



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:01 PM GMT

PDB ID : 1W8D  
Title : BINARY STRUCTURE OF HUMAN DECR.  
Authors : Alphey, M.S.; Byres, E.; Hunter, W.N.  
Deposited on : 2004-09-20  
Resolution : 2.20 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

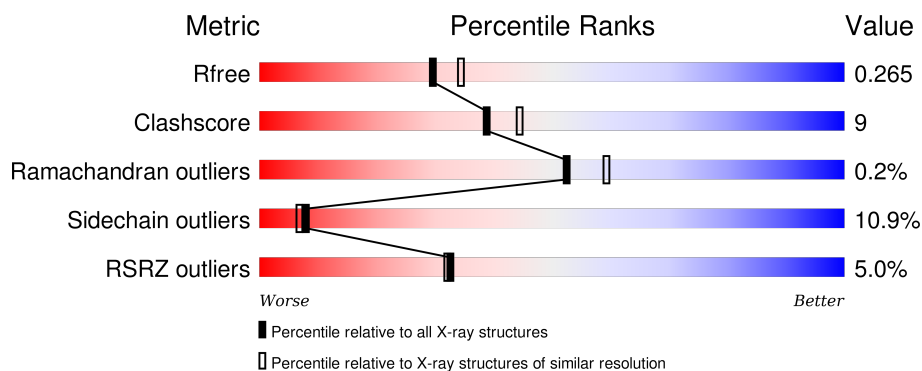
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	302	 7% 75% 16% • 5%
1	B	302	 3% 73% 18% • 7%
1	C	302	 6% 71% 20% • 6%
1	D	302	 3% 75% 15% • 7%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	1329	-	-	-	X
2	GOL	D	1328	-	-	-	X

## 2 Entry composition [i](#)

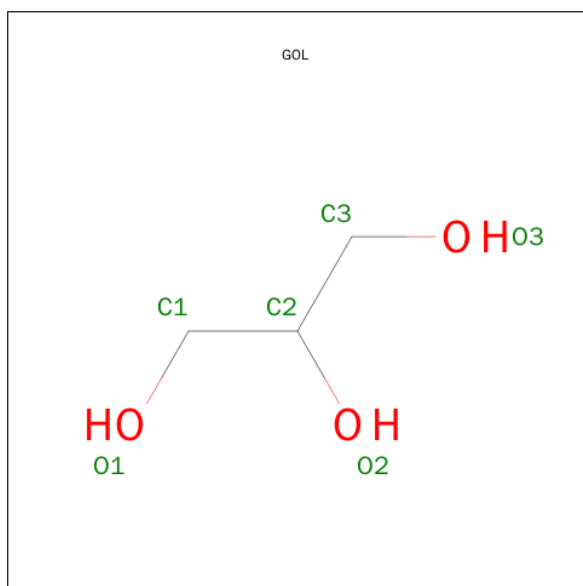
There are 4 unique types of molecules in this entry. The entry contains 8986 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRE-CURSOR.

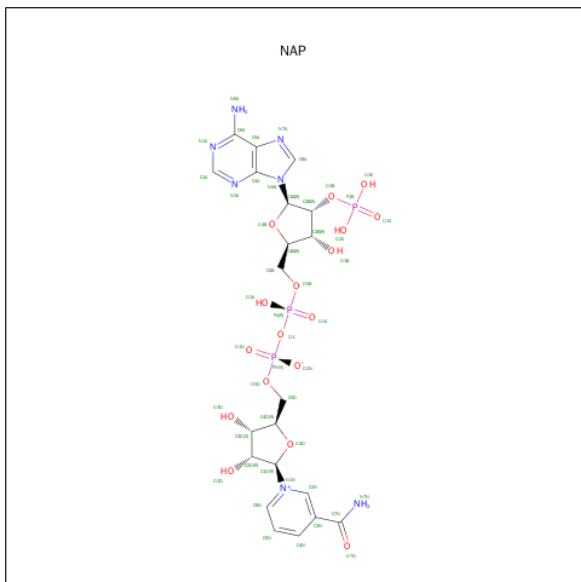
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	Se	0	5	0
			2178	1380	370	417	4	7			
1	B	282	Total	C	N	O	S	Se	0	5	0
			2137	1354	363	408	4	8			
1	C	284	Total	C	N	O	S	Se	0	5	0
			2148	1361	363	413	4	7			
1	D	280	Total	C	N	O	S	Se	0	1	0
			2102	1332	357	401	4	8			

- Molecule 2 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
2	A	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).



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

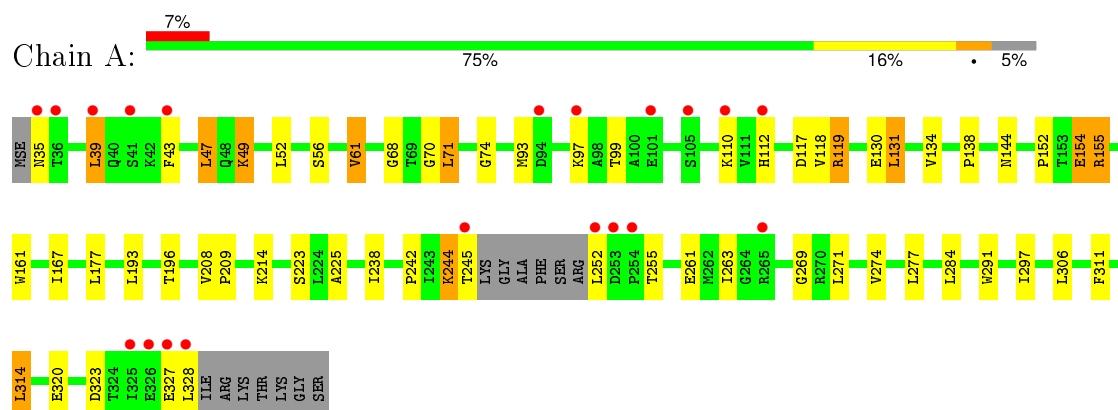
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total	O	0	0
			49	49		
4	B	58	Total	O	0	0
			58	58		
4	C	49	Total	O	0	0
			49	49		
4	D	61	Total	O	0	0
			61	61		

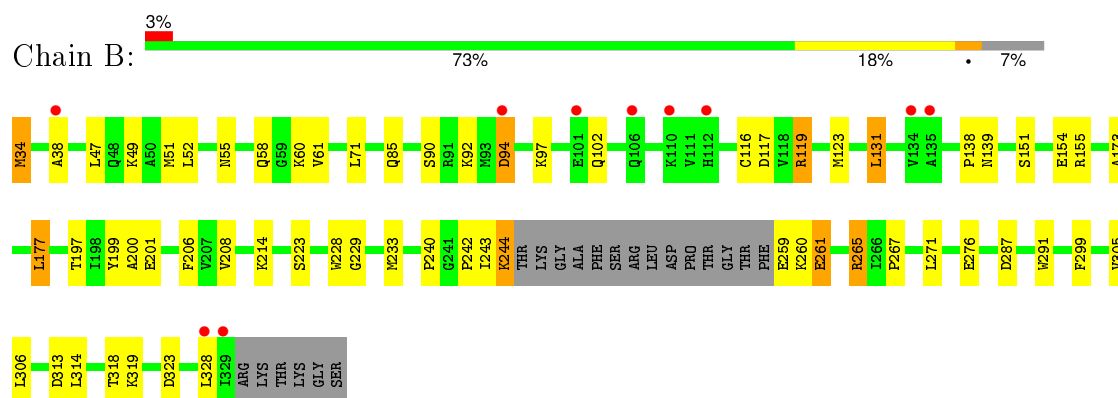
### 3 Residue-property plots

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.

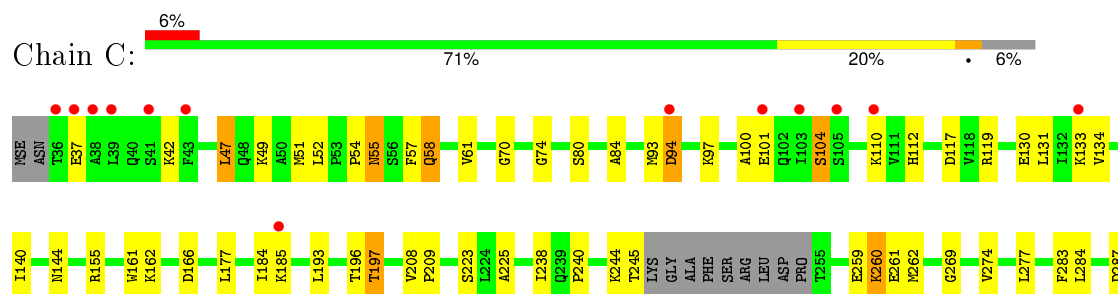
- Molecule 1: 2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR

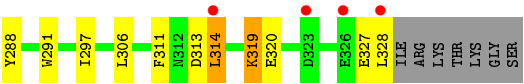


- Molecule 1: 2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR

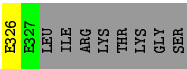
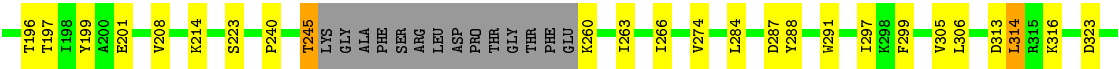
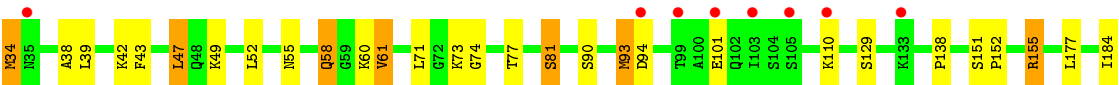
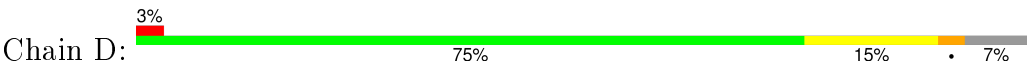


- Molecule 1: 2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR





● Molecule 1: 2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL PRECURSOR



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.87Å 131.70Å 70.59Å 90.00° 92.56° 90.00°	Depositor
Resolution (Å)	70.71 – 2.20 62.17 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (70.71-2.20) 97.6 (62.17-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.219 , 0.265 0.219 , 0.265	Depositor DCC
$R_{free}$ test set	2934 reflections (5.46%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.1	Xtriage
Anisotropy	1.114	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.1	EDS
Estimated twinning fraction	0.077 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 56715 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8986	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% 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

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

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	0.49	0/2229	0.73	2/3004 (0.1%)
1	B	0.48	0/2188	0.69	4/2944 (0.1%)
1	C	0.47	0/2198	0.70	5/2961 (0.2%)
1	D	0.46	0/2134	0.69	3/2873 (0.1%)
All	All	0.48	0/8749	0.70	14/11782 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	94[A]	ASP	CB-CG-OD2	6.06	123.75	118.30
1	C	94[B]	ASP	CB-CG-OD2	6.06	123.75	118.30
1	D	94	ASP	CB-CG-OD2	6.00	123.70	118.30
1	C	166	ASP	CB-CG-OD2	5.91	123.62	118.30
1	C	313	ASP	CB-CG-OD2	5.84	123.55	118.30
1	D	313	ASP	CB-CG-OD2	5.68	123.41	118.30
1	B	323	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	323	ASP	CB-CG-OD2	5.53	123.28	118.30
1	A	117	ASP	CB-CG-OD2	5.32	123.09	118.30
1	B	94[A]	ASP	CB-CG-OD2	5.21	122.98	118.30
1	B	94[B]	ASP	CB-CG-OD2	5.21	122.98	118.30
1	D	323	ASP	CB-CG-OD2	5.18	122.97	118.30
1	C	287	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	287	ASP	CB-CG-OD2	5.09	122.88	118.30

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	2178	0	2200	43	0
1	B	2137	0	2165	44	0
1	C	2148	0	2169	37	0
1	D	2102	0	2133	47	0
2	A	6	0	8	1	0
2	D	6	0	8	0	0
3	A	48	0	25	2	0
3	B	48	0	25	2	0
3	C	48	0	25	2	0
3	D	48	0	25	2	0
4	A	49	0	0	23	0
4	B	58	0	0	17	0
4	C	49	0	0	11	0
4	D	61	0	0	21	0
All	All	8986	0	8783	159	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 9.

All (159) 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:245:THR:HA	4:C:2035:HOH:O	1.47	1.15
1:C:240:PRO:HD2	4:C:2023:HOH:O	1.61	1.00
1:D:55:ASN:ND2	4:D:2003:HOH:O	1.93	1.00
1:C:197:THR:HA	4:C:2023:HOH:O	1.62	0.96
1:A:269:GLY:HA2	4:A:2042:HOH:O	1.63	0.96
1:D:326:GLU:HB2	4:D:2060:HOH:O	1.66	0.94
1:A:112[A]:HIS:CG	4:A:2007:HOH:O	2.21	0.92
1:B:61:VAL:HG22	1:B:138:PRO:HA	1.51	0.92
1:D:101:GLU:HG3	4:D:2009:HOH:O	1.69	0.91
1:D:73:LYS:HE2	4:D:2006:HOH:O	1.69	0.89
1:D:155:ARG:HD3	4:D:2020:HOH:O	1.72	0.88
1:D:58:GLN:HG3	4:D:2004:HOH:O	1.73	0.87
1:A:39:LEU:HD23	4:A:2001:HOH:O	1.73	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:ASN:HA	4:B:2014:HOH:O	1.78	0.83
1:B:244:LYS:C	4:B:2036:HOH:O	2.18	0.81
1:A:112[B]:HIS:CG	4:A:2007:HOH:O	2.34	0.81
1:A:154:GLU:HG2	1:C:184:ILE:HD13	1.63	0.81
1:D:284:LEU:HD11	1:D:297:ILE:HD12	1.68	0.75
1:C:54:PRO:HA	4:C:2001:HOH:O	1.87	0.75
4:A:2004:HOH:O	1:B:51:MSE:HG2	1.85	0.75
1:D:61:VAL:HG22	1:D:138:PRO:HA	1.70	0.73
1:D:49:LYS:HB2	4:D:2002:HOH:O	1.87	0.73
1:D:93:MSE:HE2	4:D:2011:HOH:O	1.89	0.73
1:C:55[B]:ASN:ND2	1:C:58[B]:GLN:OE1	2.24	0.71
1:A:43:PHE:CD1	4:A:2001:HOH:O	2.45	0.70
4:A:2021:HOH:O	1:C:162:LYS:HG3	1.91	0.69
1:C:196:THR:O	4:C:2023:HOH:O	2.09	0.68
1:B:313:ASP:O	4:B:2053:HOH:O	2.11	0.68
1:A:43:PHE:HD1	4:A:2001:HOH:O	1.77	0.67
1:B:318:THR:HA	4:B:2056:HOH:O	1.95	0.67
1:A:112[B]:HIS:CB	4:A:2007:HOH:O	2.44	0.66
1:C:319:LYS:HE3	4:D:2038:HOH:O	1.97	0.64
1:A:223:SER:HB3	1:C:208:VAL:HG22	1.79	0.64
1:A:134:VAL:CG2	4:A:2007:HOH:O	2.45	0.64
1:A:112[A]:HIS:CB	4:A:2007:HOH:O	2.44	0.64
1:A:49:LYS:HB3	4:A:2003:HOH:O	1.98	0.63
1:D:245:THR:HG23	4:D:2041:HOH:O	1.99	0.63
1:B:71:LEU:HB2	3:B:1330:NAP:H51N	1.82	0.62
1:B:318:THR:HB	4:B:2056:HOH:O	2.01	0.61
1:D:314:LEU:HD13	4:D:2058:HOH:O	2.01	0.61
1:D:201:GLU:CD	4:D:2033:HOH:O	2.39	0.60
1:A:208:VAL:HG22	1:C:223:SER:HB3	1.83	0.60
1:B:259:GLU:HA	4:B:2037:HOH:O	2.00	0.60
1:A:61:VAL:HG22	1:A:138:PRO:HA	1.83	0.60
1:D:274:VAL:HG23	4:D:2043:HOH:O	2.03	0.59
1:D:152:PRO:HB2	1:D:155:ARG:HG3	1.83	0.59
1:A:130:GLU:O	1:A:134:VAL:HG22	2.03	0.58
1:A:49:LYS:CB	4:A:2003:HOH:O	2.50	0.58
1:A:134:VAL:HG21	4:A:2007:HOH:O	2.01	0.58
1:A:244:LYS:HE3	4:A:2040:HOH:O	2.04	0.58
1:D:60:LYS:HE2	4:D:2005:HOH:O	2.04	0.57
1:A:74:GLY:HA3	1:A:274:VAL:CG1	2.35	0.56
1:B:55:ASN:ND2	4:B:2002:HOH:O	2.33	0.56
1:C:117:ASP:OD1	1:C:119:ARG:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:LYS:CE	4:D:2006:HOH:O	2.41	0.56
1:D:274:VAL:HB	4:D:2043:HOH:O	2.06	0.55
1:B:318:THR:CA	4:B:2056:HOH:O	2.54	0.55
1:B:318:THR:CB	4:B:2056:HOH:O	2.54	0.55
1:B:55:ASN:ND2	1:B:58[A]:GLN:OE1	2.39	0.55
1:D:274:VAL:CB	4:D:2043:HOH:O	2.56	0.54
1:A:56:SER:O	2:A:1329:GOL:H11	2.08	0.54
1:D:49:LYS:CB	4:D:2002:HOH:O	2.49	0.53
1:B:242:PRO:HB2	1:B:271:LEU:HD22	1.90	0.53
1:C:100:ALA:O	1:C:104:SER:HB2	2.09	0.53
1:B:92:LYS:HD2	3:B:1330:NAP:O1X	2.10	0.52
1:C:259:GLU:HA	1:C:262:MSE:HE3	1.91	0.52
1:D:34:MSE:HE1	1:D:42:LYS:HD3	1.92	0.52
1:B:92:LYS:HE2	4:B:2009:HOH:O	2.11	0.51
1:D:34:MSE:HG3	1:D:38:ALA:HB3	1.92	0.51
1:A:209:PRO:HD2	4:A:2013:HOH:O	2.11	0.51
1:A:225:ALA:HB3	1:B:305:VAL:HG21	1.93	0.51
1:C:130:GLU:O	1:C:134:VAL:HG22	2.10	0.51
1:A:242:PRO:HB2	1:A:271:LEU:HD22	1.93	0.51
1:D:60:LYS:CE	4:D:2005:HOH:O	2.59	0.50
1:B:154:GLU:HG2	1:D:184:ILE:HD13	1.94	0.50
1:B:173:ALA:O	1:B:177:LEU:HB2	2.12	0.50
1:C:51:MSE:HB2	1:D:288:TYR:CD1	2.46	0.50
1:C:260:LYS:HE2	4:C:2037:HOH:O	2.12	0.50
1:B:201:GLU:HA	4:B:2023:HOH:O	2.10	0.49
1:A:154:GLU:HG2	1:C:184:ILE:CD1	2.38	0.49
1:D:77:THR:O	1:D:81:SER:HB3	2.12	0.49
1:A:311:PHE:O	1:A:314:LEU:HB2	2.13	0.48
1:A:71:LEU:HB2	3:A:1330:NAP:H51N	1.95	0.48
1:C:284:LEU:HD11	1:C:297:ILE:HD12	1.95	0.48
1:C:209:PRO:HG2	4:C:2027:HOH:O	2.13	0.48
1:A:119:ARG:HD3	1:A:167:ILE:HG13	1.96	0.48
4:A:2004:HOH:O	1:B:51:MSE:SE	2.82	0.48
1:C:288:TYR:CE1	1:D:47:LEU:HD13	2.48	0.48
1:B:117:ASP:OD1	1:B:119:ARG:HG2	2.13	0.48
1:B:223:SER:HB3	1:D:208:VAL:HG22	1.96	0.47
1:A:118:VAL:HG13	3:A:1330:NAP:H2A	1.96	0.47
1:D:71:LEU:HB2	3:D:1329:NAP:H51N	1.95	0.47
1:B:131:LEU:HD21	1:B:138:PRO:HG3	1.95	0.47
3:C:1329:NAP:H6N	4:C:2023:HOH:O	2.14	0.47
1:B:228:TRP:HB3	1:B:233:MSE:HE3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLY:HA2	1:A:99:THR:HG21	1.95	0.47
1:A:154:GLU:OE2	4:A:2016:HOH:O	2.21	0.47
1:A:167:ILE:HD11	4:A:2049:HOH:O	2.14	0.47
4:A:2004:HOH:O	1:B:51:MSE:HE3	2.15	0.46
1:C:197:THR:CA	4:C:2023:HOH:O	2.37	0.46
1:D:274:VAL:CG2	4:D:2043:HOH:O	2.62	0.46
1:D:39:LEU:HD23	1:D:43:PHE:HE1	1.80	0.46
1:B:261:GLU:CD	1:B:265[B]:ARG:HH12	2.19	0.46
1:D:196:THR:HA	1:D:214:LYS:HD2	1.98	0.46
1:A:131:LEU:HD21	1:A:138:PRO:HG3	1.97	0.46
1:B:197:THR:HG21	1:B:199:TYR:CZ	2.51	0.45
1:D:197:THR:HG21	1:D:199:TYR:CE1	2.52	0.45
1:A:161:TRP:C	1:A:161:TRP:CD1	2.89	0.45
1:D:263:ILE:HA	1:D:266:ILE:HD12	1.99	0.45
1:B:229:GLY:N	4:B:2033:HOH:O	2.45	0.45
1:C:74:GLY:HA3	1:C:274:VAL:CG1	2.46	0.45
1:A:71:LEU:HG	1:A:277:LEU:HD22	1.99	0.45
1:D:90:SER:HB2	3:D:1329:NAP:P2B	2.57	0.44
1:B:60:LYS:CE	4:B:2005:HOH:O	2.64	0.44
1:B:60:LYS:HE2	4:B:2005:HOH:O	2.16	0.44
1:A:284:LEU:HD11	1:A:297:ILE:HD12	1.99	0.44
1:B:208:VAL:HG22	1:D:223:SER:HB3	1.99	0.44
1:A:74:GLY:HA3	1:A:274:VAL:HG12	1.99	0.44
1:C:269:GLY:HA2	4:C:2038:HOH:O	2.16	0.44
1:C:57:PHE:CE2	1:C:140:ILE:HD11	2.53	0.44
1:B:139:ASN:CB	4:B:2014:HOH:O	2.66	0.44
1:D:245:THR:C	4:D:2041:HOH:O	2.57	0.44
1:C:57:PHE:HB3	1:C:84:ALA:HB2	2.00	0.43
1:C:47:LEU:HD13	1:D:288:TYR:CE1	2.53	0.43
1:B:60:LYS:NZ	4:B:2005:HOH:O	2.34	0.43
1:C:193:LEU:HD11	1:C:238:ILE:HG13	2.01	0.43
1:A:284:LEU:HD21	1:A:297:ILE:CD1	2.49	0.43
1:B:200:ALA:HB2	1:B:214:LYS:HB3	1.99	0.43
1:D:240:PRO:HA	1:D:299:PHE:O	2.19	0.43
1:C:74:GLY:HA3	1:C:274:VAL:HG12	2.01	0.43
1:C:311:PHE:O	1:C:314:LEU:HB2	2.19	0.42
1:B:151:SER:O	1:B:206:PHE:HA	2.19	0.42
1:A:39:LEU:CD2	4:A:2001:HOH:O	2.47	0.42
1:C:51:MSE:HE1	1:C:283:PHE:HB2	2.00	0.42
1:A:196:THR:HA	1:A:214:LYS:HD2	2.02	0.42
1:A:152:PRO:HB2	1:A:155:ARG:HG3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:PHE:HE2	1:C:140:ILE:HD11	1.85	0.42
1:B:267:PRO:HG3	1:B:306:LEU:HD12	2.00	0.42
1:C:161:TRP:C	1:C:161:TRP:CD1	2.92	0.42
1:D:197:THR:HG21	1:D:199:TYR:CZ	2.55	0.42
1:B:139:ASN:CA	4:B:2014:HOH:O	2.52	0.42
1:C:47:LEU:HD12	1:D:287:ASP:HB2	2.01	0.42
1:A:193:LEU:HD11	1:A:238:ILE:HG13	2.02	0.42
1:B:240:PRO:HB3	1:B:243:ILE:HD11	2.02	0.42
1:C:225:ALA:HB3	1:D:305:VAL:HG21	2.02	0.42
1:C:51:MSE:HB2	1:D:288:TYR:CE1	2.55	0.42
1:B:116:CYS:HA	1:B:123:MSE:HE2	2.01	0.42
1:C:110:LYS:HD2	1:C:112[A]:HIS:CE1	2.55	0.41
1:D:74:GLY:HA3	1:D:274:VAL:CG1	2.50	0.41
1:A:47:LEU:HD23	1:A:47:LEU:HA	1.98	0.41
4:A:2004:HOH:O	1:B:51:MSE:CG	2.56	0.41
1:D:34:MSE:HG2	1:D:39:LEU:HG	2.02	0.41
1:D:34:MSE:HG3	1:D:38:ALA:CB	2.50	0.41
1:B:34:MSE:HE2	1:B:38:ALA:O	2.21	0.41
3:C:1329:NAP:C6N	4:C:2023:HOH:O	2.68	0.41
1:A:269:GLY:CA	4:A:2042:HOH:O	2.42	0.40
1:D:39:LEU:HD23	1:D:43:PHE:CE1	2.56	0.40
1:B:276:GLU:HB3	1:B:299:PHE:HZ	1.86	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	289/302 (96%)	280 (97%)	8 (3%)	1 (0%)	46	50
1	B	281/302 (93%)	273 (97%)	8 (3%)	0	100	100
1	C	285/302 (94%)	275 (96%)	9 (3%)	1 (0%)	39	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	277/302 (92%)	267 (96%)	10 (4%)	0	100	100
All	All	1132/1208 (94%)	1095 (97%)	35 (3%)	2 (0%)	52	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	70	GLY
1	A	70	GLY

### 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	236/235 (100%)	208 (88%)	28 (12%)	6	5
1	B	231/235 (98%)	207 (90%)	24 (10%)	9	8
1	C	233/235 (99%)	198 (85%)	35 (15%)	3	3
1	D	226/235 (96%)	208 (92%)	18 (8%)	15	15
All	All	926/940 (98%)	821 (89%)	105 (11%)	8	6

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	39	LEU
1	A	47	LEU
1	A	49	LYS
1	A	52	LEU
1	A	61	VAL
1	A	71	LEU
1	A	93	MSE
1	A	97	LYS
1	A	110	LYS
1	A	119	ARG
1	A	131	LEU

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Mol	Chain	Res	Type
1	A	144	ASN
1	A	154	GLU
1	A	155	ARG
1	A	177	LEU
1	A	244	LYS
1	A	245	THR
1	A	252	LEU
1	A	255	THR
1	A	261	GLU
1	A	263	ILE
1	A	291	TRP
1	A	306	LEU
1	A	314	LEU
1	A	320	GLU
1	A	327	GLU
1	A	328	LEU
1	B	34	MSE
1	B	47	LEU
1	B	49	LYS
1	B	52	LEU
1	B	85[A]	GLN
1	B	85[B]	GLN
1	B	90	SER
1	B	94[A]	ASP
1	B	94[B]	ASP
1	B	97	LYS
1	B	102	GLN
1	B	119	ARG
1	B	131	LEU
1	B	155	ARG
1	B	177	LEU
1	B	244	LYS
1	B	260	LYS
1	B	261	GLU
1	B	265[A]	ARG
1	B	265[B]	ARG
1	B	291	TRP
1	B	314	LEU
1	B	319	LYS
1	B	328	LEU
1	C	37	GLU
1	C	42	LYS

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Mol	Chain	Res	Type
1	C	47	LEU
1	C	49	LYS
1	C	52	LEU
1	C	55[A]	ASN
1	C	55[B]	ASN
1	C	58[A]	GLN
1	C	58[B]	GLN
1	C	61	VAL
1	C	80	SER
1	C	93	MSE
1	C	94[A]	ASP
1	C	94[B]	ASP
1	C	97	LYS
1	C	101	GLU
1	C	104	SER
1	C	131	LEU
1	C	133	LYS
1	C	144	ASN
1	C	155	ARG
1	C	177	LEU
1	C	185	LYS
1	C	197	THR
1	C	244	LYS
1	C	260	LYS
1	C	261	GLU
1	C	277	LEU
1	C	291	TRP
1	C	306	LEU
1	C	314	LEU
1	C	319	LYS
1	C	320	GLU
1	C	327	GLU
1	C	328	LEU
1	D	34	MSE
1	D	47	LEU
1	D	52	LEU
1	D	58	GLN
1	D	61	VAL
1	D	81	SER
1	D	93	MSE
1	D	110	LYS
1	D	129	SER

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Mol	Chain	Res	Type
1	D	151	SER
1	D	155	ARG
1	D	177	LEU
1	D	245	THR
1	D	260	LYS
1	D	291	TRP
1	D	306	LEU
1	D	314	LEU
1	D	316	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	126	ASN
1	A	187	GLN
1	B	126	ASN
1	B	321	GLN
1	C	126	ASN
1	C	187	GLN
1	D	58	GLN
1	D	85	GLN
1	D	126	ASN

### 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](#)

6 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	GOL	A	1329	-	5,5,5	0.37	0	5,5,5	0.18	0
3	NAP	A	1330	-	42,52,52	1.60	3 (7%)	54,80,80	1.89	5 (9%)
3	NAP	B	1330	-	42,52,52	1.64	3 (7%)	54,80,80	1.63	4 (7%)
3	NAP	C	1329	-	42,52,52	1.53	3 (7%)	54,80,80	1.93	3 (5%)
2	GOL	D	1328	-	5,5,5	0.37	0	5,5,5	0.28	0
3	NAP	D	1329	-	42,52,52	1.58	3 (7%)	54,80,80	1.78	2 (3%)

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	GOL	A	1329	-	-	0/4/4/4	0/0/0/0
3	NAP	A	1330	-	-	0/27/67/67	0/5/5/5
3	NAP	B	1330	-	-	0/27/67/67	0/5/5/5
3	NAP	C	1329	-	-	0/27/67/67	0/5/5/5
2	GOL	D	1328	-	-	0/4/4/4	0/0/0/0
3	NAP	D	1329	-	-	0/27/67/67	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1329	NAP	C2A-N1A	2.21	1.38	1.33
3	D	1329	NAP	C2A-N1A	2.58	1.38	1.33
3	A	1330	NAP	C2A-N1A	2.61	1.38	1.33
3	B	1330	NAP	C2A-N1A	2.66	1.39	1.33
3	C	1329	NAP	C2A-N3A	3.27	1.38	1.32
3	D	1329	NAP	C2A-N3A	3.49	1.38	1.32
3	A	1330	NAP	C2A-N3A	3.60	1.38	1.32
3	B	1330	NAP	C2A-N3A	3.69	1.38	1.32
3	C	1329	NAP	O7N-C7N	8.01	1.41	1.24
3	D	1329	NAP	O7N-C7N	8.12	1.41	1.24
3	A	1330	NAP	O7N-C7N	8.20	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1330	NAP	O7N-C7N	8.31	1.41	1.24

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1329	NAP	N3A-C2A-N1A	-11.89	119.79	128.89
3	A	1330	NAP	N3A-C2A-N1A	-11.71	119.93	128.89
3	D	1329	NAP	N3A-C2A-N1A	-11.31	120.24	128.89
3	B	1330	NAP	N3A-C2A-N1A	-9.89	121.32	128.89
3	A	1330	NAP	PN-O3-PA	-3.01	124.27	132.73
3	C	1329	NAP	PN-O3-PA	-2.99	124.33	132.73
3	B	1330	NAP	C4A-C5A-N7A	-2.54	107.14	109.48
3	B	1330	NAP	PN-O3-PA	-2.39	126.02	132.73
3	A	1330	NAP	C5B-C4B-C3B	-2.34	105.94	115.21
3	A	1330	NAP	O4D-C1D-N1N	2.01	110.34	108.13
3	B	1330	NAP	O4B-C1B-N9A	2.12	112.55	108.10
3	A	1330	NAP	C3N-C7N-N7N	2.36	120.40	117.82
3	D	1329	NAP	O4D-C1D-N1N	2.75	111.16	108.13
3	C	1329	NAP	O4D-C1D-N1N	3.16	111.61	108.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1329	GOL	1	0
3	A	1330	NAP	2	0
3	B	1330	NAP	2	0
3	C	1329	NAP	2	0
3	D	1329	NAP	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	281/302 (93%)	0.52	20 (7%) 19 18	27, 45, 81, 99	0
1	B	274/302 (90%)	0.42	10 (3%) 46 45	29, 47, 67, 104	0
1	C	277/302 (91%)	0.48	17 (6%) 25 24	28, 47, 81, 100	0
1	D	272/302 (90%)	0.41	8 (2%) 55 54	32, 49, 69, 82	0
All	All	1104/1208 (91%)	0.46	55 (4%) 32 32	27, 47, 75, 104	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	36	THR	9.2
1	C	328	LEU	6.4
1	B	329	ILE	6.1
1	A	35	ASN	5.0
1	A	252	LEU	5.0
1	A	39	LEU	4.3
1	A	325	ILE	4.2
1	A	36	THR	3.8
1	C	43	PHE	3.7
1	D	99	THR	3.4
1	A	110	LYS	3.3
1	A	326	GLU	3.3
1	C	185	LYS	3.2
1	D	110	LYS	3.2
1	A	254	PRO	3.2
1	C	326	GLU	3.2
1	A	41	SER	3.0
1	D	103	ILE	2.9
1	A	105	SER	2.9
1	A	101	GLU	2.9
1	A	43	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	327	GLU	2.8
1	B	328	LEU	2.8
1	C	39	LEU	2.7
1	C	103	ILE	2.7
1	C	37	GLU	2.6
1	C	41	SER	2.5
1	C	94[A]	ASP	2.5
1	B	134	VAL	2.5
1	D	105	SER	2.5
1	A	253	ASP	2.5
1	C	110	LYS	2.5
1	A	245	THR	2.5
1	B	110	LYS	2.4
1	C	105	SER	2.4
1	B	38	ALA	2.4
1	B	135	ALA	2.3
1	D	94	ASP	2.3
1	A	265[A]	ARG	2.3
1	B	101	GLU	2.3
1	B	94[A]	ASP	2.3
1	A	328	LEU	2.2
1	A	97	LYS	2.2
1	C	314	LEU	2.2
1	C	101	GLU	2.2
1	C	133	LYS	2.2
1	A	112[A]	HIS	2.2
1	C	38	ALA	2.2
1	A	94[A]	ASP	2.1
1	D	101	GLU	2.1
1	C	323	ASP	2.1
1	D	35	ASN	2.1
1	B	106	GLN	2.0
1	B	112[A]	HIS	2.0
1	D	133	LYS	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 [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	GOL	A	1329	6/6	0.50	0.47	11.10	89,90,90,90	0
2	GOL	D	1328	6/6	0.85	0.36	5.90	60,61,62,64	0
3	NAP	C	1329	48/48	0.92	0.18	1.10	39,70,87,88	0
3	NAP	B	1330	48/48	0.91	0.17	1.06	42,57,64,66	0
3	NAP	D	1329	48/48	0.89	0.16	0.33	41,67,70,71	0
3	NAP	A	1330	48/48	0.93	0.16	0.33	37,52,59,60	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.