W O R L D W I D E

wwPDB

P R O T E I N D A T A B A N K

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 12:46 AM GMT

PDB ID	:	2BFA
Title	:	LEISHMANIA MAJOR PTERIDINE REDUCTASE 1 IN COMPLEX WITH NADP AND CB3717
Authors	:	Schuettelkopf, A.W.; Hunter, W.N.
Deposited on	:	2004-12-06
Resolution	:	2.70 Å(reported)

The following versions of software and data (see references (i)) 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 2.70 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.
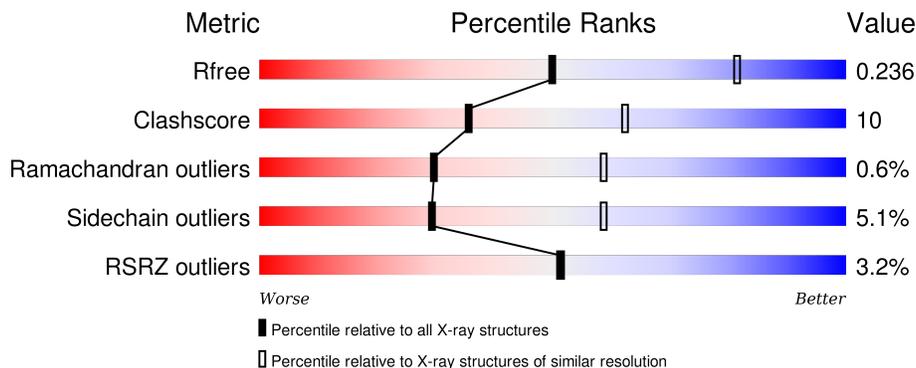
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 >=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 <=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	288	2% / 72% / 18% / • / 8%
1	B	288	3% / 71% / 19% / • / 8%
1	C	288	3% / 72% / 14% / • / 12%
1	D	288	3% / 72% / 16% / • / 11%

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	CB3	A	1290	-	-	-	X
3	CB3	B	1290	-	-	-	X
3	CB3	C	1290	-	-	-	X
3	CB3	D	1290	-	-	-	X
4	EDO	A	1291	-	-	X	X
4	EDO	A	1292	-	-	-	X
4	EDO	A	1293	-	-	X	X
4	EDO	B	1291	-	-	X	X
4	EDO	D	1291	-	-	X	X
4	EDO	D	1292	-	-	X	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8319 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 PTERIDINE REDUCTASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			1980	1248	352	369	11			
1	B	266	Total	C	N	O	S	0	0	0
			1984	1250	353	370	11			
1	C	253	Total	C	N	O	S	0	0	0
			1885	1189	337	349	10			
1	D	255	Total	C	N	O	S	0	0	0
			1903	1199	341	353	10			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).
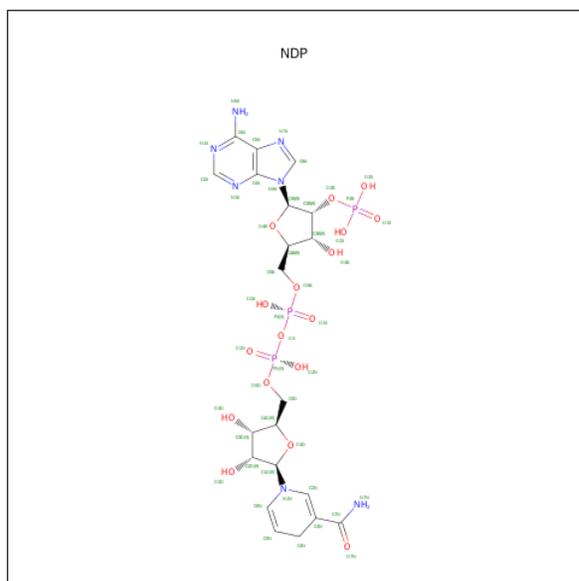
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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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		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLIC ACID (three-letter code: CB3) (formula: $C_{24}H_{23}N_5O_6$).
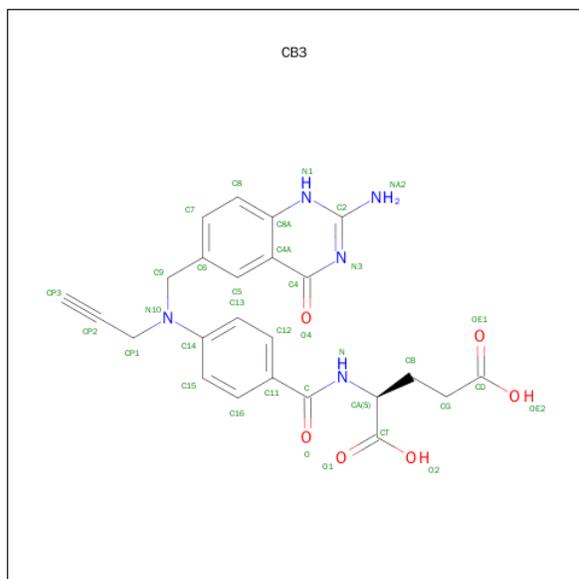
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			35	24	5	6		
3	B	1	Total	C	N	O	0	0
			35	24	5	6		
3	C	1	Total	C	N	O	0	0
			35	24	5	6		
3	D	1	Total	C	N	O	0	0
			35	24	5	6		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).
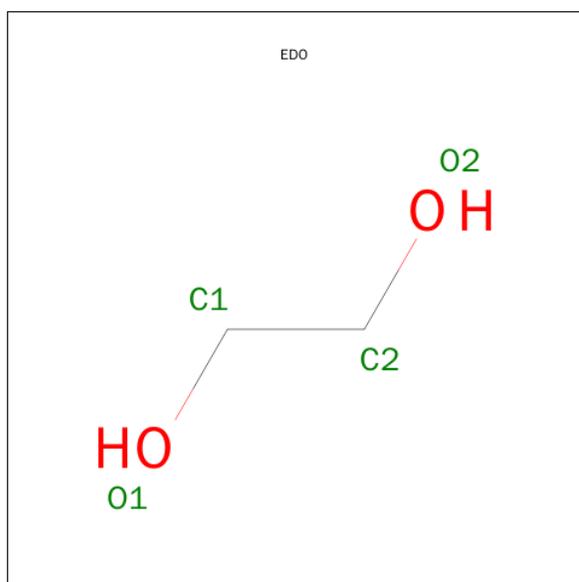
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	A	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	59	Total 59	O 59	0	0
5	B	42	Total 42	O 42	0	0
5	C	63	Total 63	O 63	0	0
5	D	47	Total 47	O 47	0	0

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: PTERIDINE REDUCTASE 1
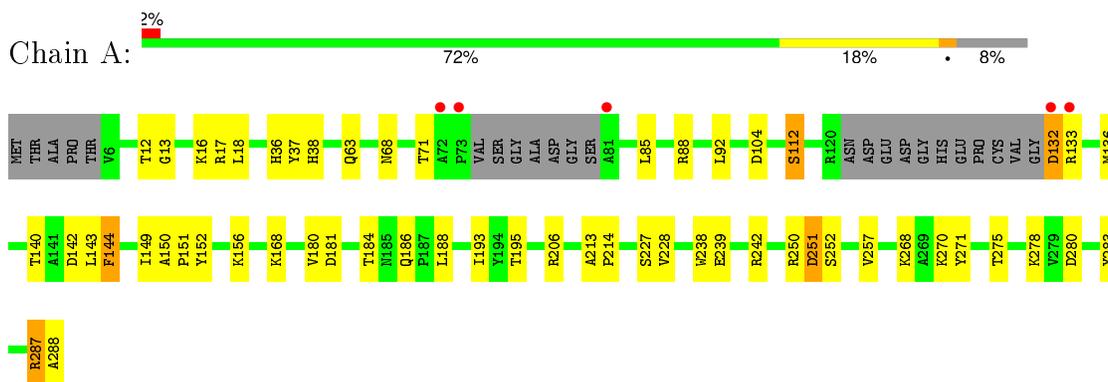
Chain A:

2%

72%　　　　18%　　·　　8%

- Molecule 1: PTERIDINE REDUCTASE 1

Chain B:

3%

71%　　　　19%　　·　　8%

- Molecule 1: PTERIDINE REDUCTASE 1

Chain C:

3%

72%　　　　14%　　·　　12%
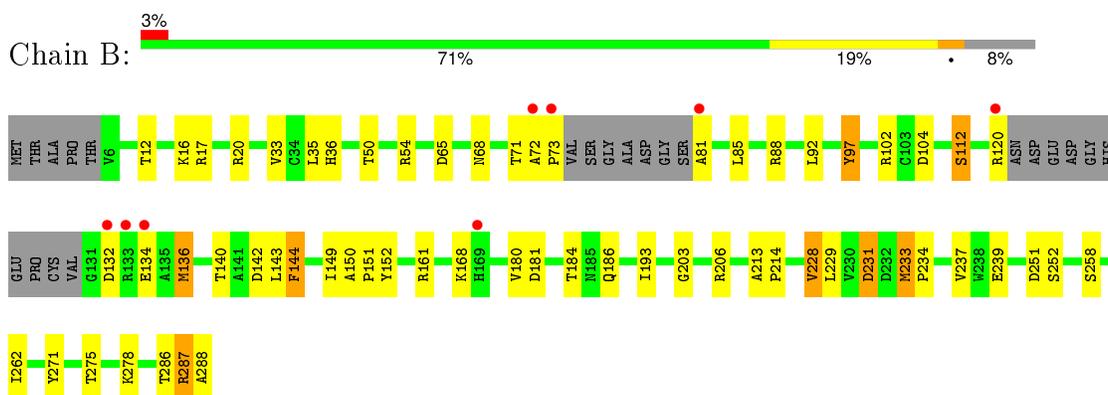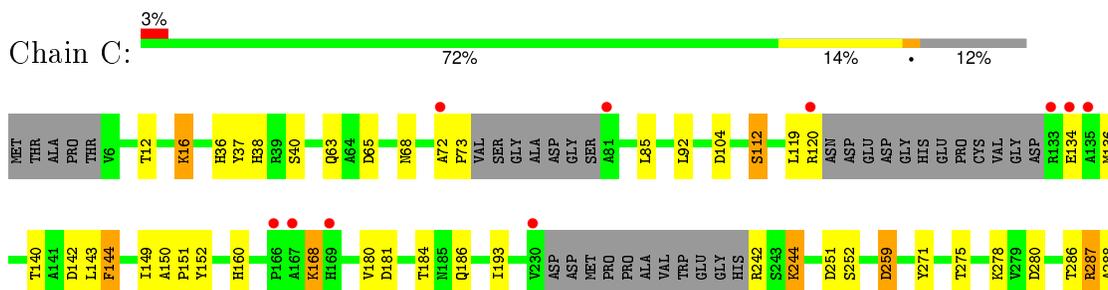
- Molecule 1: PTERIDINE REDUCTASE 1
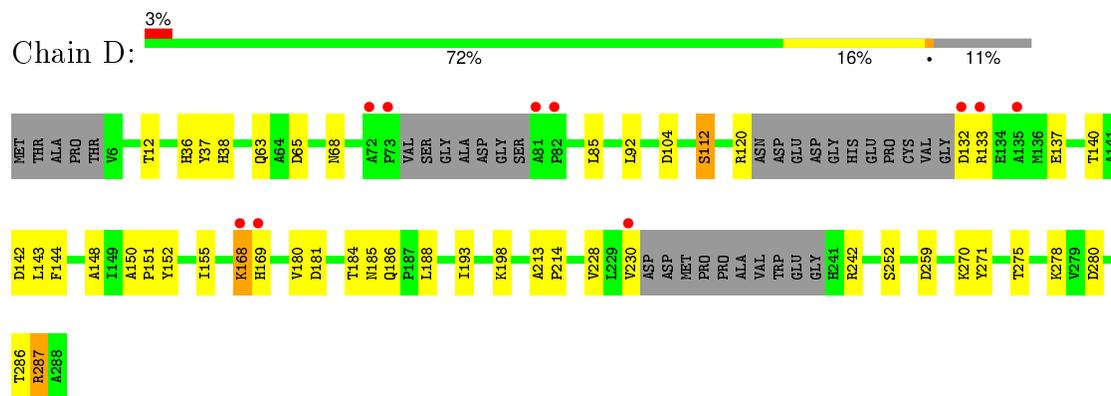
4 Data and refinement statistics (i)

| Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	94.54Å　　103.83Å　　137.04Å 90.00°　　　90.00°　　　90.00°	Depositor
Resolution (Å)	24.50　　–　　2.70 29.45　　–　　2.69	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.50-2.70) 92.7 (29.45-2.69)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.09 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.203　　,　　0.236 0.203　　,　　0.236	Depositor DCC
R_{free} test set	1765 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Outliers	1 of 35454 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8319	wwPDB-VP
Average B, all atoms (Å^2)	28.0	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 29.00 % 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 1.6721e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1] Intensities estimated from amplitudes.
[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CB3, EDO, NDP

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	0.40	0/2019	0.65	5/2750 (0.2%)
1	B	0.46	2/2023 (0.1%)	0.64	6/2755 (0.2%)
1	C	0.40	0/1918	0.62	6/2608 (0.2%)
1	D	0.43	0/1937	0.63	5/2634 (0.2%)
All	All	0.42	2/7897 (0.0%)	0.64	22/10747 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	97	TYR	CE1-CZ	-5.88	1.30	1.38
1	B	97	TYR	CE2-CZ	-5.64	1.31	1.38

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	104	ASP	CB-CG-OD2	6.27	123.94	118.30
1	A	104	ASP	CB-CG-OD2	5.97	123.67	118.30
1	B	104	ASP	CB-CG-OD2	5.95	123.66	118.30
1	D	104	ASP	CB-CG-OD2	5.80	123.52	118.30
1	B	132	ASP	CB-CG-OD2	5.55	123.29	118.30
1	B	231	ASP	CB-CG-OD2	5.53	123.27	118.30
1	D	280	ASP	CB-CG-OD2	5.43	123.19	118.30
1	D	65	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	132	ASP	CB-CG-OD2	5.35	123.12	118.30
1	C	251	ASP	CB-CG-OD2	5.34	123.11	118.30
1	D	142	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	251	ASP	CB-CG-OD2	5.28	123.05	118.30
1	B	142	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	142	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	65	ASP	CB-CG-OD2	5.18	122.96	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	65	ASP	CB-CG-OD2	5.17	122.95	118.30
1	C	259	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	280	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	280	ASP	CB-CG-OD2	5.03	122.82	118.30
1	C	142	ASP	CB-CG-OD2	5.02	122.82	118.30
1	D	259	ASP	CB-CG-OD2	5.01	122.81	118.30
1	A	251	ASP	CB-CG-OD2	5.01	122.81	118.30

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	1980	0	1987	46	0
1	B	1984	0	1990	55	0
1	C	1885	0	1911	36	0
1	D	1903	0	1922	36	0
2	A	48	0	26	1	0
2	B	48	0	26	2	0
2	C	48	0	26	1	0
2	D	48	0	26	2	0
3	A	35	0	21	7	0
3	B	35	0	21	6	0
3	C	35	0	21	4	0
3	D	35	0	21	7	0
4	A	12	0	18	16	0
4	B	4	0	6	7	0
4	D	8	0	12	12	0
5	A	59	0	0	1	0
5	B	42	0	0	1	0
5	C	63	0	0	1	0
5	D	47	0	0	1	0
All	All	8319	0	8034	156	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 10.

All (156) 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:68:ASN:HD22	4:B:1291:EDO:H21	1.17	1.07
1:B:275:THR:HG21	1:D:278:LYS:HB2	1.43	0.99
1:A:278:LYS:HB2	1:C:275:THR:HG21	1.46	0.98
3:A:1290:CB3:H12	1:D:287:ARG:HH21	1.27	0.97
1:C:149:ILE:CD1	4:D:1292:EDO:H21	1.95	0.96
1:D:188:LEU:HD22	4:D:1291:EDO:H21	1.46	0.96
1:B:278:LYS:HB2	1:D:275:THR:HG21	1.49	0.93
1:A:188:LEU:HD22	4:A:1291:EDO:H21	1.53	0.90
1:A:275:THR:HG21	1:C:278:LYS:HB2	1.51	0.89
1:B:68:ASN:ND2	4:B:1291:EDO:H21	1.89	0.86
1:B:12:THR:HA	1:B:36:HIS:HB3	1.56	0.85
3:A:1290:CB3:H12	1:D:287:ARG:NH2	1.93	0.84
1:D:68:ASN:HD22	4:D:1292:EDO:H12	1.42	0.84
3:A:1290:CB3:H13	4:A:1291:EDO:O2	1.77	0.83
1:A:287:ARG:HH21	3:D:1290:CB3:H12	1.43	0.83
1:A:181:ASP:OD2	4:A:1291:EDO:H12	1.79	0.82
1:C:149:ILE:HD11	4:D:1292:EDO:H21	1.65	0.79
1:A:287:ARG:NH2	3:D:1290:CB3:H12	1.97	0.78
1:B:68:ASN:HD22	4:B:1291:EDO:C2	1.96	0.77
4:A:1293:EDO:H21	1:B:203:GLY:CA	2.14	0.77
1:B:287:ARG:HH21	3:C:1290:CB3:H12	1.50	0.76
1:A:186:GLN:O	1:D:287:ARG:NH1	2.21	0.73
1:A:195:THR:CG2	4:A:1293:EDO:H12	2.17	0.73
1:A:242:ARG:NH1	1:A:251:ASP:OD1	2.23	0.72
1:B:17:ARG:NH1	1:B:228:VAL:HG23	2.05	0.72
1:C:168:LYS:H	1:C:168:LYS:HD3	1.53	0.71
1:B:97:TYR:CE1	1:B:102:ARG:HA	2.26	0.71
1:C:12:THR:HA	1:C:36:HIS:HB3	1.74	0.69
1:C:181:ASP:HB3	1:C:184:THR:HG23	1.73	0.69
1:A:287:ARG:NH1	1:D:186:GLN:O	2.26	0.68
4:A:1293:EDO:H21	1:B:203:GLY:HA3	1.74	0.67
1:D:12:THR:HA	1:D:36:HIS:HB3	1.77	0.67
1:C:112:SER:HB2	1:C:143:LEU:HD23	1.77	0.67
1:B:228:VAL:O	1:B:228:VAL:HG23	1.94	0.67
1:A:112:SER:HB2	1:A:143:LEU:HD23	1.74	0.67
1:D:181:ASP:HB3	1:D:184:THR:HG23	1.75	0.66
1:B:112:SER:HB2	1:B:143:LEU:HD23	1.77	0.66
1:A:12:THR:HA	1:A:36:HIS:HB3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1290:CB3:H13	5:C:2057:HOH:O	1.94	0.66
3:B:1290:CB3:H12	1:C:287:ARG:NH2	2.10	0.66
1:D:112:SER:HB2	1:D:143:LEU:HD23	1.79	0.65
1:D:133:ARG:O	1:D:137:GLU:HG2	1.97	0.65
1:A:252:SER:HB3	1:C:271:TYR:CE2	2.32	0.65
1:D:68:ASN:ND2	4:D:1292:EDO:H12	2.12	0.64
3:B:1290:CB3:H12	1:C:287:ARG:HH21	1.63	0.64
1:A:242:ARG:HB3	1:A:250:ARG:HA	1.81	0.63
3:A:1290:CB3:H7	4:A:1291:EDO:H22	1.79	0.63
1:A:288:ALA:HB2	1:D:286:THR:HB	1.82	0.62
1:B:229:LEU:HD11	3:B:1290:CB3:H15	1.81	0.62
1:C:150:ALA:HB3	1:C:151:PRO:HD3	1.82	0.62
1:A:181:ASP:HB3	1:A:184:THR:HG23	1.81	0.61
1:B:97:TYR:CE2	1:B:161:ARG:HB3	2.35	0.61
3:D:1290:CB3:H7	4:D:1291:EDO:H22	1.82	0.61
1:B:287:ARG:NH2	3:C:1290:CB3:H12	2.15	0.61
1:B:287:ARG:NH1	1:C:186:GLN:O	2.31	0.60
1:D:150:ALA:HB3	1:D:151:PRO:HD3	1.83	0.60
3:A:1290:CB3:C7	4:A:1291:EDO:H22	2.31	0.60
1:A:150:ALA:HB3	1:A:151:PRO:HD3	1.84	0.60
1:B:288:ALA:HB2	1:C:286:THR:HB	1.83	0.59
1:B:186:GLN:O	1:C:287:ARG:NH1	2.33	0.59
1:A:149:ILE:HD11	4:B:1291:EDO:H12	1.85	0.59
1:A:271:TYR:CE2	1:C:252:SER:HB3	2.38	0.58
4:A:1293:EDO:H21	1:B:203:GLY:HA2	1.85	0.58
1:A:278:LYS:HB2	1:C:275:THR:CG2	2.29	0.58
1:B:271:TYR:CE2	1:D:252:SER:HB3	2.38	0.58
1:A:195:THR:HG22	4:A:1293:EDO:H12	1.85	0.57
1:B:150:ALA:HB3	1:B:151:PRO:HD3	1.84	0.57
1:C:193:ILE:HD11	1:D:152:TYR:CE2	2.40	0.57
1:D:132:ASP:C	1:D:132:ASP:OD1	2.43	0.57
1:A:206:ARG:HH22	4:A:1292:EDO:H11	1.69	0.56
1:B:149:ILE:HD11	4:B:1291:EDO:H11	1.86	0.56
1:B:181:ASP:HB3	1:B:184:THR:HG23	1.87	0.56
1:A:268:LYS:HG2	1:C:259:ASP:OD2	2.06	0.56
1:B:17:ARG:HH12	1:B:228:VAL:HG23	1.71	0.55
1:B:50:THR:HG21	1:B:54:ARG:HH21	1.73	0.54
1:B:252:SER:HB3	1:D:271:TYR:CE2	2.43	0.54
1:A:149:ILE:CD1	4:B:1291:EDO:H12	2.39	0.53
1:A:278:LYS:CB	1:C:275:THR:HG21	2.30	0.53
1:C:152:TYR:CE2	1:D:193:ILE:HD11	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:THR:CG2	1:B:54:ARG:HH21	2.22	0.52
1:C:149:ILE:HD11	4:D:1292:EDO:C2	2.38	0.52
1:A:13:GLY:HA2	5:A:2058:HOH:O	2.09	0.52
1:A:193:ILE:HD11	1:B:152:TYR:CE2	2.46	0.51
1:B:286:THR:HB	1:C:288:ALA:HB2	1.91	0.50
1:C:140:THR:O	1:C:144:PHE:HB2	2.10	0.50
1:C:68:ASN:HA	1:C:85:LEU:HD22	1.94	0.50
1:B:97:TYR:CE2	1:B:161:ARG:CB	2.94	0.49
2:B:1289:NDP:H41N	3:B:1290:CB3:C7	2.41	0.49
1:A:156:LYS:HE3	1:B:136:MET:HE3	1.93	0.49
1:A:287:ARG:NH2	4:D:1291:EDO:O2	2.39	0.49
1:A:283:TYR:OH	3:A:1290:CB3:O	2.28	0.48
1:A:71:THR:HG23	1:A:88:ARG:NH1	2.28	0.48
1:A:140:THR:O	1:A:144:PHE:HB2	2.14	0.48
1:B:233:MET:HB2	1:B:234:PRO:HD2	1.96	0.48
1:B:140:THR:O	1:B:144:PHE:HB2	2.14	0.47
1:A:156:LYS:HE3	1:B:136:MET:CE	2.44	0.47
1:B:68:ASN:HA	1:B:85:LEU:HD22	1.96	0.47
2:D:1289:NDP:H41N	3:D:1290:CB3:C7	2.44	0.47
1:B:73:PRO:HG3	1:B:81:ALA:O	2.14	0.46
1:A:206:ARG:HH22	4:A:1292:EDO:C1	2.27	0.46
1:D:68:ASN:HD22	4:D:1292:EDO:C1	2.21	0.46
2:D:1289:NDP:H2D	3:D:1290:CB3:C2	2.45	0.46
1:A:275:THR:CG2	1:C:278:LYS:HB2	2.34	0.46
2:A:1289:NDP:H41N	3:A:1290:CB3:C7	2.46	0.45
1:D:140:THR:O	1:D:144:PHE:HB2	2.16	0.45
4:A:1293:EDO:O1	1:B:206:ARG:NE	2.39	0.45
1:D:151:PRO:O	1:D:155:ILE:HG13	2.17	0.45
1:D:168:LYS:HE2	1:D:169:HIS:CE1	2.52	0.45
1:C:193:ILE:HD11	1:D:152:TYR:CD2	2.51	0.45
1:A:17:ARG:NH1	1:A:228:VAL:HG23	2.32	0.44
1:B:258:SER:O	1:B:262:ILE:HD13	2.18	0.44
1:C:119:LEU:O	1:C:120:ARG:C	2.55	0.44
1:D:185:ASN:HB2	5:D:2017:HOH:O	2.18	0.44
4:A:1293:EDO:O1	1:B:203:GLY:HA2	2.18	0.44
1:C:16:LYS:HE3	1:C:40:SER:OG	2.18	0.44
1:C:181:ASP:HB3	1:C:184:THR:CG2	2.46	0.44
1:B:278:LYS:CB	1:D:275:THR:HG21	2.35	0.43
1:D:181:ASP:HB3	1:D:184:THR:CG2	2.46	0.43
1:B:71:THR:HG23	1:B:88:ARG:NH1	2.33	0.43
1:A:18:LEU:HD13	1:A:257:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:VAL:HG12	1:B:35:LEU:HD23	1.99	0.43
2:B:1289:NDP:H2D	3:B:1290:CB3:C2	2.48	0.43
1:C:149:ILE:CD1	4:D:1292:EDO:C2	2.84	0.43
1:D:68:ASN:HA	1:D:85:LEU:HD22	2.01	0.43
1:A:193:ILE:HD11	1:B:152:TYR:CD2	2.54	0.43
3:D:1290:CB3:C7	4:D:1291:EDO:H22	2.48	0.43
4:A:1293:EDO:H22	1:B:206:ARG:HH21	1.83	0.43
1:B:288:ALA:O	1:C:244:LYS:HD2	2.19	0.42
1:D:37:TYR:CE1	1:D:63:GLN:HG2	2.54	0.42
1:D:148:ALA:C	1:D:151:PRO:HD2	2.40	0.42
5:B:2039:HOH:O	3:C:1290:CB3:H13	2.19	0.42
1:B:233:MET:HG3	1:B:237:VAL:HB	2.01	0.42
1:A:152:TYR:CE2	1:B:193:ILE:HD11	2.55	0.42
1:D:36:HIS:CG	1:D:37:TYR:N	2.88	0.42
1:B:213:ALA:N	1:B:214:PRO:CD	2.82	0.42
1:A:68:ASN:HA	1:A:85:LEU:HD22	2.01	0.42
1:D:198:LYS:HD2	1:D:198:LYS:HA	1.90	0.42
3:D:1290:CB3:H13	4:D:1291:EDO:C2	2.51	0.41
1:A:213:ALA:N	1:A:214:PRO:CD	2.82	0.41
1:A:37:TYR:O	1:A:63:GLN:HA	2.20	0.41
1:D:38:HIS:HD2	1:D:63:GLN:NE2	2.18	0.41
1:C:38:HIS:HD2	1:C:63:GLN:NE2	2.19	0.41
1:A:38:HIS:HD2	1:A:63:GLN:NE2	2.19	0.41
1:D:213:ALA:N	1:D:214:PRO:CD	2.84	0.41
1:C:160:HIS:HB2	1:D:120:ARG:NH1	2.36	0.41
4:A:1293:EDO:C2	1:B:203:GLY:HA2	2.51	0.41
2:C:1289:NDP:H41N	3:C:1290:CB3:C7	2.51	0.41
1:B:228:VAL:O	1:B:228:VAL:CG2	2.65	0.41
1:C:72:ALA:O	1:C:73:PRO:C	2.58	0.40
1:B:149:ILE:CD1	4:B:1291:EDO:C2	3.00	0.40
1:A:227:SER:O	1:A:228:VAL:C	2.59	0.40
1:C:37:TYR:O	1:C:63:GLN:HA	2.21	0.40
1:A:238:TRP:CZ2	1:A:242:ARG:HD2	2.57	0.40
1:B:72:ALA:HA	1:B:73:PRO:HD3	1.80	0.40
1:A:152:TYR:CD2	1:B:193:ILE:HD11	2.57	0.40
1:B:213:ALA:HB3	1:B:214:PRO:HD3	2.04	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	259/288 (90%)	241 (93%)	17 (7%)	1 (0%)	39	69
1	B	260/288 (90%)	244 (94%)	14 (5%)	2 (1%)	24	51
1	C	245/288 (85%)	229 (94%)	15 (6%)	1 (0%)	39	69
1	D	247/288 (86%)	233 (94%)	12 (5%)	2 (1%)	24	51
All	All	1011/1152 (88%)	947 (94%)	58 (6%)	6 (1%)	30	59

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	VAL
1	B	180	VAL
1	C	180	VAL
1	D	180	VAL
1	B	228	VAL
1	D	228	VAL

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	206/223 (92%)	195 (95%)	11 (5%)	28	57
1	B	206/223 (92%)	193 (94%)	13 (6%)	22	48
1	C	196/223 (88%)	186 (95%)	10 (5%)	29	59
1	D	198/223 (89%)	191 (96%)	7 (4%)	43	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	806/892 (90%)	765 (95%)	41 (5%)	29 59

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	92	LEU
1	A	112	SER
1	A	132	ASP
1	A	133	ARG
1	A	136	MET
1	A	144	PHE
1	A	168	LYS
1	A	239	GLU
1	A	270	LYS
1	A	287	ARG
1	B	16	LYS
1	B	20	ARG
1	B	92	LEU
1	B	112	SER
1	B	120	ARG
1	B	134	GLU
1	B	136	MET
1	B	144	PHE
1	B	168	LYS
1	B	231	ASP
1	B	233	MET
1	B	239	GLU
1	B	287	ARG
1	C	16	LYS
1	C	92	LEU
1	C	112	SER
1	C	134	GLU
1	C	136	MET
1	C	144	PHE
1	C	168	LYS
1	C	242	ARG
1	C	244	LYS
1	C	287	ARG
1	D	92	LEU
1	D	112	SER
1	D	168	LYS

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Mol	Chain	Res	Type
1	D	230	VAL
1	D	242	ARG
1	D	270	LYS
1	D	287	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	63	GLN
1	A	185	ASN
1	B	38	HIS
1	B	63	GLN
1	B	68	ASN
1	B	185	ASN
1	C	38	HIS
1	C	63	GLN
1	C	169	HIS
1	C	185	ASN
1	D	38	HIS
1	D	63	GLN
1	D	68	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)

14 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	NDP	A	1289	-	42,52,52	1.61	6 (14%)	55,80,80	1.90	5 (9%)
3	CB3	A	1290	-	31,37,37	2.76	12 (38%)	35,51,51	1.83	6 (17%)
4	EDO	A	1291	-	3,3,3	0.36	0	2,2,2	0.19	0
4	EDO	A	1292	-	3,3,3	0.31	0	2,2,2	0.44	0
4	EDO	A	1293	-	3,3,3	0.30	0	2,2,2	0.45	0
2	NDP	B	1289	-	42,52,52	1.63	6 (14%)	55,80,80	1.87	5 (9%)
3	CB3	B	1290	-	31,37,37	2.80	12 (38%)	35,51,51	1.86	7 (20%)
4	EDO	B	1291	-	3,3,3	0.38	0	2,2,2	0.18	0
2	NDP	C	1289	-	42,52,52	1.65	6 (14%)	55,80,80	1.88	8 (14%)
3	CB3	C	1290	-	31,37,37	2.78	11 (35%)	35,51,51	1.81	6 (17%)
2	NDP	D	1289	-	42,52,52	1.64	6 (14%)	55,80,80	1.91	7 (12%)
3	CB3	D	1290	-	31,37,37	2.77	13 (41%)	35,51,51	1.84	7 (20%)
4	EDO	D	1291	-	3,3,3	0.33	0	2,2,2	0.26	0
4	EDO	D	1292	-	3,3,3	0.32	0	2,2,2	0.32	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	NDP	A	1289	-	-	0/30/77/77	0/5/5/5
3	CB3	A	1290	-	-	0/21/28/28	0/3/3/3
4	EDO	A	1291	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1292	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1293	-	-	0/1/1/1	0/0/0/0
2	NDP	B	1289	-	-	0/30/77/77	0/5/5/5
3	CB3	B	1290	-	-	0/21/28/28	0/3/3/3
4	EDO	B	1291	-	-	0/1/1/1	0/0/0/0
2	NDP	C	1289	-	-	0/30/77/77	0/5/5/5
3	CB3	C	1290	-	-	0/21/28/28	0/3/3/3
2	NDP	D	1289	-	-	0/30/77/77	0/5/5/5
3	CB3	D	1290	-	-	0/21/28/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	D	1291	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1292	-	-	0/1/1/1	0/0/0/0

All (72) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1289	NDP	C4N-C5N	-4.64	1.39	1.49
2	B	1289	NDP	C4N-C5N	-4.51	1.39	1.49
2	A	1289	NDP	C4N-C5N	-4.47	1.39	1.49
2	D	1289	NDP	C4N-C5N	-4.43	1.39	1.49
3	B	1290	CB3	C11-C	-2.09	1.45	1.50
3	A	1290	CB3	C11-C	-2.09	1.45	1.50
2	D	1289	NDP	C2N-C3N	2.00	1.39	1.34
3	A	1290	CB3	C4A-C8A	2.05	1.45	1.41
2	C	1289	NDP	C2N-C3N	2.08	1.39	1.34
3	D	1290	CB3	C4A-C8A	2.12	1.46	1.41
3	D	1290	CB3	C12-C11	2.14	1.43	1.39
3	D	1290	CB3	C7-C6	2.21	1.43	1.38
3	C	1290	CB3	C7-C6	2.24	1.43	1.38
2	B	1289	NDP	C2N-C3N	2.27	1.40	1.34
2	A	1289	NDP	C2N-C3N	2.30	1.40	1.34
3	A	1290	CB3	C16-C15	2.33	1.43	1.38
2	D	1289	NDP	C2A-N1A	2.36	1.38	1.33
3	B	1290	CB3	C16-C15	2.39	1.43	1.38
2	B	1289	NDP	C2A-N1A	2.45	1.38	1.33
3	D	1290	CB3	C16-C15	2.48	1.43	1.38
3	D	1290	CB3	C13-C14	2.48	1.44	1.39
3	A	1290	CB3	C13-C14	2.52	1.44	1.39
2	C	1289	NDP	C2A-N1A	2.53	1.38	1.33
3	C	1290	CB3	C13-C14	2.56	1.44	1.39
3	C	1290	CB3	C16-C15	2.57	1.43	1.38
3	B	1290	CB3	C13-C14	2.59	1.44	1.39
2	A	1289	NDP	C2A-N1A	2.67	1.39	1.33
3	A	1290	CB3	C16-C11	2.70	1.43	1.39
3	B	1290	CB3	C16-C11	2.79	1.44	1.39
3	C	1290	CB3	C16-C11	2.96	1.44	1.39
2	C	1289	NDP	C6N-C5N	2.96	1.39	1.33
3	B	1290	CB3	C4-N3	3.02	1.38	1.33
3	D	1290	CB3	C16-C11	3.02	1.44	1.39
3	A	1290	CB3	C5-C6	3.09	1.44	1.37
3	C	1290	CB3	C5-C6	3.09	1.44	1.37
2	B	1289	NDP	C6N-C5N	3.15	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1289	NDP	C6N-C5N	3.19	1.39	1.33
2	D	1289	NDP	C6N-C5N	3.19	1.39	1.33
3	D	1290	CB3	C5-C6	3.22	1.45	1.37
3	B	1290	CB3	C5-C6	3.22	1.45	1.37
3	D	1290	CB3	C4-N3	3.23	1.39	1.33
2	B	1289	NDP	C2A-N3A	3.24	1.37	1.32
3	C	1290	CB3	C4-N3	3.28	1.39	1.33
2	A	1289	NDP	C2A-N3A	3.29	1.38	1.32
3	A	1290	CB3	C4-N3	3.33	1.39	1.33
3	A	1290	CB3	C8-C7	3.42	1.43	1.36
3	B	1290	CB3	C8-C7	3.47	1.43	1.36
2	D	1289	NDP	C2A-N3A	3.51	1.38	1.32
2	C	1289	NDP	C2A-N3A	3.51	1.38	1.32
3	C	1290	CB3	C8-C7	3.57	1.44	1.36
3	D	1290	CB3	C8-C7	3.60	1.44	1.36
3	B	1290	CB3	CA-N	3.72	1.52	1.46
3	B	1290	CB3	C15-C14	4.08	1.47	1.39
3	D	1290	CB3	C15-C14	4.13	1.47	1.39
3	C	1290	CB3	C15-C14	4.15	1.47	1.39
3	A	1290	CB3	C15-C14	4.20	1.47	1.39
3	B	1290	CB3	O4-C4	5.88	1.38	1.24
3	C	1290	CB3	O4-C4	5.97	1.39	1.24
3	D	1290	CB3	O4-C4	6.02	1.39	1.24
3	A	1290	CB3	O4-C4	6.30	1.39	1.24
2	A	1289	NDP	O7N-C7N	6.31	1.40	1.24
3	D	1290	CB3	C9-N10	6.59	1.55	1.46
3	C	1290	CB3	C9-N10	6.62	1.55	1.46
2	B	1289	NDP	O7N-C7N	6.68	1.41	1.24
3	B	1290	CB3	C9-N10	6.70	1.55	1.46
2	C	1289	NDP	O7N-C7N	6.76	1.41	1.24
2	D	1289	NDP	O7N-C7N	6.83	1.41	1.24
3	A	1290	CB3	C9-N10	6.83	1.55	1.46
3	A	1290	CB3	CP1-N10	7.10	1.52	1.46
3	B	1290	CB3	CP1-N10	7.28	1.52	1.46
3	D	1290	CB3	CP1-N10	7.42	1.52	1.46
3	C	1290	CB3	CP1-N10	7.67	1.53	1.46

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1289	NDP	N3A-C2A-N1A	-11.54	120.06	128.89
2	A	1289	NDP	N3A-C2A-N1A	-11.53	120.06	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1289	NDP	N3A-C2A-N1A	-11.28	120.26	128.89
2	C	1289	NDP	N3A-C2A-N1A	-11.05	120.43	128.89
3	B	1290	CB3	N1-C2-N3	-5.28	119.40	127.44
3	A	1290	CB3	N1-C2-N3	-5.27	119.42	127.44
3	D	1290	CB3	N1-C2-N3	-5.15	119.59	127.44
3	C	1290	CB3	N1-C2-N3	-5.15	119.60	127.44
2	D	1289	NDP	PN-O3-PA	-3.59	122.63	132.73
3	D	1290	CB3	CP1-CP2-CP3	-3.34	173.43	177.76
2	C	1289	NDP	PN-O3-PA	-3.20	123.74	132.73
2	D	1289	NDP	C4B-O4B-C1B	-3.13	106.28	109.72
2	A	1289	NDP	C4B-O4B-C1B	-3.10	106.32	109.72
2	A	1289	NDP	PN-O3-PA	-3.10	124.04	132.73
2	C	1289	NDP	C4B-O4B-C1B	-3.01	106.41	109.72
2	B	1289	NDP	PN-O3-PA	-2.84	124.75	132.73
3	C	1290	CB3	CP1-CP2-CP3	-2.72	174.22	177.76
3	B	1290	CB3	CP1-CP2-CP3	-2.69	174.26	177.76
3	A	1290	CB3	CP1-CP2-CP3	-2.68	174.28	177.76
3	A	1290	CB3	C4-C4A-C8A	-2.60	116.01	118.54
2	B	1289	NDP	C3N-C2N-N1N	-2.54	119.50	123.14
2	C	1289	NDP	C3N-C2N-N1N	-2.50	119.55	123.14
3	B	1290	CB3	C4-C4A-C8A	-2.48	116.12	118.54
2	B	1289	NDP	C4B-O4B-C1B	-2.47	107.00	109.72
3	D	1290	CB3	C4-C4A-C8A	-2.40	116.20	118.54
2	D	1289	NDP	C3N-C2N-N1N	-2.35	119.77	123.14
2	D	1289	NDP	C4N-C5N-C6N	-2.27	118.83	122.58
2	D	1289	NDP	C4A-C5A-N7A	-2.26	107.40	109.48
2	C	1289	NDP	C4A-C5A-N7A	-2.16	107.49	109.48
2	C	1289	NDP	C4N-C5N-C6N	-2.08	119.15	122.58
2	A	1289	NDP	C3N-C2N-N1N	-2.02	120.24	123.14
3	D	1290	CB3	C8-C8A-N1	2.03	121.95	118.73
3	B	1290	CB3	C8-C8A-N1	2.15	122.14	118.73
3	C	1290	CB3	C8-C8A-N1	2.18	122.20	118.73
2	C	1289	NDP	O4B-C1B-N9A	2.45	113.22	108.10
3	C	1290	CB3	NA2-C2-N1	2.57	122.73	117.80
3	D	1290	CB3	NA2-C2-N1	2.63	122.84	117.80
2	B	1289	NDP	C5N-C4N-C3N	2.71	119.98	112.52
2	A	1289	NDP	C5N-C4N-C3N	2.76	120.14	112.52
3	A	1290	CB3	NA2-C2-N1	2.77	123.11	117.80
2	C	1289	NDP	C5N-C4N-C3N	2.82	120.29	112.52
2	D	1289	NDP	C5N-C4N-C3N	2.88	120.46	112.52
3	B	1290	CB3	NA2-C2-N1	2.95	123.47	117.80
3	A	1290	CB3	C6-C9-N10	4.01	121.18	114.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	1290	CB3	C6-C9-N10	4.28	121.63	114.51
3	B	1290	CB3	C6-C9-N10	4.35	121.74	114.51
3	D	1290	CB3	C6-C9-N10	4.39	121.81	114.51
3	C	1290	CB3	C4-N3-C2	4.55	122.26	115.94
3	D	1290	CB3	C4-N3-C2	4.72	122.49	115.94
3	B	1290	CB3	C4-N3-C2	4.91	122.76	115.94
3	A	1290	CB3	C4-N3-C2	4.95	122.81	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 53 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1289	NDP	1	0
3	A	1290	CB3	7	0
4	A	1291	EDO	5	0
4	A	1292	EDO	2	0
4	A	1293	EDO	9	0
2	B	1289	NDP	2	0
3	B	1290	CB3	6	0
4	B	1291	EDO	7	0
2	C	1289	NDP	1	0
3	C	1290	CB3	4	0
2	D	1289	NDP	2	0
3	D	1290	CB3	7	0
4	D	1291	EDO	5	0
4	D	1292	EDO	7	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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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^2)	Q<0.9
1	A	265/288 (92%)	-0.40	5 (1%)	70	70	17, 25, 45, 93	1 (0%)
1	B	266/288 (92%)	-0.30	8 (3%)	54	54	17, 26, 51, 67	2 (0%)
1	C	253/288 (87%)	-0.39	10 (3%)	42	41	17, 25, 46, 92	0
1	D	255/288 (88%)	-0.21	10 (3%)	43	43	17, 25, 52, 75	3 (1%)
All	All	1039/1152 (90%)	-0.33	33 (3%)	51	51	17, 25, 51, 93	6 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	ASP	5.1
1	B	132	ASP	4.7
1	A	81	ALA	4.2
1	C	133	ARG	4.2
1	D	132	ASP	3.9
1	C	230	VAL	3.8
1	D	135	ALA	3.7
1	D	72	ALA	3.5
1	D	81	ALA	3.5
1	C	134	GLU	3.4
1	B	120	ARG	3.3
1	D	73	PRO	3.2
1	D	169	HIS	3.2
1	A	133	ARG	3.1
1	D	230	VAL	3.0
1	D	133	ARG	2.9
1	B	81	ALA	2.9
1	C	166	PRO	2.9
1	C	72	ALA	2.7
1	B	73	PRO	2.6
1	A	72	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	72	ALA	2.5
1	C	169	HIS	2.3
1	B	134	GLU	2.2
1	A	73	PRO	2.2
1	D	82	PRO	2.2
1	C	167	ALA	2.1
1	D	168	LYS	2.1
1	B	169	HIS	2.1
1	C	135	ALA	2.1
1	C	81	ALA	2.1
1	C	120	ARG	2.0
1	B	133	ARG	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, 95th 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^2)	Q<0.9
4	EDO	D	1291	4/4	0.95	0.42	9.47	48,49,49,50	0
3	CB3	A	1290	35/35	0.79	0.33	7.61	39,66,82,83	9
3	CB3	C	1290	35/35	0.63	0.48	7.22	50,81,93,93	9
3	CB3	D	1290	35/35	0.61	0.47	5.32	48,64,69,70	9
3	CB3	B	1290	35/35	0.80	0.34	4.26	41,73,89,89	9
4	EDO	A	1293	4/4	0.96	0.20	4.15	50,51,51,51	0
4	EDO	A	1292	4/4	0.96	0.19	3.57	37,39,40,41	0
4	EDO	A	1291	4/4	0.93	0.21	3.31	46,47,47,48	0
4	EDO	B	1291	4/4	0.93	0.17	2.46	24,25,26,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
4	EDO	D	1292	4/4	0.93	0.22	2.25	34,36,37,39	0
2	NDP	A	1289	48/48	0.97	0.14	0.08	26,29,31,33	0
2	NDP	B	1289	48/48	0.97	0.12	0.03	26,29,31,33	0
2	NDP	C	1289	48/48	0.97	0.11	-0.77	26,29,32,33	0
2	NDP	D	1289	48/48	0.96	0.11	-0.80	26,29,32,33	0

6.5 Other polymers (i)

There are no such residues in this entry.