



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 03:40 AM GMT

PDB ID : 4I3L
Title : Crystal structure of a metabolic reductase with 6-benzyl-1-hydroxy-4-methylpyridin-2(1H)-one
Authors : Zheng, B.; Yao, Y.; Liu, Z.; Deng, L.; Anglin, J.L.; Jiang, H.; Prasad, B.V.V.; Song, Y.
Deposited on : 2012-11-26
Resolution : 3.29 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

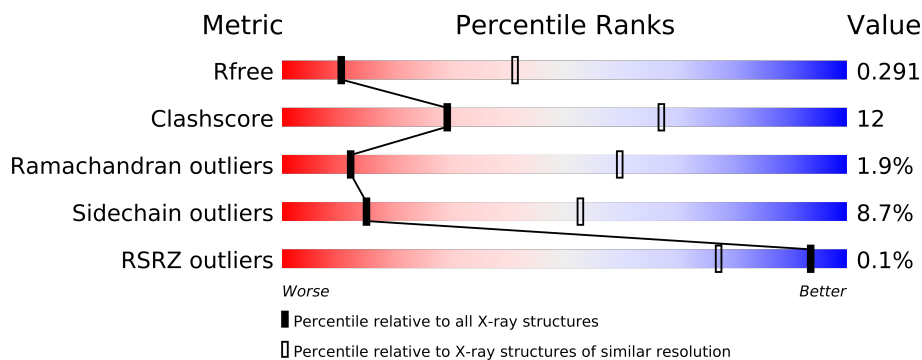
The following versions of software and data (see [references](#)) were used in the production of this report:

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

1 Overall quality at a glance

The reported resolution of this entry is 3.29 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1341 (3.40-3.20)
Clashscore	79885	1696 (3.40-3.20)
Ramachandran outliers	78287	1664 (3.40-3.20)
Sidechain outliers	78261	1662 (3.40-3.20)
RSRZ outliers	66119	1342 (3.40-3.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	414	
1	B	414	

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5888 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

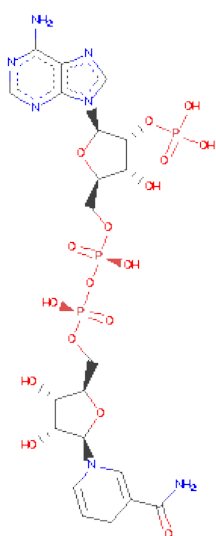
- Molecule 1 is a protein called Isocitrate dehydrogenase [NADP] cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2922	1863	493	549	17			
1	B	358	Total	C	N	O	S	0	0	0
			2844	1814	478	535	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	HIS	ARG	ENGINEERED MUTATION	UNP O75874
B	132	HIS	ARG	ENGINEERED MUTATION	UNP O75874

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



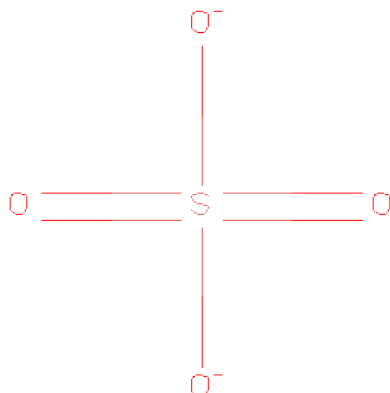
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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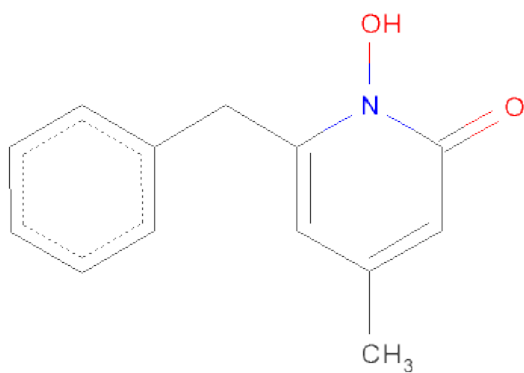
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 6-BENZYL-1-HYDROXY-4-METHYLPYRIDIN-2(1H)-ONE (three-letter code: 1BZ) (formula: C₁₃H₁₃NO₂).



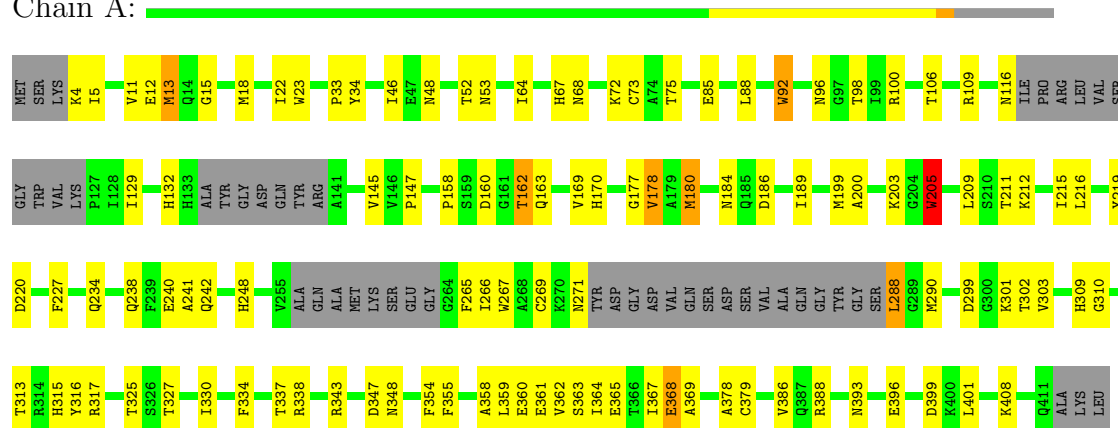
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	16	13	1	2	0	0

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.

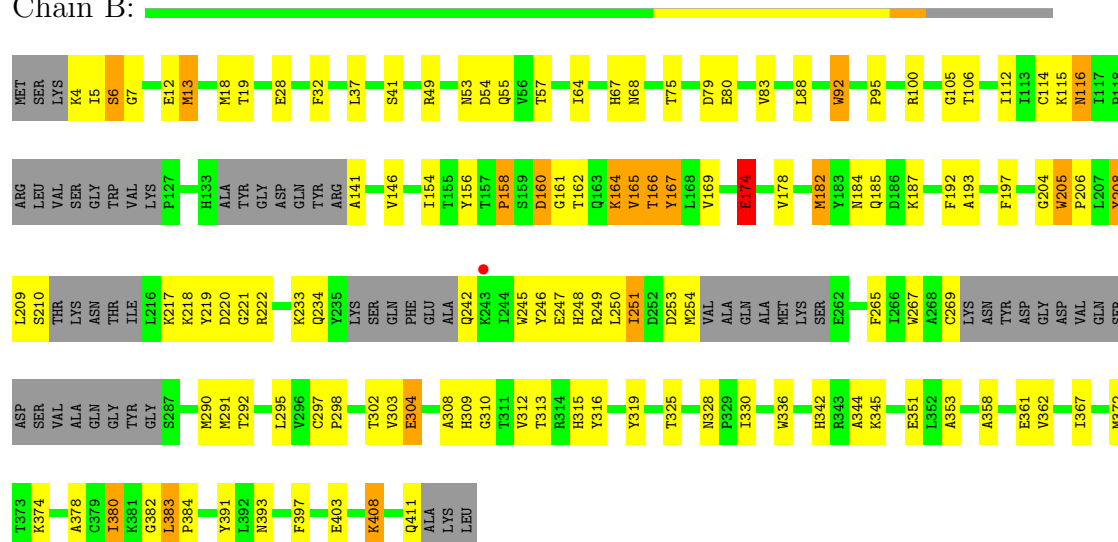
- Molecule 1: Isocitrate dehydrogenase [NADP] cytoplasmic

Chain A:



- Molecule 1: Isocitrate dehydrogenase [NADP] cytoplasmic

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.85Å 80.85Å 304.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.73 – 3.29 45.73 – 3.29	Depositor EDS
% Data completeness (in resolution range)	95.8 (45.73-3.29) 95.8 (45.73-3.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.43 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.293 0.220 , 0.291	Depositor DCC
R_{free} test set	774 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 11.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 15546 reflections	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5888	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, 1BZ, SO4

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	0.61	3/2980 (0.1%)	0.69	0/4012
1	B	0.61	4/2900 (0.1%)	0.68	0/3903
All	All	0.61	7/5880 (0.1%)	0.69	0/7915

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	205	TRP	CD2-CE2	5.87	1.48	1.41
1	B	92	TRP	CD2-CE2	5.61	1.48	1.41
1	B	336	TRP	CD2-CE2	5.37	1.47	1.41
1	A	92	TRP	CD2-CE2	5.29	1.47	1.41
1	B	205	TRP	CD2-CE2	5.14	1.47	1.41
1	A	267	TRP	CD2-CE2	5.10	1.47	1.41
1	B	245	TRP	CD2-CE2	5.03	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2922	0	2899	69	0
1	B	2844	0	2811	75	0
2	A	48	0	26	5	0
2	B	48	0	26	1	0
3	A	10	0	0	0	0
4	A	16	0	13	1	0
All	All	5888	0	5775	143	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (143) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:13:MET:CE	1:B:64:ILE:HD11	1.74	1.16
1:B:13:MET:HE1	1:B:64:ILE:HD11	1.34	1.03
1:B:13:MET:HE3	1:B:64:ILE:HD11	1.53	0.91
1:B:206:PRO:HB2	1:B:208:TYR:HE1	1.45	0.81
1:A:200:ALA:HA	1:A:266:ILE:CD1	2.10	0.81
1:B:83:VAL:HA	1:B:88:LEU:HD12	1.63	0.79
1:A:361:GLU:O	1:A:365:GLU:HG2	1.87	0.73
1:A:325:THR:O	1:A:393:ASN:HB2	1.89	0.72
1:B:18:MET:HB2	1:B:316:TYR:HB2	1.72	0.71
1:B:7:GLY:HA3	1:B:37:LEU:HD23	1.74	0.69
1:B:291:MET:HB3	1:B:308:ALA:HB3	1.76	0.67
1:A:75:THR:H	2:A:501:NDP:H71N	1.40	0.67
1:B:303:VAL:HB	1:B:342:HIS:CD2	2.31	0.65
1:B:13:MET:HE3	1:B:64:ILE:CD1	2.27	0.65
1:B:167:TYR:N	1:B:167:TYR:CD1	2.65	0.64
1:A:288:LEU:C	1:A:290:MET:H	2.01	0.64
1:B:297:CYS:HB3	1:B:298:PRO:HD2	1.81	0.62
1:A:378:ALA:HA	1:A:386:VAL:HG21	1.81	0.62
1:B:164:LYS:O	1:B:166:THR:HG22	2.00	0.62
1:A:330:ILE:HD12	1:A:363:SER:HB3	1.81	0.61
1:A:200:ALA:HA	1:A:266:ILE:HD12	1.82	0.61
1:B:313:THR:OG1	2:B:501:NDP:H51N	2.01	0.60
1:A:334:PHE:O	1:A:338:ARG:HG2	2.01	0.60
1:B:167:TYR:HD1	1:B:167:TYR:H	1.48	0.60
1:A:288:LEU:HD22	1:A:309:HIS:HB3	1.83	0.60
1:A:367:ILE:C	1:A:369:ALA:H	2.05	0.60
1:B:13:MET:CE	1:B:64:ILE:CD1	2.67	0.58
1:A:53:ASN:HA	1:A:92:TRP:CH2	2.38	0.58
1:B:325:THR:O	1:B:393:ASN:HB2	2.04	0.58
1:B:164:LYS:O	1:B:164:LYS:CG	2.51	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:96:ASN:O	1:A:100:ARG:HB2	2.04	0.58
1:A:5:ILE:HD12	1:A:34:TYR:O	2.03	0.58
1:A:162:THR:HG22	1:A:163:GLN:H	1.70	0.57
1:A:158:PRO:HG2	1:A:162:THR:HB	1.86	0.56
1:B:164:LYS:O	1:B:165:VAL:C	2.43	0.56
1:A:177:GLY:O	1:A:178:VAL:HG13	2.05	0.56
1:B:13:MET:HE1	1:B:64:ILE:CD1	2.24	0.56
1:B:403:GLU:OE1	1:B:403:GLU:HA	2.06	0.56
1:A:23:TRP:CD2	1:A:73:CYS:HB2	2.42	0.55
1:A:378:ALA:HA	1:A:386:VAL:CG2	2.36	0.55
1:B:164:LYS:O	1:B:164:LYS:HG3	2.06	0.55
1:B:112:ILE:HD11	1:B:292:THR:OG1	2.06	0.55
1:B:105:GLY:HA3	1:B:297:CYS:HA	1.89	0.54
1:A:337:THR:HG23	1:A:359:LEU:HD23	1.90	0.54
1:A:358:ALA:O	1:A:362:VAL:HG23	2.07	0.54
1:A:75:THR:O	2:A:501:NDP:H2N	2.08	0.54
1:A:211:THR:OG1	1:A:248:HIS:HE1	1.90	0.54
1:B:309:HIS:HD2	1:B:310:GLY:O	1.91	0.54
1:A:367:ILE:O	1:A:369:ALA:N	2.41	0.53
1:B:219:TYR:C	1:B:221:GLY:N	2.60	0.53
1:A:378:ALA:CA	1:A:386:VAL:HG21	2.37	0.53
1:B:5:ILE:HG22	1:B:6:SER:N	2.24	0.53
1:A:313:THR:OG1	2:A:501:NDP:H51N	2.09	0.53
1:A:205:TRP:HB3	1:A:265:PHE:HA	1.91	0.53
1:A:5:ILE:H	1:A:5:ILE:HD12	1.74	0.53
1:A:211:THR:HB	1:A:220:ASP:HB3	1.90	0.53
1:B:67:HIS:O	1:B:68:ASN:HB2	2.10	0.52
1:B:248:HIS:O	1:B:249:ARG:HD2	2.10	0.52
2:A:501:NDP:H42N	4:A:504:1BZ:H5	1.92	0.52
1:A:169:VAL:O	1:A:170:HIS:HB2	2.11	0.51
1:B:304:GLU:HG3	1:B:304:GLU:O	2.10	0.51
1:B:141:ALA:HB2	1:B:182:MET:HG3	1.91	0.51
1:B:154:ILE:HG22	1:B:169:VAL:HG22	1.91	0.51
1:A:367:ILE:C	1:A:369:ALA:N	2.65	0.50
1:B:372:MET:HA	1:B:397:PHE:CE1	2.47	0.50
1:A:48:ASN:O	1:A:52:THR:HG23	2.12	0.50
1:B:247:GLU:OE2	1:B:249:ARG:NH1	2.44	0.49
1:B:351:GLU:CD	1:B:351:GLU:H	2.16	0.49
1:A:309:HIS:HD2	1:A:310:GLY:O	1.95	0.49
1:A:337:THR:CG2	1:A:359:LEU:HD23	2.43	0.49
1:A:18:MET:HB2	1:A:316:TYR:HB2	1.96	0.48
1:A:240:GLU:C	1:A:242:GLN:H	2.16	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:358:ALA:O	1:B:362:VAL:HG23	2.13	0.48
1:A:72:LYS:NZ	2:A:501:NDP:H72N	2.12	0.48
1:B:383:LEU:N	1:B:384:PRO:HD2	2.29	0.48
1:B:68:ASN:HA	1:B:302:THR:HG23	1.96	0.48
1:A:288:LEU:C	1:A:290:MET:N	2.65	0.48
1:B:219:TYR:C	1:B:221:GLY:H	2.18	0.47
1:A:158:PRO:HB2	1:A:160:ASP:OD1	2.14	0.47
1:B:100:ARG:HG2	1:B:295:LEU:HD22	1.96	0.47
1:A:15:GLY:HA2	1:A:75:THR:HG22	1.96	0.47
1:A:13:MET:HG3	1:A:72:LYS:HA	1.97	0.47
1:B:116:ASN:O	1:B:380:ILE:CD1	2.63	0.46
1:B:49:ARG:NH1	1:B:95:PRO:HD3	2.30	0.46
1:B:112:ILE:HD12	1:B:290:MET:O	2.16	0.46
1:B:344:ALA:HB1	1:B:353:ALA:HB2	1.97	0.46
1:B:374:LYS:HD2	1:B:391:TYR:CZ	2.50	0.46
1:A:343:ARG:NE	1:A:347:ASP:OD2	2.49	0.46
1:A:186:ASP:HA	1:A:189:ILE:HD12	1.98	0.46
1:B:53:ASN:HA	1:B:92:TRP:CH2	2.51	0.46
1:A:363:SER:HA	1:A:401:LEU:HD21	1.98	0.45
1:B:79:ASP:O	1:B:83:VAL:HG23	2.17	0.45
1:A:396:GLU:O	1:A:399:ASP:HB2	2.16	0.45
1:B:267:TRP:C	1:B:267:TRP:CD1	2.90	0.45
1:B:53:ASN:O	1:B:55:GLN:N	2.49	0.45
1:B:233:LYS:HG3	1:B:234:GLN:HG3	1.98	0.45
1:B:205:TRP:HB3	1:B:265:PHE:HA	1.99	0.44
1:A:334:PHE:CE2	1:A:360:GLU:HG2	2.52	0.44
1:A:67:HIS:O	1:A:68:ASN:HB2	2.18	0.44
1:A:212:LYS:HD3	1:A:215:ILE:HD12	1.99	0.44
1:B:204:GLY:O	1:B:205:TRP:HD1	2.01	0.44
1:A:355:PHE:O	1:A:358:ALA:HB3	2.18	0.44
1:B:160:ASP:O	1:B:162:THR:HG23	2.18	0.44
1:A:4:LYS:HE2	1:A:33:PRO:O	2.19	0.43
1:B:193:ALA:O	1:B:197:PHE:CD1	2.72	0.43
1:B:251:ILE:H	1:B:251:ILE:HG13	1.55	0.43
1:B:209:LEU:HD12	1:B:210:SER:N	2.34	0.43
1:A:209:LEU:HD22	1:A:227:PHE:CG	2.53	0.43
1:B:328:ASN:OD1	1:B:330:ILE:HG12	2.19	0.43
1:A:216:LEU:HB3	1:A:219:TYR:HB3	2.00	0.43
1:B:206:PRO:HB2	1:B:208:TYR:CE1	2.37	0.42
1:B:378:ALA:O	1:B:382:GLY:N	2.49	0.42
1:B:205:TRP:HA	1:B:206:PRO:HD2	1.83	0.42
1:B:246:TYR:CZ	1:B:247:GLU:O	2.73	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:316:TYR:O	1:B:319:TYR:HB3	2.19	0.42
1:A:299:ASP:C	1:A:301:LYS:H	2.23	0.42
1:A:116:ASN:OD1	1:A:368:GLU:HA	2.18	0.42
1:B:4:LYS:HE2	1:B:32:PHE:O	2.19	0.42
1:A:211:THR:OG1	1:A:248:HIS:CE1	2.71	0.42
1:B:184:ASN:HB2	1:B:219:TYR:OH	2.19	0.42
1:A:13:MET:CE	1:A:64:ILE:HD11	2.50	0.42
1:A:46:ILE:HG13	1:A:88:LEU:HD21	2.01	0.42
1:A:12:GLU:HG2	1:A:13:MET:N	2.34	0.42
1:B:174:GLU:CD	1:B:174:GLU:H	2.23	0.42
1:A:315:HIS:O	1:A:325:THR:HG21	2.20	0.41
1:A:145:VAL:HG23	1:B:218:LYS:HB3	2.01	0.41
1:A:240:GLU:C	1:A:242:GLN:N	2.74	0.41
1:B:361:GLU:OE1	1:B:408:LYS:NZ	2.48	0.41
1:A:354:PHE:C	1:A:354:PHE:CD2	2.92	0.41
1:A:11:VAL:HG21	1:A:64:ILE:HA	2.01	0.41
1:B:154:ILE:HG22	1:B:169:VAL:CG2	2.50	0.41
1:A:85:GLU:OE2	1:A:317:ARG:NH2	2.53	0.41
1:A:234:GLN:O	1:A:238:GLN:NE2	2.54	0.41
1:B:254:MET:H	1:B:254:MET:HG2	1.67	0.41
1:A:68:ASN:HA	1:A:302:THR:HG23	2.01	0.41
1:A:22:ILE:HD11	1:A:327:THR:HB	2.03	0.41
1:B:312:VAL:HG12	1:B:315:HIS:HB2	2.02	0.41
1:A:180:MET:HG2	1:B:219:TYR:CE1	2.56	0.40
1:B:116:ASN:HD21	1:B:367:ILE:HG22	1.86	0.40
1:B:193:ALA:O	1:B:197:PHE:HD1	2.04	0.40
1:B:156:TYR:CE1	1:B:158:PRO:HD3	2.57	0.40
1:B:209:LEU:HD12	1:B:210:SER:H	1.87	0.40
1:A:129:ILE:HD11	1:A:203:LYS:HE3	2.03	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	357/414 (86%)	323 (90%)	29 (8%)	5 (1%)	16	67
1	B	344/414 (83%)	298 (87%)	38 (11%)	8 (2%)	10	54
All	All	701/828 (85%)	621 (89%)	67 (10%)	13 (2%)	12	60

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	54	ASP
1	B	220	ASP
1	A	132	HIS
1	B	161	GLY
1	B	217	LYS
1	A	241	ALA
1	B	158	PRO
1	B	174	GLU
1	B	380	ILE
1	A	368	GLU
1	B	251	ILE
1	A	147	PRO
1	A	162	THR

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	314/350 (90%)	296 (94%)	18 (6%)	29	74
1	B	305/350 (87%)	269 (88%)	36 (12%)	8	34
All	All	619/700 (88%)	565 (91%)	54 (9%)	15	53

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	MET
1	A	98	THR
1	A	106	THR
1	A	109	ARG

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Mol	Chain	Res	Type
1	A	178	VAL
1	A	180	MET
1	A	184	ASN
1	A	199	MET
1	A	205	TRP
1	A	269	CYS
1	A	271	ASN
1	A	288	LEU
1	A	303	VAL
1	A	348	ASN
1	A	364	ILE
1	A	379	CYS
1	A	388	ARG
1	A	408	LYS
1	B	6	SER
1	B	12	GLU
1	B	13	MET
1	B	19	THR
1	B	28	GLU
1	B	41	SER
1	B	57	THR
1	B	75	THR
1	B	80	GLU
1	B	106	THR
1	B	114	CYS
1	B	115	LYS
1	B	116	ASN
1	B	146	VAL
1	B	160	ASP
1	B	164	LYS
1	B	165	VAL
1	B	166	THR
1	B	167	TYR
1	B	174	GLU
1	B	178	VAL
1	B	182	MET
1	B	185	GLN
1	B	187	LYS
1	B	192	PHE
1	B	208	TYR
1	B	222	ARG
1	B	242	GLN

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Mol	Chain	Res	Type
1	B	250	LEU
1	B	253	ASP
1	B	269	CYS
1	B	304	GLU
1	B	345	LYS
1	B	383	LEU
1	B	408	LYS
1	B	411	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	242	GLN
1	A	248	HIS
1	A	309	HIS
1	A	385	ASN
1	B	116	ASN
1	B	132	HIS
1	B	170	HIS
1	B	171	ASN
1	B	309	HIS
1	B	348	ASN
1	B	357	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

5 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	501	-	52,52,52	1.15	5 (9%)	80,80,80	1.50	11 (13%)
3	SO4	A	502	-	4,4,4	0.44	0	6,6,6	0.14	0
3	SO4	A	503	-	4,4,4	0.50	0	6,6,6	0.12	0
4	1BZ	A	504	-	17,17,17	1.68	2 (11%)	21,23,23	1.48	3 (14%)
2	NDP	B	501	-	52,52,52	1.15	6 (11%)	80,80,80	1.42	6 (7%)

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	501	-	-	0/35/77/77	0/3/5/5
3	SO4	A	502	-	-	0/0/0/0	0/0/0/0
3	SO4	A	503	-	-	0/0/0/0	0/0/0/0
4	1BZ	A	504	-	-	0/4/4/4	0/2/2/2
2	NDP	B	501	-	-	0/35/77/77	0/3/5/5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	504	1BZ	O2-N1	-5.37	1.31	1.38
2	B	501	NDP	C6N-C5N	3.77	1.41	1.33
2	A	501	NDP	C5A-C4A	3.54	1.48	1.40
4	A	504	1BZ	C2-N1	3.27	1.38	1.36
2	A	501	NDP	C6N-C5N	3.21	1.40	1.33
2	B	501	NDP	C5A-C4A	3.12	1.47	1.40
2	B	501	NDP	C2N-C3N	2.77	1.40	1.34
2	A	501	NDP	C2N-C3N	2.66	1.39	1.34
2	B	501	NDP	C4A-N9A	-2.63	1.33	1.37
2	A	501	NDP	C4A-N9A	-2.23	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	NDP	O4B-C1B	2.18	1.44	1.41
2	A	501	NDP	C2A-N3A	2.07	1.36	1.32
2	B	501	NDP	C7N-C3N	2.03	1.51	1.47

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NDP	N3A-C4A-N9A	5.33	135.06	125.43
2	B	501	NDP	N3A-C4A-N9A	5.32	135.04	125.43
2	A	501	NDP	N3A-C2A-N1A	-5.22	124.34	128.71
2	B	501	NDP	N3A-C2A-N1A	-4.82	124.68	128.71
4	A	504	1BZ	C2-C6-C10	-4.57	107.01	114.15
2	A	501	NDP	C4A-C5A-N7A	-3.96	106.13	109.52
2	A	501	NDP	O4B-C1B-N9A	3.82	111.99	108.44
2	A	501	NDP	C5A-C4A-N3A	-3.62	117.82	125.70
2	B	501	NDP	PN-O3-PA	-3.52	121.35	131.68
2	B	501	NDP	C1D-N1N-C2N	-3.28	115.43	121.02
2	B	501	NDP	C4A-C5A-N7A	-3.20	106.78	109.52
2	B	501	NDP	C5A-C4A-N3A	-3.18	118.79	125.70
2	A	501	NDP	P2B-O2B-C2B	2.88	128.03	121.96
2	A	501	NDP	PN-O3-PA	-2.72	123.72	131.68
2	A	501	NDP	O2B-P2B-O1X	-2.54	99.70	106.79
4	A	504	1BZ	C3-C4-C5	2.53	120.30	117.94
2	A	501	NDP	C2A-N3A-C4A	2.48	121.07	114.01
4	A	504	1BZ	C6-C2-N1	2.37	121.44	117.97
2	A	501	NDP	C3D-C2D-C1D	2.18	105.69	101.35
2	A	501	NDP	O4B-C1B-C2B	-2.13	104.95	106.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	367/414 (88%)	-0.11	0 100 100	26, 45, 76, 100	0
1	B	358/414 (86%)	-0.10	1 (0%) 91 63	23, 44, 81, 115	0
All	All	725/828 (87%)	-0.11	1 (0%) 93 77	23, 45, 78, 115	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	LYS	2.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	1BZ	A	504	16/16	0.32	1.99	88,94,100,101	0
3	SO4	A	502	5/5	0.27	1.11	89,92,94,96	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NDP	A	501	48/48	0.22	0.31	49,58,79,82	0
2	NDP	B	501	48/48	0.17	-0.38	32,45,69,70	0
3	SO4	A	503	5/5	0.17	-1.77	83,83,86,88	0

6.5 Other polymers ⓘ

There are no such residues in this entry.