	4/4	0.12	3.07	48,48,49,50	0
3	EDO	B	704	4/4	0.13	2.76	52,54,54,57	0
5	GOL	C	706	6/6	0.17	1.81	49,63,66,67	0
2	NAP	C	604	48/48	0.09	-0.23	26,33,37,40	0
2	NAP	D	603	48/48	0.09	-0.40	15,27,32,35	0
2	NAP	B	602	48/48	0.08	-0.52	18,26,30,37	0
2	NAP	A	601	48/48	0.08	-0.75	18,28,36,37	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.