



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:49 AM GMT

PDB ID : 2EGH
Title : Crystal structure of 1-deoxy-D-xylulose 5-phosphate reductoisomerase complexed with a magnesium ion, NADPH and fosmidomycin
Authors : Yajima, S.; Hara, K.; Iino, D.; Sasaki, Y.; Kuzuyama, T.; Seto, H.
Deposited on : 2007-03-01
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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

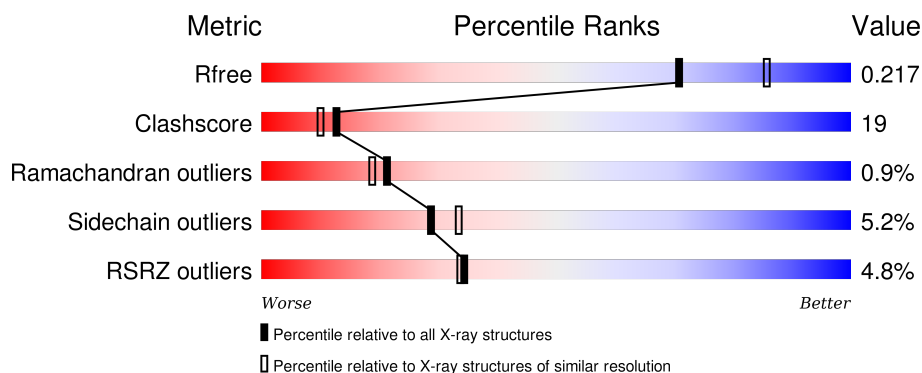
1 Overall quality at a glance

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 ≥ 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	424	
1	B	424	

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
4	NDP	A	3001	-	-	-	X
4	NDP	B	3002	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6482 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	0	0
			3036	1895	536	579	26			
1	B	398	Total	C	N	O	S	0	0	0
			3025	1889	534	576	26			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	CLONING ARTIFACT	UNP P45568
A	-9	ARG	-	CLONING ARTIFACT	UNP P45568
A	-8	GLY	-	CLONING ARTIFACT	UNP P45568
A	-7	SER	-	CLONING ARTIFACT	UNP P45568
A	-6	HIS	-	CLONING ARTIFACT	UNP P45568
A	-5	HIS	-	CLONING ARTIFACT	UNP P45568
A	-4	HIS	-	CLONING ARTIFACT	UNP P45568
A	-3	HIS	-	CLONING ARTIFACT	UNP P45568
A	-2	HIS	-	CLONING ARTIFACT	UNP P45568
A	-1	HIS	-	CLONING ARTIFACT	UNP P45568
A	0	GLY	-	CLONING ARTIFACT	UNP P45568
A	398	SER	-	CLONING ARTIFACT	UNP P45568
A	399	ALA	-	CLONING ARTIFACT	UNP P45568
A	400	CYS	-	CLONING ARTIFACT	UNP P45568
A	401	ASP	-	CLONING ARTIFACT	UNP P45568
A	402	LEU	-	CLONING ARTIFACT	UNP P45568
A	403	GLY	-	CLONING ARTIFACT	UNP P45568
A	404	THR	-	CLONING ARTIFACT	UNP P45568
A	405	PRO	-	CLONING ARTIFACT	UNP P45568
A	406	GLY	-	CLONING ARTIFACT	UNP P45568
A	407	ARG	-	CLONING ARTIFACT	UNP P45568
A	408	PRO	-	CLONING ARTIFACT	UNP P45568
A	409	ALA	-	CLONING ARTIFACT	UNP P45568
A	410	ALA	-	CLONING ARTIFACT	UNP P45568
A	411	LYS	-	CLONING ARTIFACT	UNP P45568

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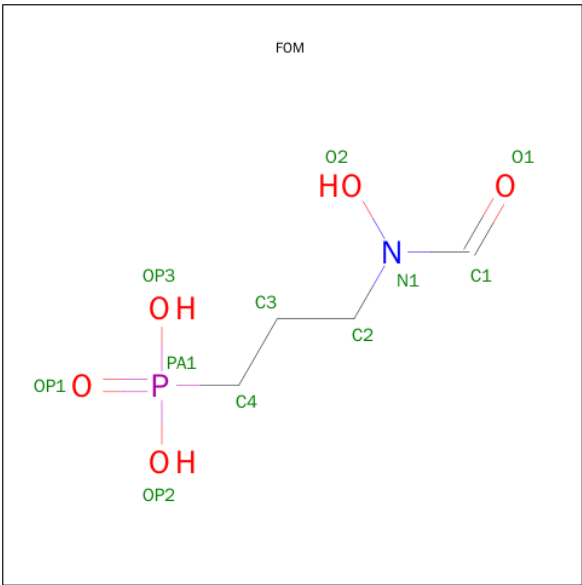
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Chain	Residue	Modelled	Actual	Comment	Reference
A	412	LEU	-	CLONING ARTIFACT	UNP P45568
A	413	ASN	-	CLONING ARTIFACT	UNP P45568
B	-10	MET	-	CLONING ARTIFACT	UNP P45568
B	-9	ARG	-	CLONING ARTIFACT	UNP P45568
B	-8	GLY	-	CLONING ARTIFACT	UNP P45568
B	-7	SER	-	CLONING ARTIFACT	UNP P45568
B	-6	HIS	-	CLONING ARTIFACT	UNP P45568
B	-5	HIS	-	CLONING ARTIFACT	UNP P45568
B	-4	HIS	-	CLONING ARTIFACT	UNP P45568
B	-3	HIS	-	CLONING ARTIFACT	UNP P45568
B	-2	HIS	-	CLONING ARTIFACT	UNP P45568
B	-1	HIS	-	CLONING ARTIFACT	UNP P45568
B	0	GLY	-	CLONING ARTIFACT	UNP P45568
B	398	SER	-	CLONING ARTIFACT	UNP P45568
B	399	ALA	-	CLONING ARTIFACT	UNP P45568
B	400	CYS	-	CLONING ARTIFACT	UNP P45568
B	401	ASP	-	CLONING ARTIFACT	UNP P45568
B	402	LEU	-	CLONING ARTIFACT	UNP P45568
B	403	GLY	-	CLONING ARTIFACT	UNP P45568
B	404	THR	-	CLONING ARTIFACT	UNP P45568
B	405	PRO	-	CLONING ARTIFACT	UNP P45568
B	406	GLY	-	CLONING ARTIFACT	UNP P45568
B	407	ARG	-	CLONING ARTIFACT	UNP P45568
B	408	PRO	-	CLONING ARTIFACT	UNP P45568
B	409	ALA	-	CLONING ARTIFACT	UNP P45568
B	410	ALA	-	CLONING ARTIFACT	UNP P45568
B	411	LYS	-	CLONING ARTIFACT	UNP P45568
B	412	LEU	-	CLONING ARTIFACT	UNP P45568
B	413	ASN	-	CLONING ARTIFACT	UNP P45568

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

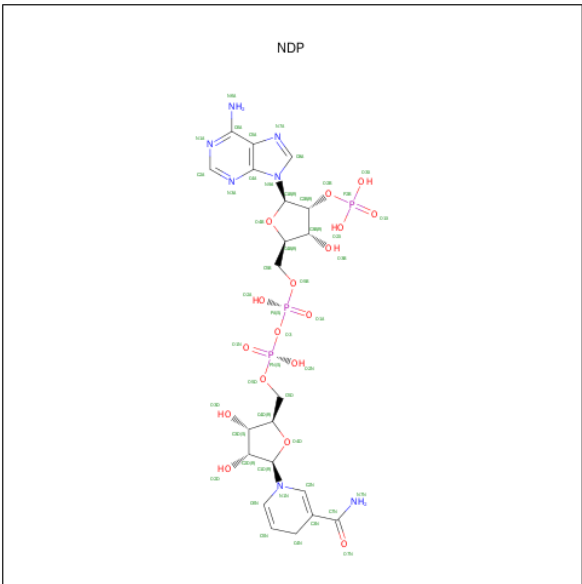
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0

- Molecule 3 is 3-[FORMYL(HYDROXY)AMINO]PROPYLPHOSPHONIC ACID (three-letter code: FOM) (formula: C₄H₁₀NO₅P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			11	4	1	5	1		
3	B	1	Total	C	N	O	P	0	0
			11	4	1	5	1		

- Molecule 4 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



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

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

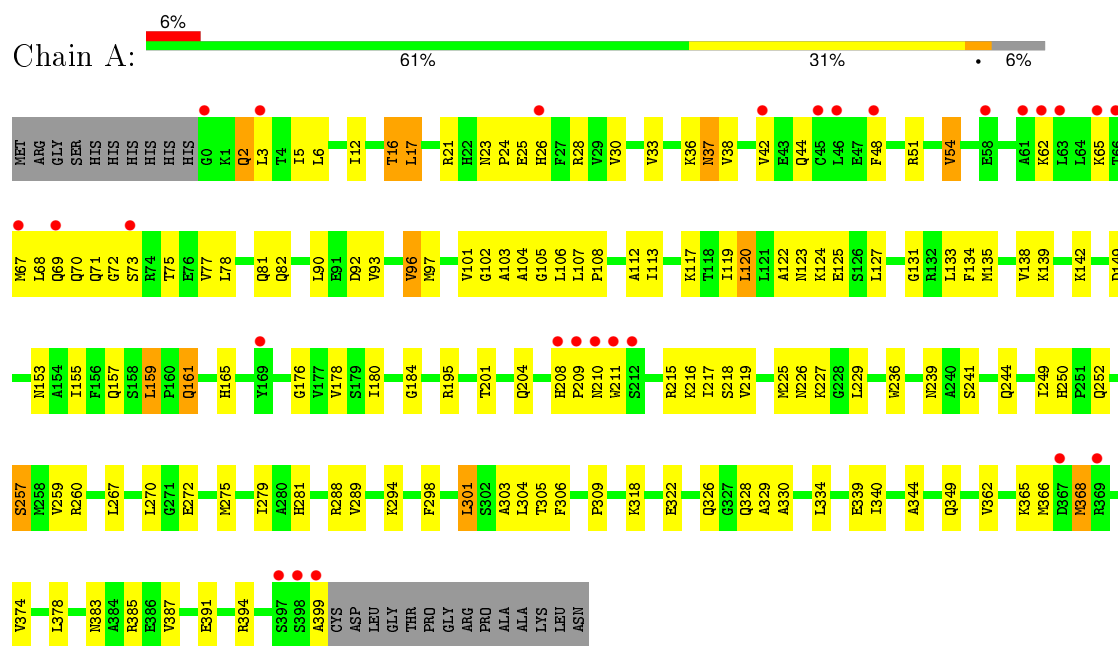
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	150	Total	O	0	0
			150	150		
5	B	151	Total	O	0	0
			151	151		

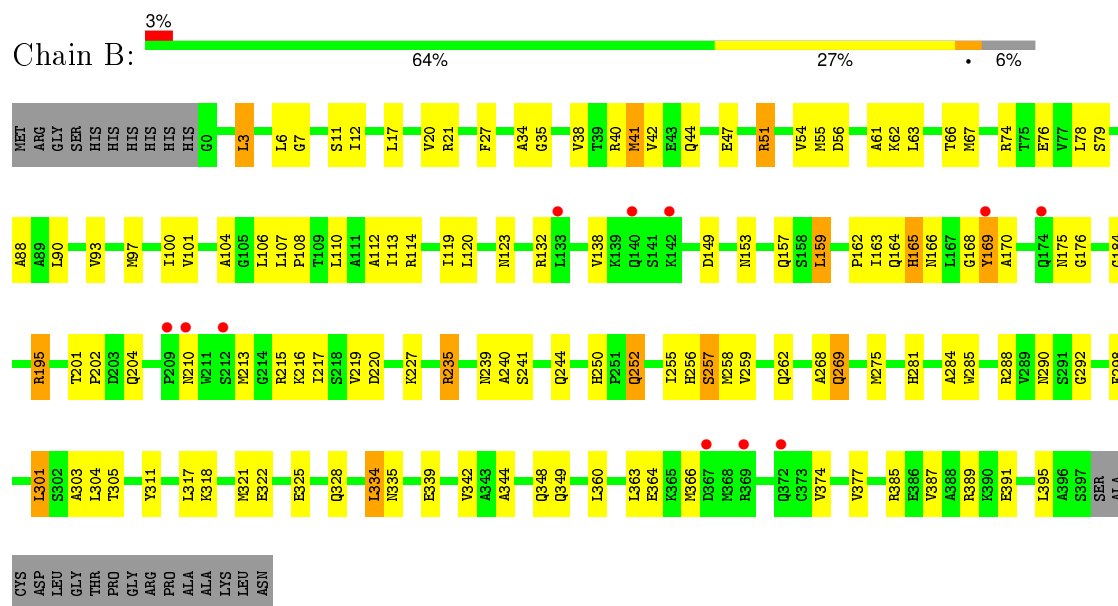
3 Residue-property plots

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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	180.59 Å 59.12 Å 87.05 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.21 – 2.20 47.20 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.4 (47.21-2.20) 98.2 (47.20-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.20 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.225 0.220 , 0.217	Depositor DCC
R_{free} test set	2412 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 88408 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6482	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NDP, MG, FOM

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	0.37	1/3084 (0.0%)	0.60	0/4181
1	B	0.35	0/3073	0.62	1/4166 (0.0%)
All	All	0.36	1/6157 (0.0%)	0.61	1/8347 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	ASN	C-N	5.52	1.46	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	165	HIS	N-CA-C	-5.46	96.26	111.00

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	3036	0	3059	120	0
1	B	3025	0	3049	125	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	11	0	8	0	0
3	B	11	0	7	0	0
4	A	48	0	26	10	0
4	B	48	0	26	19	0
5	A	150	0	0	7	0
5	B	151	0	0	5	0
All	All	6482	0	6175	239	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 19.

All (239) 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:149:ASP:HA	4:B:3002:NDP:H5N	1.40	1.00
1:B:256:HIS:HD2	1:B:269:GLN:HE22	1.13	0.95
1:B:256:HIS:CD2	1:B:269:GLN:HE22	1.91	0.87
1:B:123:ASN:HA	4:B:3002:NDP:O3D	1.79	0.83
1:A:123:ASN:HA	4:A:3001:NDP:O3D	1.81	0.81
1:B:7:GLY:CA	1:B:100:ILE:HD13	2.13	0.79
1:B:241:SER:H	1:B:244:GLN:HE21	1.30	0.79
1:A:12:ILE:O	1:A:16:THR:HG23	1.81	0.79
1:B:159:LEU:HD13	1:B:259:VAL:HG21	1.65	0.79
1:A:159:LEU:HD13	1:A:259:VAL:HG21	1.64	0.78
1:A:73:SER:OG	1:A:75:THR:HG22	1.83	0.77
1:B:201:THR:HG22	1:B:204:GLN:HG3	1.66	0.76
1:A:101:VAL:HG22	1:A:102:GLY:N	2.01	0.75
1:A:149:ASP:HA	4:A:3001:NDP:H5N	1.68	0.75
1:A:107:LEU:HD21	1:A:374:VAL:HG21	1.68	0.74
1:A:249:ILE:HD11	1:A:309:PRO:HB3	1.70	0.72
1:A:303:ALA:HB1	1:B:303:ALA:HB1	1.74	0.70
1:A:184:GLY:HA3	1:A:227:LYS:HE3	1.74	0.69
1:A:33:VAL:HG22	1:A:54:VAL:HG13	1.73	0.69
1:A:155:ILE:HD12	1:A:180:ILE:HG23	1.75	0.68
1:B:275:MET:CE	4:B:3002:NDP:H42N	2.23	0.68
1:A:252:GLN:HE22	1:A:305:THR:H	1.40	0.68
1:B:195:ARG:HH11	1:B:195:ARG:HB3	1.60	0.67
1:A:241:SER:H	1:A:244:GLN:HE21	1.40	0.66
1:A:344:ALA:HA	1:A:349:GLN:HE21	1.61	0.66
1:B:113:ILE:HD12	1:B:138:VAL:HG22	1.79	0.65
1:B:166:ASN:HA	1:B:169:TYR:CZ	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:GLY:HA3	1:B:100:ILE:HD13	1.78	0.65
1:A:298:PHE:HA	1:A:301:LEU:HD22	1.79	0.64
1:A:270:LEU:HD22	1:B:258:MET:HE1	1.78	0.64
1:B:201:THR:HG22	1:B:204:GLN:CG	2.27	0.64
1:A:33:VAL:HG22	1:A:54:VAL:CG1	2.27	0.63
1:A:249:ILE:CD1	1:A:309:PRO:HB3	2.28	0.62
1:B:252:GLN:HE22	1:B:305:THR:H	1.45	0.62
1:B:21:ARG:HD3	1:B:47:GLU:OE2	2.00	0.62
1:B:100:ILE:HD12	4:B:3002:NDP:N3A	2.15	0.62
1:B:164:GLN:NE2	1:B:285:TRP:HE1	1.98	0.61
1:B:298:PHE:HA	1:B:301:LEU:HD22	1.81	0.61
1:B:275:MET:HG3	4:B:3002:NDP:O7N	2.01	0.61
1:A:134:PHE:O	1:A:138:VAL:HG13	2.00	0.61
1:B:63:LEU:O	1:B:67:MET:HG2	2.01	0.61
1:B:252:GLN:NE2	1:B:305:THR:H	1.99	0.60
1:B:201:THR:HG23	1:B:204:GLN:H	1.65	0.60
1:B:255:ILE:HD11	1:B:304:LEU:HD13	1.83	0.60
1:B:3:LEU:HD21	1:B:27:PHE:HB3	1.83	0.59
1:A:101:VAL:CG2	1:A:102:GLY:N	2.64	0.59
1:A:195:ARG:HG3	5:A:3073:HOH:O	2.01	0.59
1:B:7:GLY:CA	1:B:100:ILE:CD1	2.80	0.58
1:B:217:ILE:H	1:B:217:ILE:HD12	1.68	0.58
1:A:252:GLN:NE2	1:A:305:THR:H	2.01	0.58
1:B:54:VAL:HG22	1:B:78:LEU:HB2	1.86	0.57
1:A:101:VAL:HG23	4:A:3001:NDP:H3D	1.86	0.57
1:B:162:PRO:HB2	1:B:175:ASN:ND2	2.20	0.57
1:A:12:ILE:HD13	1:A:122:ALA:HB1	1.87	0.57
1:A:329:ALA:HB1	1:A:368:MET:HE2	1.86	0.57
1:B:387:VAL:O	1:B:391:GLU:HG2	2.04	0.56
1:B:162:PRO:HB2	1:B:175:ASN:HD21	1.69	0.56
1:A:122:ALA:O	4:A:3001:NDP:O4D	2.23	0.56
1:B:100:ILE:HD12	4:B:3002:NDP:C4A	2.35	0.56
1:B:149:ASP:CA	4:B:3002:NDP:H5N	2.25	0.56
1:B:395:LEU:O	1:B:395:LEU:HD13	2.04	0.56
1:A:90:LEU:O	1:A:117:LYS:HE3	2.05	0.56
1:B:41:MET:HG3	1:B:55:MET:SD	2.45	0.56
1:A:123:ASN:CA	4:A:3001:NDP:O3D	2.54	0.56
1:A:2:GLN:HB3	1:A:93:VAL:HA	1.86	0.56
1:B:184:GLY:HA3	1:B:227:LYS:HE3	1.87	0.56
1:B:258:MET:HG2	1:B:268:ALA:HB2	1.86	0.56
1:B:255:ILE:CD1	1:B:304:LEU:HD13	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:LEU:HD22	1:B:258:MET:CE	2.36	0.55
1:A:101:VAL:CG2	4:A:3001:NDP:H3D	2.35	0.55
1:A:67:MET:O	1:A:71:GLN:HG2	2.06	0.55
1:B:40:ARG:O	1:B:44:GLN:HG3	2.06	0.55
1:A:329:ALA:HB3	1:A:368:MET:HG3	1.89	0.55
1:A:161:GLN:HG3	1:A:165:HIS:HD2	1.72	0.55
1:B:344:ALA:HA	1:B:349:GLN:HE21	1.70	0.55
1:A:362:VAL:O	1:A:366:MET:HG2	2.07	0.54
1:A:102:GLY:CA	1:A:125:GLU:HG3	2.38	0.54
1:B:216:LYS:HD2	1:B:342:VAL:HG11	1.89	0.54
1:B:166:ASN:HA	1:B:169:TYR:CE1	2.43	0.54
1:B:235:ARG:NH2	1:B:325:GLU:OE2	2.41	0.54
1:B:7:GLY:N	1:B:100:ILE:CD1	2.70	0.54
1:A:23:ASN:HB3	1:A:26:HIS:CD2	2.43	0.54
1:B:318:LYS:O	1:B:322:GLU:HG3	2.07	0.53
1:B:107:LEU:N	1:B:107:LEU:HD22	2.24	0.53
1:A:3:LEU:HD12	1:A:5:ILE:HD11	1.90	0.53
1:A:340:ILE:HD11	1:A:385:ARG:HG2	1.90	0.53
1:A:107:LEU:CD2	1:A:374:VAL:HG21	2.39	0.53
1:A:155:ILE:HD11	1:A:257:SER:HB3	1.91	0.53
1:A:288:ARG:HB2	1:B:176:GLY:HA3	1.90	0.53
1:A:62:LYS:O	1:A:65:LYS:HB3	2.09	0.53
1:A:101:VAL:CG2	1:A:102:GLY:H	2.22	0.53
1:B:275:MET:HE2	4:B:3002:NDP:H42N	1.92	0.52
1:B:168:GLY:O	1:B:239:ASN:HB2	2.09	0.52
1:B:153:ASN:ND2	1:B:157:GLN:HE21	2.08	0.52
1:A:12:ILE:O	1:A:16:THR:CG2	2.55	0.52
1:A:155:ILE:CD1	1:A:257:SER:HB3	2.39	0.52
1:A:101:VAL:HG22	1:A:102:GLY:H	1.72	0.52
1:A:103:ALA:O	1:A:106:LEU:HB2	2.10	0.52
1:A:241:SER:H	1:A:244:GLN:NE2	2.06	0.51
1:B:258:MET:HE2	1:B:268:ALA:HB2	1.92	0.51
1:A:36:LYS:O	1:A:38:VAL:N	2.42	0.51
1:A:394:ARG:HG2	1:A:399:ALA:HB3	1.92	0.51
1:A:96:VAL:HG11	1:A:112:ALA:HB1	1.90	0.51
1:A:102:GLY:C	1:A:125:GLU:HG3	2.31	0.51
1:B:164:GLN:HE22	1:B:285:TRP:HE1	1.58	0.51
1:A:340:ILE:HD11	1:A:385:ARG:CG	2.42	0.50
1:B:101:VAL:HG23	4:B:3002:NDP:H3D	1.92	0.50
1:B:104:ALA:HB1	4:B:3002:NDP:N6A	2.26	0.50
1:B:90:LEU:O	1:B:93:VAL:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:GLY:N	1:B:100:ILE:HD11	2.27	0.49
1:A:105:GLY:C	1:A:108:PRO:HD2	2.33	0.49
1:B:195:ARG:H	1:B:195:ARG:NH1	2.10	0.49
1:B:290:ASN:ND2	1:B:292:GLY:H	2.09	0.49
1:B:256:HIS:HE1	5:B:3016:HOH:O	1.94	0.49
1:B:201:THR:CG2	1:B:204:GLN:H	2.26	0.49
1:A:3:LEU:H	1:A:3:LEU:HD23	1.78	0.49
1:B:215:ARG:HD3	5:B:3078:HOH:O	2.13	0.49
1:A:215:ARG:O	1:A:219:VAL:HG23	2.13	0.49
1:A:3:LEU:HD23	1:A:3:LEU:N	2.28	0.49
1:B:217:ILE:N	1:B:217:ILE:HD12	2.27	0.48
1:B:201:THR:CG2	1:B:204:GLN:HG3	2.39	0.48
1:A:2:GLN:HG3	1:A:30:VAL:CG2	2.43	0.48
1:B:252:GLN:NE2	1:B:252:GLN:H	2.11	0.48
1:A:217:ILE:HG12	5:A:3079:HOH:O	2.13	0.48
1:A:23:ASN:HB3	1:A:26:HIS:HD2	1.78	0.48
1:B:17:LEU:HA	1:B:20:VAL:HG13	1.96	0.48
1:B:258:MET:HG2	1:B:268:ALA:CB	2.43	0.48
1:B:216:LYS:HE2	1:B:220:ASP:OD1	2.14	0.47
1:A:133:LEU:H	1:A:328:GLN:HE22	1.62	0.47
1:B:112:ALA:HB1	1:B:119:ILE:HD11	1.95	0.47
1:B:114:ARG:HG3	1:B:114:ARG:HH11	1.79	0.47
1:A:3:LEU:CD1	1:A:5:ILE:HD11	2.45	0.47
1:B:97:MET:HA	1:B:120:LEU:HB2	1.97	0.47
1:B:132:ARG:HB3	1:B:328:GLN:NE2	2.28	0.47
1:B:385:ARG:O	1:B:389:ARG:HG3	2.15	0.47
1:B:275:MET:CG	4:B:3002:NDP:O7N	2.63	0.47
1:B:61:ALA:CB	1:B:79:SER:HB3	2.44	0.47
1:B:35:GLY:H	4:B:3002:NDP:P2B	2.38	0.46
1:A:77:VAL:O	1:A:78:LEU:HD23	2.15	0.46
1:A:153:ASN:HD21	1:A:281:HIS:CD2	2.34	0.46
1:B:157:GLN:HG2	1:B:281:HIS:CE1	2.51	0.46
1:A:16:THR:HG21	1:A:97:MET:HG2	1.97	0.46
1:B:256:HIS:CD2	1:B:269:GLN:NE2	2.73	0.46
1:B:107:LEU:HD22	1:B:107:LEU:H	1.80	0.46
1:A:178:VAL:CG2	1:A:260:ARG:HD2	2.46	0.46
1:A:102:GLY:O	1:A:104:ALA:O	2.33	0.46
1:B:153:ASN:HD21	1:B:157:GLN:HE21	1.62	0.46
1:A:225:MET:HE2	1:A:229:LEU:HG	1.96	0.46
1:A:272:GLU:OE2	1:A:294:LYS:HE3	2.16	0.46
1:B:241:SER:H	1:B:244:GLN:NE2	2.05	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:LEU:HD12	1:A:270:LEU:N	2.31	0.46
1:A:135:MET:O	1:A:138:VAL:HG22	2.16	0.46
1:B:112:ALA:HB1	1:B:119:ILE:CD1	2.46	0.46
1:B:215:ARG:O	1:B:219:VAL:HG23	2.16	0.45
1:B:334:LEU:HG	1:B:363:LEU:HD11	1.98	0.45
1:A:127:LEU:HD11	1:A:135:MET:CE	2.47	0.45
1:A:157:GLN:HG2	1:A:281:HIS:CE1	2.52	0.45
1:B:348:GLN:HA	5:B:3074:HOH:O	2.17	0.45
1:B:275:MET:HE1	4:B:3002:NDP:H42N	1.97	0.45
1:A:124:LYS:HE2	1:A:226:ASN:ND2	2.32	0.45
1:A:123:ASN:CB	4:A:3001:NDP:O3D	2.64	0.45
1:B:12:ILE:HD11	4:B:3002:NDP:C7N	2.47	0.45
1:A:96:VAL:HG11	1:A:112:ALA:CB	2.47	0.45
1:B:360:LEU:O	1:B:364:GLU:HG3	2.16	0.45
1:B:100:ILE:CD1	4:B:3002:NDP:N3A	2.80	0.45
1:A:131:GLY:HA3	1:A:236:TRP:CD1	2.52	0.45
1:B:288:ARG:NE	5:B:3109:HOH:O	2.21	0.45
1:A:17:LEU:HG	1:A:48:PHE:CZ	2.52	0.44
1:A:374:VAL:O	1:A:378:LEU:HG	2.18	0.44
1:A:250:HIS:CE1	1:A:252:GLN:HE21	2.35	0.44
1:B:11:SER:HB3	4:B:3002:NDP:O1N	2.17	0.44
1:A:275:MET:CE	4:A:3001:NDP:H42N	2.47	0.44
1:B:7:GLY:N	1:B:100:ILE:HD13	2.33	0.44
1:A:97:MET:HA	1:A:120:LEU:HB2	2.00	0.44
1:B:38:VAL:O	1:B:42:VAL:HG23	2.18	0.44
1:A:3:LEU:HD23	1:A:28:ARG:O	2.17	0.44
1:A:51:ARG:HH11	1:A:51:ARG:HG3	1.81	0.44
1:B:374:VAL:O	1:B:377:VAL:HG22	2.17	0.44
1:A:178:VAL:HG21	1:A:260:ARG:HD2	1.99	0.44
1:A:161:GLN:HG3	1:A:165:HIS:CD2	2.52	0.44
1:A:365:LYS:HE2	1:A:391:GLU:OE2	2.18	0.44
1:B:149:ASP:HA	4:B:3002:NDP:C5N	2.29	0.43
1:B:288:ARG:NH2	5:B:3109:HOH:O	2.51	0.43
1:A:81:GLN:HG3	5:A:3036:HOH:O	2.18	0.43
1:B:163:ILE:HD13	1:B:170:ALA:CB	2.49	0.43
1:A:281:HIS:HE1	5:A:3002:HOH:O	2.01	0.43
1:A:326:GLN:HB2	1:A:330:ALA:CB	2.48	0.43
1:B:339:GLU:OE1	1:B:385:ARG:NH2	2.39	0.43
1:A:82:GLN:HB2	5:A:3034:HOH:O	2.18	0.43
1:B:113:ILE:CD1	1:B:119:ILE:HG13	2.49	0.43
1:B:176:GLY:HA2	1:B:262:GLN:NE2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:HIS:CE1	1:B:252:GLN:HE21	2.37	0.42
1:A:304:LEU:HB2	1:B:304:LEU:HB2	2.01	0.42
1:A:44:GLN:O	1:A:48:PHE:HD1	2.01	0.42
1:A:106:LEU:HD12	1:A:106:LEU:HA	1.92	0.42
1:A:208:HIS:CD2	1:A:218:SER:OG	2.72	0.42
1:A:176:GLY:HA3	1:B:288:ARG:HB2	2.01	0.42
1:A:211:TRP:HZ3	1:A:275:MET:SD	2.43	0.42
1:A:139:LYS:O	1:A:142:LYS:HD2	2.19	0.42
1:A:318:LYS:HE3	1:A:322:GLU:OE1	2.18	0.42
1:B:317:LEU:O	1:B:321:MET:HG3	2.19	0.42
1:A:329:ALA:CB	1:A:368:MET:HE2	2.49	0.42
1:A:70:GLN:C	1:A:72:GLY:H	2.21	0.42
1:A:21:ARG:O	1:A:24:PRO:HD3	2.19	0.42
1:B:107:LEU:HB2	1:B:108:PRO:HD3	2.02	0.42
1:B:132:ARG:HB3	1:B:328:GLN:HE22	1.85	0.42
1:A:216:LYS:HD3	1:A:216:LYS:O	2.19	0.42
1:A:68:LEU:HD13	1:A:75:THR:CG2	2.50	0.42
1:B:62:LYS:O	1:B:66:THR:HG23	2.20	0.42
1:B:88:ALA:HB1	1:B:112:ALA:HB2	2.01	0.41
1:B:61:ALA:HB2	1:B:79:SER:HB3	2.01	0.41
1:B:34:ALA:HB1	4:B:3002:NDP:O2X	2.20	0.41
1:B:123:ASN:CA	4:B:3002:NDP:O3D	2.61	0.41
1:A:102:GLY:O	1:A:125:GLU:HG3	2.20	0.41
1:A:16:THR:HA	1:A:279:ILE:HG21	2.01	0.41
1:A:101:VAL:HB	4:A:3001:NDP:H51N	2.02	0.41
1:A:12:ILE:HD11	4:A:3001:NDP:C2N	2.50	0.41
1:B:256:HIS:O	1:B:257:SER:CB	2.68	0.41
1:B:201:THR:OG1	1:B:202:PRO:HD2	2.21	0.41
1:B:311:TYR:CE1	1:B:318:LYS:HD3	2.55	0.41
1:B:335:ASN:O	1:B:339:GLU:HG3	2.20	0.41
1:A:42:VAL:HA	1:A:68:LEU:HD21	2.01	0.41
1:A:249:ILE:O	1:A:306:PHE:HA	2.21	0.41
1:B:165:HIS:O	1:B:166:ASN:HB2	2.20	0.41
1:B:284:ALA:O	1:B:285:TRP:C	2.59	0.41
1:B:235:ARG:CD	1:B:240:ALA:O	2.69	0.41
1:B:51:ARG:NH1	1:B:76:GLU:OE2	2.53	0.41
1:A:68:LEU:O	1:A:73:SER:HB3	2.21	0.41
1:B:132:ARG:HH11	1:B:132:ARG:HG2	1.85	0.41
1:A:339:GLU:HG2	5:A:3125:HOH:O	2.20	0.41
1:A:383:ASN:O	1:A:387:VAL:HG23	2.21	0.41
1:A:113:ILE:CG1	1:A:119:ILE:HD13	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:THR:OG1	1:A:204:GLN:HG3	2.21	0.41
1:B:255:ILE:HD12	1:B:255:ILE:N	2.35	0.40
1:B:90:LEU:HB2	1:B:93:VAL:HG13	2.03	0.40
1:A:113:ILE:HA	1:A:119:ILE:HD11	2.04	0.40
1:A:92:ASP:OD1	1:A:92:ASP:N	2.52	0.40
1:B:113:ILE:HD13	1:B:119:ILE:HG13	2.04	0.40
1:A:216:LYS:HE3	5:A:3125:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	398/424 (94%)	385 (97%)	9 (2%)	4 (1%)	19	16
1	B	396/424 (93%)	384 (97%)	9 (2%)	3 (1%)	24	22
All	All	794/848 (94%)	769 (97%)	18 (2%)	7 (1%)	21	19

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	ASN
1	B	210	ASN
1	A	257	SER
1	B	257	SER
1	A	37	ASN
1	A	209	PRO
1	B	366	MET

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	328/347 (94%)	311 (95%)	17 (5%)	29	33
1	B	327/347 (94%)	310 (95%)	17 (5%)	29	33
All	All	655/694 (94%)	621 (95%)	34 (5%)	29	33

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	6	LEU
1	A	16	THR
1	A	17	LEU
1	A	25	GLU
1	A	54	VAL
1	A	69	GLN
1	A	96	VAL
1	A	120	LEU
1	A	159	LEU
1	A	161	GLN
1	A	239	ASN
1	A	267	LEU
1	A	289	VAL
1	A	301	LEU
1	A	334	LEU
1	A	368	MET
1	B	3	LEU
1	B	6	LEU
1	B	41	MET
1	B	51	ARG
1	B	56	ASP
1	B	74	ARG
1	B	106	LEU
1	B	110	LEU
1	B	159	LEU
1	B	169	TYR

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Mol	Chain	Res	Type
1	B	195	ARG
1	B	213	MET
1	B	235	ARG
1	B	252	GLN
1	B	269	GLN
1	B	301	LEU
1	B	334	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	123	ASN
1	A	144	GLN
1	A	161	GLN
1	A	164	GLN
1	A	165	HIS
1	A	175	ASN
1	A	208	HIS
1	A	210	ASN
1	A	226	ASN
1	A	239	ASN
1	A	244	GLN
1	A	252	GLN
1	A	256	HIS
1	A	281	HIS
1	A	328	GLN
1	A	349	GLN
1	B	2	GLN
1	B	26	HIS
1	B	69	GLN
1	B	70	GLN
1	B	144	GLN
1	B	152	HIS
1	B	153	ASN
1	B	161	GLN
1	B	164	GLN
1	B	175	ASN
1	B	210	ASN
1	B	244	GLN
1	B	252	GLN
1	B	256	HIS

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Mol	Chain	Res	Type
1	B	262	GLN
1	B	269	GLN
1	B	281	HIS
1	B	290	ASN
1	B	349	GLN
1	B	372	GLN
1	B	383	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	FOM	A	1001	2	8,10,10	1.97	2 (25%)	8,13,13	2.04	2 (25%)
4	NDP	A	3001	-	42,52,52	2.50	13 (30%)	55,80,80	4.25	32 (58%)
3	FOM	B	2001	2	8,10,10	1.95	1 (12%)	8,13,13	2.06	2 (25%)
4	NDP	B	3002	-	42,52,52	2.52	13 (30%)	55,80,80	4.20	32 (58%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FOM	A	1001	2	-	0/6/9/9	0/0/0/0
4	NDP	A	3001	-	-	0/30/77/77	0/5/5/5
3	FOM	B	2001	2	-	0/6/9/9	0/0/0/0
4	NDP	B	3002	-	-	0/30/77/77	0/5/5/5

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	3001	NDP	PN-O2N	-7.88	1.21	1.54
4	B	3002	NDP	PN-O2N	-7.86	1.21	1.54
4	A	3001	NDP	PA-O1A	-5.54	1.30	1.51
4	B	3002	NDP	PA-O1A	-4.98	1.33	1.51
4	B	3002	NDP	P2B-O2X	-3.42	1.42	1.54
4	B	3002	NDP	PN-O1N	-3.07	1.39	1.51
4	A	3001	NDP	P2B-O2X	-2.99	1.44	1.54
4	A	3001	NDP	PN-O1N	-2.58	1.41	1.51
4	A	3001	NDP	O5D-C5D	-2.31	1.35	1.44
4	B	3002	NDP	O5D-C5D	-2.26	1.35	1.44
4	A	3001	NDP	C3D-C4D	-2.06	1.47	1.53
4	B	3002	NDP	C7N-N7N	2.10	1.39	1.33
3	A	1001	FOM	PA1-OP2	2.14	1.60	1.54
4	B	3002	NDP	O4D-C1D	2.86	1.49	1.42
4	A	3001	NDP	O4D-C1D	2.91	1.49	1.42
4	B	3002	NDP	C4N-C5N	3.12	1.55	1.49
4	A	3001	NDP	C4N-C5N	3.14	1.55	1.49
4	B	3002	NDP	O3B-C3B	3.88	1.52	1.43
4	B	3002	NDP	C2D-C3D	3.93	1.64	1.53
4	A	3001	NDP	C2D-C3D	3.94	1.64	1.53
4	A	3001	NDP	O5B-C5B	4.04	1.61	1.44
4	B	3002	NDP	O5B-C5B	4.05	1.61	1.44
4	A	3001	NDP	O3B-C3B	4.08	1.52	1.43
4	A	3001	NDP	O4B-C1B	4.16	1.46	1.41
3	A	1001	FOM	PA1-OP1	4.35	1.60	1.50
4	B	3002	NDP	C3B-C2B	4.64	1.63	1.53
3	B	2001	FOM	PA1-OP1	4.76	1.61	1.50
4	A	3001	NDP	C3B-C2B	4.89	1.64	1.53
4	B	3002	NDP	O4B-C1B	5.35	1.48	1.41

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3002	NDP	O2B-C2B-C3B	-9.25	75.53	111.51
4	A	3001	NDP	O2B-C2B-C3B	-9.15	75.91	111.51
4	A	3001	NDP	C1B-N9A-C4A	-8.12	114.69	126.94
4	B	3002	NDP	C1B-N9A-C4A	-7.87	115.07	126.94
4	A	3001	NDP	C2D-C3D-C4D	-7.87	86.44	102.61
4	B	3002	NDP	O3-PA-O5B	-7.15	83.98	102.94
4	B	3002	NDP	C2D-C3D-C4D	-6.55	89.14	102.61
4	A	3001	NDP	O3-PA-O5B	-6.42	85.90	102.94
4	A	3001	NDP	O2A-PA-O3	-6.17	77.09	105.09
4	B	3002	NDP	O2N-PN-O5D	-6.06	77.91	108.46
4	A	3001	NDP	O2N-PN-O5D	-5.93	78.54	108.46
4	B	3002	NDP	O2A-PA-O3	-5.84	78.60	105.09
4	B	3002	NDP	O4D-C1D-N1N	-4.93	97.66	108.07
4	A	3001	NDP	P2B-O2B-C2B	-4.87	109.88	121.56
4	B	3002	NDP	P2B-O2B-C2B	-4.79	110.08	121.56
4	A	3001	NDP	N3A-C2A-N1A	-4.71	125.29	128.89
4	A	3001	NDP	O4D-C1D-N1N	-4.64	98.27	108.07
4	B	3002	NDP	O3B-C3B-C4B	-4.34	98.05	111.05
4	B	3002	NDP	N3A-C2A-N1A	-4.32	125.59	128.89
4	A	3001	NDP	C4D-O4D-C1D	-4.12	100.45	109.52
4	B	3002	NDP	C4D-O4D-C1D	-4.05	100.60	109.52
4	B	3002	NDP	C3B-C2B-C1B	-4.03	94.94	102.73
4	A	3001	NDP	C3B-C2B-C1B	-3.94	95.11	102.73
4	A	3001	NDP	O3B-C3B-C4B	-3.82	99.60	111.05
4	B	3002	NDP	O4B-C1B-N9A	-3.51	100.74	108.10
4	A	3001	NDP	O4B-C1B-N9A	-3.04	101.73	108.10
3	B	2001	FOM	OP2-PA1-OP1	-3.04	104.62	112.40
3	A	1001	FOM	OP2-PA1-OP1	-2.90	104.99	112.40
4	B	3002	NDP	O3D-C3D-C4D	-2.89	102.37	111.05
4	A	3001	NDP	O2N-PN-O1N	-2.37	99.66	112.53
4	B	3002	NDP	O5D-C5D-C4D	-2.36	100.42	109.12
4	A	3001	NDP	O5D-C5D-C4D	-2.28	100.73	109.12
4	B	3002	NDP	C5D-C4D-C3D	-2.22	106.40	115.21
4	B	3002	NDP	O2N-PN-O1N	-2.21	100.54	112.53
4	B	3002	NDP	O2N-PN-O3	-2.20	95.09	105.09
4	A	3001	NDP	O2N-PN-O3	-2.14	95.39	105.09
4	A	3001	NDP	O3D-C3D-C4D	-2.10	104.75	111.05
4	A	3001	NDP	O3X-P2B-O2X	2.09	115.34	107.38
4	A	3001	NDP	C4N-C5N-C6N	2.13	126.09	122.58
4	B	3002	NDP	O2X-P2B-O1X	2.18	117.60	110.58
4	A	3001	NDP	O2X-P2B-O1X	2.20	117.67	110.58
4	B	3002	NDP	C4N-C5N-C6N	2.25	126.30	122.58
4	B	3002	NDP	O2A-PA-O1A	3.26	130.21	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	3001	NDP	O3D-C3D-C2D	3.26	122.44	111.83
4	B	3002	NDP	O3D-C3D-C2D	3.28	122.50	111.83
4	B	3002	NDP	O5D-PN-O1N	3.30	122.42	109.62
4	A	3001	NDP	O2A-PA-O1A	3.31	130.48	112.53
4	A	3001	NDP	O5D-PN-O1N	3.34	122.58	109.62
4	A	3001	NDP	C2B-C3B-C4B	3.52	110.19	101.85
4	B	3002	NDP	C2B-C3B-C4B	3.59	110.35	101.85
4	A	3001	NDP	O2B-C2B-C1B	3.69	124.39	110.02
4	A	3001	NDP	C2D-C1D-N1N	3.70	123.33	113.34
4	B	3002	NDP	O4B-C1B-C2B	3.71	113.31	106.60
4	B	3002	NDP	O2B-C2B-C1B	3.76	124.67	110.02
4	A	3001	NDP	O4B-C4B-C5B	3.83	123.01	109.32
4	B	3002	NDP	O4B-C4B-C5B	3.85	123.09	109.32
4	B	3002	NDP	C2D-C1D-N1N	3.92	123.92	113.34
3	B	2001	FOM	OP3-PA1-C4	3.94	116.67	106.89
3	A	1001	FOM	OP3-PA1-C4	4.05	116.95	106.89
4	A	3001	NDP	O4B-C1B-C2B	4.14	114.10	106.60
4	B	3002	NDP	O4D-C4D-C5D	4.34	124.84	109.32
4	A	3001	NDP	O4D-C4D-C5D	4.53	125.51	109.32
4	A	3001	NDP	O4D-C4D-C3D	6.27	117.79	105.15
4	B	3002	NDP	O4D-C4D-C3D	7.47	120.20	105.15
4	B	3002	NDP	O3-PN-O5D	9.08	127.03	102.94
4	A	3001	NDP	O3-PN-O5D	9.78	128.89	102.94
4	B	3002	NDP	PN-O3-PA	13.95	171.90	132.73
4	A	3001	NDP	PN-O3-PA	14.77	174.21	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3001	NDP	10	0
4	B	3002	NDP	19	0

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, 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	400/424 (94%)	0.40	27 (6%) 20 20	22, 34, 72, 98	0
1	B	398/424 (93%)	0.04	11 (2%) 56 55	23, 37, 60, 86	0
All	All	798/848 (94%)	0.22	38 (4%) 34 34	22, 35, 66, 98	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	399	ALA	13.4
1	A	398	SER	9.2
1	A	210	ASN	8.1
1	A	212	SER	4.5
1	B	169	TYR	4.5
1	A	209	PRO	4.3
1	A	62	LYS	4.2
1	B	212	SER	4.1
1	A	169	TYR	3.7
1	A	211	TRP	3.7
1	B	367	ASP	3.6
1	B	369	ARG	3.6
1	A	397	SER	3.6
1	A	66	THR	3.3
1	A	208	HIS	3.3
1	A	65	LYS	3.3
1	B	372	GLN	3.2
1	B	209	PRO	3.2
1	A	48	PHE	3.1
1	A	73	SER	3.0
1	A	3	LEU	3.0
1	A	46	LEU	2.9
1	A	63	LEU	2.8
1	A	42	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	142	LYS	2.6
1	B	210	ASN	2.5
1	A	69	GLN	2.5
1	B	174	GLN	2.5
1	B	133	LEU	2.5
1	A	45	CYS	2.4
1	A	67	MET	2.4
1	A	58	GLU	2.4
1	A	26	HIS	2.4
1	A	61	ALA	2.3
1	A	367	ASP	2.2
1	A	0	GLY	2.1
1	B	140	GLN	2.1
1	A	369	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	NDP	B	3002	48/48	0.69	0.31	6.66	56,78,85,85	0
4	NDP	A	3001	48/48	0.70	0.29	2.75	59,81,91,91	0
3	FOM	B	2001	11/11	0.86	0.22	1.47	73,74,75,75	0
3	FOM	A	1001	11/11	0.84	0.24	0.47	75,77,77,78	0
2	MG	A	900	1/1	0.77	0.15	-0.84	65,65,65,65	0
2	MG	B	901	1/1	0.90	0.05	-6.80	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.