



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2016 – 12:00 AM GMT

PDB ID : 7MDH
Title : STRUCTURAL BASIS FOR LIGHT ACITVATION OF A CHLOROPLAST ENZYME. THE STRUCTURE OF SORGHUM NADP-MALATE DEHYDROGENASE IN ITS OXIDIZED FORM
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Deposited on : 1999-02-16
Resolution : 2.40 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

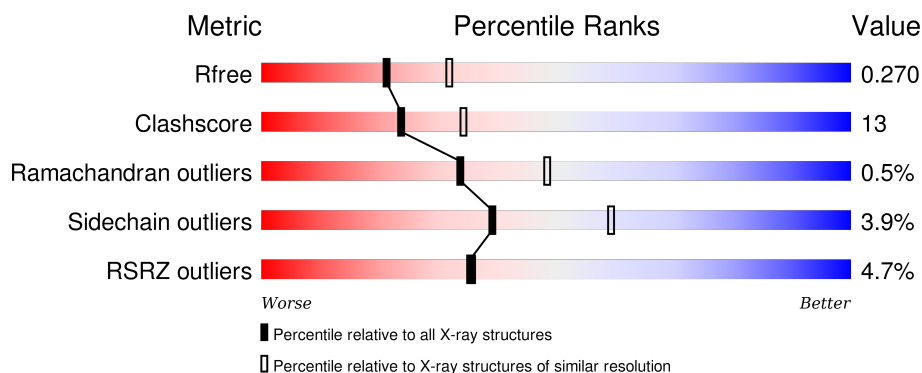
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	375	<div> <div>4%</div> <div>66%</div> <div>25%</div> <div>6%</div> </div>
1	B	375	<div> <div>4%</div> <div>74%</div> <div>20%</div> <div>6%</div> </div>
1	C	375	<div> <div>6%</div> <div>67%</div> <div>25%</div> <div>6%</div> </div>
1	D	375	<div> <div>3%</div> <div>72%</div> <div>20%</div> <div>6%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11132 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 PROTEIN (MALATE DEHYDROGENASE).

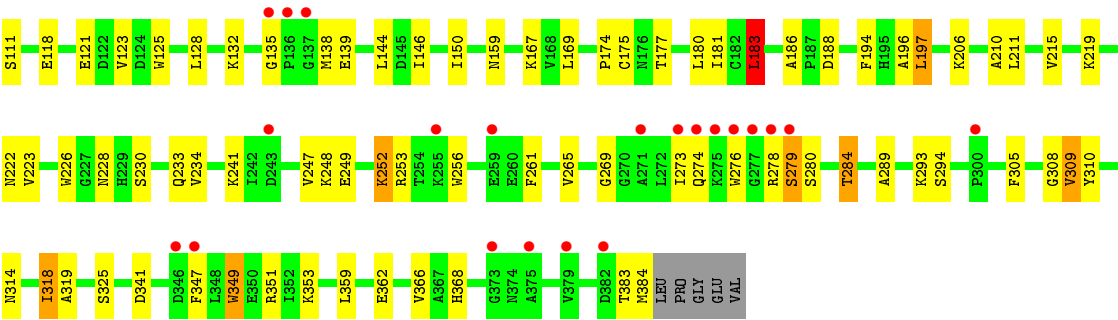
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2688	1708	453	514	13			
1	B	360	Total	C	N	O	S	0	0	0
			2765	1757	467	528	13			
1	C	352	Total	C	N	O	S	0	0	0
			2693	1709	454	517	13			
1	D	352	Total	C	N	O	S	0	0	0
			2704	1718	458	516	12			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

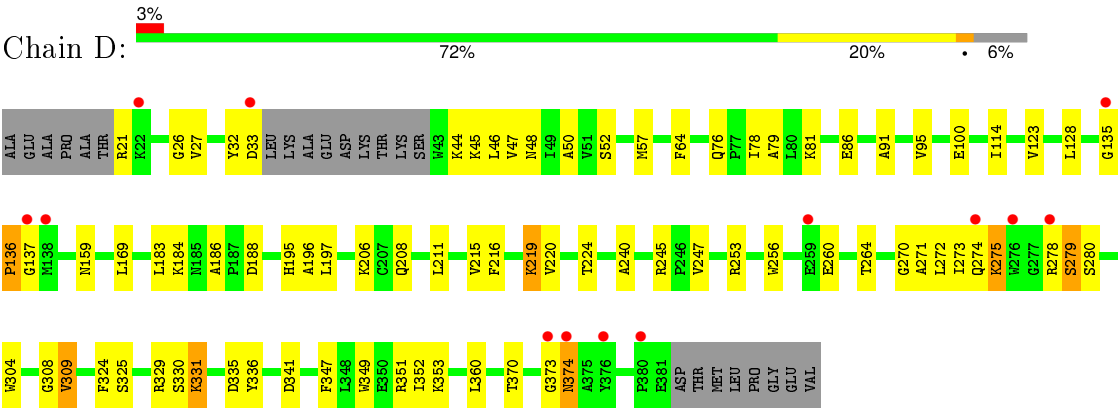
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	5	Total	Zn	0	0
			5	5		
2	A	4	Total	Zn	0	0
			4	4		
2	D	3	Total	Zn	0	0
			3	3		
2	C	5	Total	Zn	0	0
			5	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total	O	0	0
			61	61		
3	B	77	Total	O	0	0
			77	77		
3	C	41	Total	O	0	0
			41	41		
3	D	86	Total	O	0	0
			86	86		



● Molecule 1: PROTEIN (MALATE DEHYDROGENASE)



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	145.42Å 153.94Å 160.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 19.94 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.9 (50.00-2.40) 95.4 (19.94-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.30Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.221 , 0.271 0.221 , 0.270	Depositor DCC
R_{free} test set	2010 reflections (3.02%)	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.5	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 75861 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11132	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 2.49% 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: ZN

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	0.33	0/2740	0.61	1/3715 (0.0%)
1	B	0.36	0/2819	0.62	1/3821 (0.0%)
1	C	0.35	0/2745	0.62	1/3722 (0.0%)
1	D	0.38	0/2757	0.67	3/3737 (0.1%)
All	All	0.35	0/11061	0.63	6/14995 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	331	LYS	N-CA-C	-7.01	92.07	111.00
1	B	183	LEU	CA-CB-CG	6.93	131.25	115.30
1	A	183	LEU	CA-CB-CG	6.66	130.62	115.30
1	C	183	LEU	CA-CB-CG	5.87	128.79	115.30
1	D	183	LEU	CA-CB-CG	5.86	128.77	115.30
1	D	32	TYR	C-N-CA	-5.37	108.29	121.70

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	2688	0	2678	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2765	0	2759	74	0
1	C	2693	0	2678	83	0
1	D	2704	0	2693	63	0
2	A	4	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	1	0
2	D	3	0	0	0	0
3	A	61	0	0	0	0
3	B	77	0	0	2	0
3	C	41	0	0	0	0
3	D	86	0	0	1	0
All	All	11132	0	10808	282	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 13.

All (282) 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:D:278:ARG:HG2	1:D:279:SER:H	1.23	0.99
1:B:138:MET:HE3	1:B:146:ILE:HD12	1.45	0.98
1:D:159:ASN:HD21	1:D:188:ASP:H	1.16	0.90
1:B:278:ARG:HG2	1:B:279:SER:H	1.37	0.90
1:C:27:VAL:O	1:C:30:THR:HG22	1.73	0.89
1:A:278:ARG:HG2	1:A:279:SER:H	1.38	0.89
1:C:159:ASN:HD21	1:C:188:ASP:H	1.20	0.88
1:A:329:ARG:NH1	1:A:339:ALA:HA	1.91	0.86
1:B:175:CYS:HG	2:B:504:ZN:ZN	0.53	0.85
1:C:144:LEU:HD23	1:C:174:PRO:HG2	1.59	0.84
1:C:66:LEU:HD23	1:C:71:VAL:HG21	1.61	0.82
1:A:329:ARG:HH12	1:A:339:ALA:HA	1.43	0.82
1:B:159:ASN:HD21	1:B:188:ASP:H	1.27	0.80
1:C:138:MET:HE3	1:C:146:ILE:HD12	1.63	0.79
1:C:278:ARG:HG2	1:C:279:SER:H	1.47	0.78
1:D:270:GLY:O	1:D:273:ILE:HG12	1.84	0.78
1:D:278:ARG:HG2	1:D:279:SER:N	1.98	0.76
1:B:228:ASN:HB3	1:B:359:LEU:HD21	1.67	0.74
1:B:138:MET:CE	1:B:146:ILE:HD12	2.18	0.74
1:D:159:ASN:ND2	1:D:188:ASP:H	1.86	0.72
1:B:132:LYS:HE3	1:B:132:LYS:HA	1.72	0.71
1:C:230:SER:O	1:C:233:GLN:HG2	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:VAL:HG22	1:B:219:LYS:HD3	1.72	0.70
1:B:48:ASN:HD22	1:B:79:ALA:HB3	1.56	0.70
1:A:50:ALA:HB2	1:A:123:VAL:HG11	1.74	0.69
1:D:245:ARG:HD2	3:D:589:HOH:O	1.91	0.69
1:A:308:GLY:HA2	1:A:325:SER:HA	1.74	0.69
1:B:228:ASN:HB3	1:B:359:LEU:HD11	1.72	0.69
1:D:271:ALA:HA	1:D:274:GLN:HE21	1.57	0.69
1:C:253:ARG:HD2	1:C:256:TRP:HB2	1.73	0.68
1:A:206:LYS:HG2	1:A:223:VAL:HG21	1.74	0.68
1:A:318:ILE:HD13	1:A:319:ALA:N	2.09	0.68
1:A:180:LEU:HA	1:A:183:LEU:HD13	1.75	0.68
1:C:132:LYS:HE3	1:C:150:ILE:HD11	1.75	0.67
1:C:27:VAL:HG22	1:C:100:GLU:HG2	1.76	0.66
1:B:278:ARG:CG	1:B:279:SER:H	2.09	0.65
1:D:272:LEU:HD13	1:D:280:SER:HB3	1.77	0.65
1:B:228:ASN:CB	1:B:359:LEU:HD21	2.25	0.65
1:A:230:SER:O	1:A:233:GLN:HG2	1.96	0.65
1:C:222:ASN:ND2	1:C:241:LYS:HD2	2.10	0.65
1:A:368:HIS:CD2	1:A:369:LEU:HG	2.31	0.65
1:C:206:LYS:HG2	1:C:223:VAL:HG21	1.79	0.64
1:B:308:GLY:HA2	1:B:325:SER:HA	1.79	0.64
1:D:206:LYS:HE3	1:D:220:VAL:O	1.98	0.63
1:C:308:GLY:HA2	1:C:325:SER:HA	1.80	0.63
1:C:314:ASN:CG	1:C:318:ILE:HG22	2.20	0.62
1:C:132:LYS:HD2	1:C:146:ILE:CG2	2.30	0.62
1:A:180:LEU:HA	1:A:183:LEU:CD1	2.29	0.62
1:B:159:ASN:ND2	1:B:188:ASP:H	1.98	0.62
1:C:138:MET:CE	1:C:146:ILE:HD12	2.31	0.61
1:A:183:LEU:HD22	1:A:184:LYS:N	2.14	0.61
1:C:43:TRP:HB3	1:C:77:PRO:HD3	1.81	0.61
1:C:180:LEU:O	1:C:183:LEU:HD13	2.00	0.61
1:C:253:ARG:CD	1:C:256:TRP:HB2	2.30	0.61
1:A:280:SER:O	1:A:284:THR:HG23	2.01	0.61
1:A:278:ARG:HG2	1:A:279:SER:N	2.11	0.60
1:B:159:ASN:HD21	1:B:188:ASP:HB2	1.67	0.60
1:C:278:ARG:HG2	1:C:279:SER:N	2.16	0.60
1:A:82:LEU:HB2	1:A:112:ILE:HG22	1.83	0.60
1:A:278:ARG:CG	1:A:279:SER:H	2.12	0.60
1:C:159:ASN:HD22	1:C:186:ALA:HA	1.67	0.60
1:D:48:ASN:HD22	1:D:79:ALA:HB3	1.66	0.60
1:C:144:LEU:CD2	1:C:174:PRO:HG2	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:330:SER:OG	1:D:331:LYS:O	2.21	0.59
1:B:278:ARG:HG2	1:B:279:SER:N	2.13	0.59
1:B:47:VAL:CG2	1:B:78:ILE:HG22	2.32	0.59
1:B:256:TRP:CD1	1:B:260:GLU:HB2	2.37	0.59
1:D:50:ALA:HB2	1:D:123:VAL:HG11	1.84	0.58
1:C:48:ASN:HB2	1:C:123:VAL:HA	1.86	0.58
1:D:159:ASN:HD22	1:D:186:ALA:CA	2.17	0.58
1:B:50:ALA:HB2	1:B:123:VAL:HG11	1.86	0.58
1:B:132:LYS:HE3	1:B:132:LYS:CA	2.33	0.58
1:B:237:PHE:O	1:B:247:VAL:CG1	2.51	0.58
1:C:132:LYS:HD2	1:C:146:ILE:HG21	1.84	0.58
1:A:139:GLU:H	1:A:139:GLU:CD	2.06	0.58
1:B:284:THR:HG21	3:B:572:HOH:O	2.03	0.58
1:B:159:ASN:HD21	1:B:188:ASP:N	1.99	0.57
1:D:278:ARG:CG	1:D:279:SER:H	2.05	0.57
1:B:180:LEU:HA	1:B:183:LEU:CD1	2.34	0.57
1:C:81:LYS:HD2	1:C:111:SER:OG	2.05	0.57
1:C:159:ASN:HD22	1:C:186:ALA:CA	2.18	0.57
1:D:308:GLY:HA2	1:D:325:SER:HA	1.87	0.56
1:B:21:ARG:HG3	1:B:24:CYS:SG	2.45	0.56
1:B:159:ASN:ND2	1:B:188:ASP:HB2	2.20	0.56
1:B:231:THR:HG23	1:B:383:THR:O	2.05	0.56
1:D:33:ASP:CG	1:D:33:ASP:O	2.44	0.56
1:C:318:ILE:HD13	1:C:319:ALA:N	2.21	0.55
1:C:269:GLY:O	1:C:273:ILE:HG13	2.07	0.55
1:B:246:PRO:O	1:B:249:GLU:HG3	2.06	0.55
1:C:55:ALA:HB2	1:C:92:LEU:CD1	2.37	0.55
1:A:269:GLY:O	1:A:273:ILE:HG12	2.06	0.55
1:C:175:CYS:HB3	1:C:196:ALA:HB1	1.89	0.55
1:D:215:VAL:HG12	1:D:216:PHE:N	2.22	0.55
1:C:175:CYS:HG	2:C:504:ZN:ZN	1.19	0.55
1:B:139:GLU:H	1:B:139:GLU:CD	2.10	0.55
1:C:247:VAL:HG13	1:C:248:LYS:N	2.22	0.55
1:A:314:ASN:CG	1:A:318:ILE:HG22	2.26	0.54
1:A:224:THR:OG1	1:A:304:TRP:NE1	2.40	0.54
1:C:249:GLU:O	1:C:252:LYS:HE3	2.07	0.54
1:B:180:LEU:HA	1:B:183:LEU:HD13	1.89	0.54
1:B:48:ASN:HB2	1:B:123:VAL:HA	1.90	0.54
1:C:46:LEU:HD13	1:C:47:VAL:N	2.23	0.54
1:B:321:ASP:OD2	1:B:363:LYS:NZ	2.33	0.54
1:D:159:ASN:HD22	1:D:186:ALA:HA	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:VAL:O	1:A:30:THR:HG22	2.07	0.53
1:A:338:LEU:HD22	1:A:338:LEU:H	1.72	0.53
1:B:288:ILE:O	1:B:292:ILE:HG13	2.08	0.53
1:D:48:ASN:HB2	1:D:123:VAL:HA	1.89	0.53
1:A:252:LYS:N	1:A:252:LYS:HD2	2.24	0.53
1:A:215:VAL:CG1	1:A:219:LYS:HB2	2.38	0.53
1:D:169:LEU:HD13	1:D:195:HIS:HB2	1.90	0.53
1:C:349:TRP:CH2	1:C:353:LYS:HD3	2.44	0.53
1:C:177:THR:O	1:C:181:ILE:HG13	2.08	0.53
1:C:169:LEU:HB3	1:C:197:LEU:HD21	1.91	0.53
1:B:309:VAL:HG13	3:B:522:HOH:O	2.08	0.53
1:D:159:ASN:HD21	1:D:188:ASP:N	1.96	0.52
1:D:136:PRO:HG2	1:D:137:GLY:H	1.73	0.52
1:D:86:GLU:HG2	1:D:114:ILE:HD12	1.90	0.52
1:C:280:SER:O	1:C:284:THR:HG23	2.09	0.52
1:D:253:ARG:HD3	1:D:256:TRP:HB2	1.92	0.52
1:A:314:ASN:ND2	1:A:318:ILE:O	2.43	0.52
1:A:226:TRP:HA	1:A:325:SER:O	2.10	0.52
1:C:139:GLU:H	1:C:139:GLU:CD	2.13	0.52
1:D:215:VAL:HG13	1:D:219:LYS:NZ	2.25	0.52
1:B:208:GLN:NE2	1:B:208:GLN:HA	2.24	0.52
1:C:55:ALA:HB2	1:C:92:LEU:HD12	1.92	0.52
1:B:183:LEU:HD22	1:B:184:LYS:N	2.26	0.51
1:B:21:ARG:NH1	1:B:21:ARG:HG2	2.24	0.51
1:D:240:ALA:HB3	1:D:247:VAL:HG21	1.92	0.51
1:D:21:ARG:HH11	1:D:21:ARG:HG3	1.75	0.51
1:A:169:LEU:HD12	1:A:169:LEU:N	2.25	0.51
1:A:152:ALA:O	1:A:156:LYS:HG3	2.10	0.51
1:D:335:ASP:CG	1:D:336:TYR:H	2.13	0.51
1:A:27:VAL:HG12	1:B:211:LEU:HB2	1.93	0.51
1:D:197:LEU:O	1:D:197:LEU:HD23	2.11	0.51
1:A:253:ARG:HG2	1:A:256:TRP:HB2	1.92	0.51
1:A:118:GLU:O	1:A:121:GLU:HG2	2.10	0.51
1:B:197:LEU:N	1:B:197:LEU:HD23	2.26	0.50
1:D:33:ASP:O	1:D:33:ASP:OD1	2.30	0.50
1:D:44:LYS:HE2	1:D:76:GLN:OE1	2.11	0.50
1:D:52:SER:OG	1:D:128:LEU:HA	2.11	0.50
1:B:21:ARG:HG2	1:B:21:ARG:HH11	1.77	0.50
1:C:206:LYS:HG2	1:C:223:VAL:CG2	2.41	0.50
1:C:183:LEU:C	1:C:183:LEU:HD22	2.32	0.50
1:C:180:LEU:HA	1:C:183:LEU:CD1	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:THR:O	1:A:181:ILE:HG13	2.12	0.50
1:C:253:ARG:HG2	1:C:256:TRP:H	1.77	0.50
1:D:256:TRP:HA	1:D:260:GLU:HB2	1.94	0.49
1:C:103:LEU:HD13	1:D:206:LYS:HD3	1.95	0.49
1:C:159:ASN:ND2	1:C:188:ASP:H	2.00	0.49
1:A:141:ALA:HA	1:A:144:LEU:HD12	1.95	0.49
1:C:211:LEU:HD13	1:D:27:VAL:HG12	1.93	0.49
1:B:35:LYS:HD3	1:B:35:LYS:C	2.34	0.48
1:D:215:VAL:HG13	1:D:219:LYS:HZ2	1.78	0.48
1:C:351:ARG:HG3	1:C:351:ARG:NH1	2.29	0.48
1:D:329:ARG:HH22	1:D:341:ASP:CG	2.16	0.48
1:B:310:TYR:OH	1:B:321:ASP:OD1	2.29	0.48
1:C:47:VAL:CG2	1:C:78:ILE:HG22	2.43	0.48
1:A:256:TRP:CE3	1:A:257:LEU:HD23	2.48	0.48
1:A:324:PHE:CZ	1:A:352:ILE:HG23	2.49	0.48
1:B:21:ARG:CG	1:B:24:CYS:SG	3.02	0.48
1:A:87:ARG:O	1:A:87:ARG:HG3	2.12	0.48
1:A:351:ARG:HG3	1:A:351:ARG:NH1	2.29	0.48
1:C:118:GLU:O	1:C:121:GLU:HG2	2.14	0.48
1:C:197:LEU:HD23	1:C:197:LEU:N	2.28	0.47
1:C:347:PHE:CE1	1:C:351:ARG:NH2	2.82	0.47
1:C:30:THR:HG21	1:D:215:VAL:O	2.13	0.47
1:C:314:ASN:OD1	1:C:318:ILE:HG22	2.13	0.47
1:C:294:SER:HB3	1:C:305:PHE:CD2	2.49	0.47
1:A:311:THR:HG22	1:A:326:MET:CE	2.44	0.47
1:A:54:ALA:HB3	1:A:92:LEU:HD21	1.96	0.47
1:A:215:VAL:HG13	1:A:219:LYS:HB2	1.97	0.47
1:A:128:LEU:HD13	1:A:154:GLN:NE2	2.30	0.47
1:B:280:SER:O	1:B:284:THR:HG22	2.15	0.47
1:B:298:PRO:HG3	1:B:331:LYS:O	2.15	0.47
1:D:57:MET:HE1	1:D:278:ARG:HD3	1.97	0.47
1:A:103:LEU:HD13	1:B:206:LYS:HD2	1.97	0.47
1:B:351:ARG:HG3	1:B:351:ARG:NH1	2.29	0.47
1:C:228:ASN:HB3	1:C:359:LEU:HD11	1.96	0.46
1:C:210:ALA:HB1	1:C:215:VAL:O	2.15	0.46
1:D:47:VAL:CG2	1:D:78:ILE:HG22	2.45	0.46
1:A:210:ALA:HB1	1:A:215:VAL:O	2.15	0.46
1:A:63:LEU:HD12	1:A:95:VAL:HG11	1.98	0.46
1:B:146:ILE:HD11	1:C:86:GLU:HB3	1.95	0.46
1:A:351:ARG:HG3	1:A:351:ARG:HH11	1.79	0.46
1:C:261:PHE:O	1:C:265:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:THR:O	1:A:314:ASN:HB3	2.16	0.46
1:D:208:GLN:NE2	1:D:264:THR:HG21	2.31	0.46
1:B:91:ALA:O	1:B:95:VAL:HG23	2.16	0.46
1:C:309:VAL:CG1	1:C:310:TYR:N	2.79	0.46
1:D:373:GLY:O	1:D:374:ASN:C	2.54	0.45
1:C:226:TRP:HB2	1:C:234:VAL:HB	1.97	0.45
1:C:89:PHE:O	1:C:93:GLU:HG3	2.16	0.45
1:D:351:ARG:NH1	1:D:351:ARG:HG3	2.31	0.45
1:B:237:PHE:O	1:B:247:VAL:HG11	2.17	0.45
1:B:159:ASN:HD21	1:B:188:ASP:CB	2.29	0.45
1:C:46:LEU:HD13	1:C:46:LEU:C	2.36	0.45
1:C:289:ALA:O	1:C:293:LYS:HG3	2.17	0.45
1:B:54:ALA:HB1	1:B:82:LEU:HB3	1.99	0.45
1:C:159:ASN:ND2	1:C:186:ALA:HA	2.32	0.45
1:C:47:VAL:HG23	1:C:78:ILE:HG22	1.98	0.45
1:B:47:VAL:HG22	1:B:78:ILE:HG22	1.99	0.44
1:D:159:ASN:ND2	1:D:186:ALA:HA	2.32	0.44
1:C:125:TRP:CE3	1:C:167:LYS:HB2	2.52	0.44
1:D:309:VAL:HG21	1:D:336:TYR:CZ	2.52	0.44
1:B:81:LYS:HD2	1:B:111:SER:OG	2.18	0.44
1:B:308:GLY:HA2	1:B:325:SER:CA	2.48	0.44
1:C:183:LEU:HB3	1:C:194:PHE:CG	2.53	0.44
1:D:349:TRP:O	1:D:353:LYS:HG2	2.18	0.44
1:B:118:GLU:O	1:B:121:GLU:HG2	2.18	0.44
1:D:324:PHE:CZ	1:D:352:ILE:HG23	2.53	0.44
1:A:312:THR:HA	1:A:320:GLU:HB3	2.00	0.43
1:D:57:MET:HE3	1:D:278:ARG:HH11	1.82	0.43
1:B:326:MET:HB3	1:B:327:PRO:HD2	2.00	0.43
1:A:174:PRO:O	1:A:178:ASN:ND2	2.51	0.43
1:C:366:VAL:HA	1:C:368:HIS:CE1	2.53	0.43
1:A:247:VAL:HG13	1:A:248:LYS:N	2.33	0.43
1:B:280:SER:O	1:B:284:THR:CG2	2.67	0.43
1:C:159:ASN:HD22	1:C:186:ALA:C	2.21	0.43
1:C:314:ASN:ND2	1:C:318:ILE:HG22	2.32	0.43
1:B:309:VAL:HG21	1:B:336:TYR:CZ	2.53	0.43
1:D:215:VAL:CG1	1:D:216:PHE:N	2.82	0.43
1:C:230:SER:HB2	1:C:383:THR:O	2.19	0.43
1:B:201:ASP:OD2	1:B:229:HIS:NE2	2.52	0.43
1:B:236:ASP:C	1:B:236:ASP:OD1	2.57	0.43
1:C:309:VAL:HG13	1:C:310:TYR:N	2.34	0.43
1:D:184:LYS:HG3	1:D:370:THR:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ASN:CG	1:A:359:LEU:HD21	2.39	0.43
1:C:27:VAL:CG1	1:D:211:LEU:HD13	2.49	0.43
1:A:304:TRP:HB2	1:A:328:CYS:O	2.19	0.43
1:A:203:ASN:HA	1:B:103:LEU:HD11	1.99	0.43
1:B:228:ASN:HB3	1:B:359:LEU:CD1	2.45	0.42
1:A:326:MET:HB3	1:A:327:PRO:HD2	2.01	0.42
1:D:159:ASN:HD22	1:D:186:ALA:C	2.22	0.42
1:A:230:SER:HA	1:A:385:LEU:HG	2.00	0.42
1:C:46:LEU:HD11	1:C:79:ALA:HB2	2.01	0.42
1:D:21:ARG:NH1	1:D:21:ARG:HG3	2.34	0.42
1:C:144:LEU:HD11	1:C:362:GLU:HG2	2.01	0.42
1:B:52:SER:OG	1:B:128:LEU:HA	2.20	0.42
1:C:351:ARG:HG3	1:C:351:ARG:HH11	1.84	0.42
1:A:59:SER:O	1:A:63:LEU:HG	2.19	0.42
1:A:197:LEU:N	1:A:197:LEU:HD23	2.35	0.42
1:A:173:ASN:HA	1:A:174:PRO:C	2.40	0.42
1:A:278:ARG:CG	1:A:279:SER:N	2.77	0.42
1:B:228:ASN:HB3	1:B:359:LEU:CD2	2.42	0.42
1:B:368:HIS:CE1	1:D:275:LYS:NZ	2.88	0.42
1:A:97:MET:HA	1:A:100:GLU:OE2	2.19	0.42
1:A:215:VAL:HG13	1:A:219:LYS:HD3	2.02	0.42
1:A:272:LEU:HD13	1:A:280:SER:HB3	2.02	0.42
1:D:135:GLY:HA3	1:D:136:PRO:HD2	1.94	0.41
1:A:314:ASN:HA	1:A:315:PRO:HD3	1.74	0.41
1:A:324:PHE:HZ	1:A:352:ILE:HG23	1.85	0.41
1:A:115:ASP:HA	1:A:116:PRO:HD2	1.83	0.41
1:A:142:ALA:O	1:A:146:ILE:HG13	2.21	0.41
1:C:276:TRP:HA	1:C:276:TRP:CE3	2.56	0.41
1:D:224:THR:HG1	1:D:304:TRP:HE1	1.68	0.41
1:B:218:ASP:OD1	1:B:219:LYS:HG3	2.19	0.41
1:A:212:LYS:NZ	1:A:253:ARG:HD3	2.36	0.41
1:B:252:LYS:HD2	1:B:252:LYS:N	2.36	0.41
1:A:117:TYR:CE2	1:A:157:ALA:HA	2.56	0.41
1:D:91:ALA:O	1:D:95:VAL:HG23	2.21	0.41
1:B:351:ARG:HG3	1:B:351:ARG:HH11	1.85	0.41
1:C:219:LYS:HB3	1:C:219:LYS:HE2	1.88	0.41
1:C:52:SER:OG	1:C:128:LEU:HA	2.20	0.41
1:B:176:ASN:ND2	1:B:228:ASN:HA	2.36	0.41
1:A:93:GLU:O	1:A:97:MET:HG3	2.20	0.41
1:A:190:PRO:C	1:A:192:LYS:N	2.72	0.41
1:C:341:ASP:N	1:C:341:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:TRP:O	1:B:353:LYS:HG2	2.21	0.41
1:D:45:LYS:HE2	1:D:46:LEU:O	2.21	0.41
1:C:54:ALA:CB	1:C:82:LEU:HB3	2.51	0.41
1:D:196:ALA:HB3	1:D:308:GLY:HA3	2.02	0.41
1:B:253:ARG:HG2	1:B:256:TRP:H	1.86	0.40
1:C:30:THR:HG21	1:D:215:VAL:C	2.41	0.40
1:B:183:LEU:C	1:B:183:LEU:HD22	2.42	0.40
1:A:338:LEU:HD22	1:A:338:LEU:N	2.35	0.40
1:B:272:LEU:O	1:B:276:TRP:HB3	2.21	0.40
1:D:64:PHE:CD1	1:D:64:PHE:N	2.89	0.40
1:D:347:PHE:CE1	1:D:351:ARG:CZ	3.04	0.40
1:D:26:GLY:HA3	1:D:100:GLU:OE2	2.22	0.40
1:A:183:LEU:C	1:A:183:LEU:CD2	2.90	0.40
1:A:309:VAL:O	1:A:323:VAL:HA	2.22	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	347/375 (92%)	323 (93%)	24 (7%)	0	100	100
1	B	356/375 (95%)	337 (95%)	18 (5%)	1 (0%)	46	63
1	C	348/375 (93%)	319 (92%)	27 (8%)	2 (1%)	30	43
1	D	348/375 (93%)	329 (94%)	15 (4%)	4 (1%)	17	25
All	All	1399/1500 (93%)	1308 (94%)	84 (6%)	7 (0%)	34	48

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	136	PRO

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Mol	Chain	Res	Type
1	B	253	ARG
1	D	275	LYS
1	D	374	ASN
1	C	279	SER
1	D	279	SER
1	C	135	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	288/307 (94%)	272 (94%)	16 (6%)	26	41
1	B	297/307 (97%)	284 (96%)	13 (4%)	35	53
1	C	289/307 (94%)	277 (96%)	12 (4%)	36	56
1	D	289/307 (94%)	285 (99%)	4 (1%)	74	88
All	All	1163/1228 (95%)	1118 (96%)	45 (4%)	39	59

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLU
1	A	86	GLU
1	A	183	LEU
1	A	215	VAL
1	A	217	TYR
1	A	252	LYS
1	A	274	GLN
1	A	284	THR
1	A	314	ASN
1	A	318	ILE
1	A	335	ASP
1	A	344	ASN
1	A	360	LEU
1	A	368	HIS
1	A	372	GLU

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Mol	Chain	Res	Type
1	A	382	ASP
1	B	33	ASP
1	B	70	GLU
1	B	132	LYS
1	B	183	LEU
1	B	197	LEU
1	B	228	ASN
1	B	249	GLU
1	B	252	LYS
1	B	274	GLN
1	B	284	THR
1	B	360	LEU
1	B	374	ASN
1	B	384	MET
1	C	70	GLU
1	C	87	ARG
1	C	92	LEU
1	C	183	LEU
1	C	197	LEU
1	C	252	LYS
1	C	274	GLN
1	C	284	THR
1	C	309	VAL
1	C	318	ILE
1	C	349	TRP
1	C	384	MET
1	D	81	LYS
1	D	219	LYS
1	D	309	VAL
1	D	360	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	GLN
1	A	208	GLN
1	A	266	GLN
1	A	368	HIS
1	B	48	ASN
1	B	159	ASN
1	B	208	GLN
1	B	222	ASN

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Mol	Chain	Res	Type
1	B	228	ASN
1	B	266	GLN
1	B	274	GLN
1	B	368	HIS
1	B	374	ASN
1	C	149	GLN
1	C	154	GLN
1	C	159	ASN
1	C	208	GLN
1	C	222	ASN
1	C	266	GLN
1	D	48	ASN
1	D	159	ASN
1	D	208	GLN
1	D	222	ASN
1	D	266	GLN
1	D	274	GLN

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](#)

Of 17 ligands modelled in this entry, 17 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	351/375 (93%)	-0.07	15 (4%) 39 40	19, 39, 80, 98	0
1	B	360/375 (96%)	-0.17	14 (3%) 43 44	17, 31, 77, 100	0
1	C	352/375 (93%)	0.05	24 (6%) 20 20	19, 41, 83, 99	0
1	D	352/375 (93%)	-0.25	13 (3%) 45 46	15, 29, 72, 91	0
All	All	1415/1500 (94%)	-0.11	66 (4%) 35 36	15, 35, 79, 100	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	ARG	6.5
1	B	279	SER	5.9
1	B	276	TRP	5.9
1	B	137	GLY	5.3
1	D	276	TRP	5.0
1	A	278	ARG	4.9
1	C	23	ASP	4.8
1	B	275	LYS	4.7
1	C	278	ARG	4.6
1	A	136	PRO	4.4
1	D	374	ASN	4.4
1	D	135	GLY	4.3
1	C	382	ASP	4.2
1	A	137	GLY	4.2
1	C	276	TRP	4.1
1	B	274	GLN	4.1
1	D	376	TYR	3.9
1	A	135	GLY	3.8
1	C	87	ARG	3.7
1	A	259	GLU	3.7
1	A	87	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	22	LYS	3.6
1	B	373	GLY	3.6
1	A	350	GLU	3.6
1	A	276	TRP	3.5
1	C	273	ILE	3.4
1	B	374	ASN	3.3
1	C	88	SER	3.2
1	A	347	PHE	3.2
1	D	137	GLY	3.2
1	D	380	PRO	3.2
1	C	271	ALA	3.2
1	C	137	GLY	3.2
1	D	373	GLY	3.2
1	B	35	LYS	3.1
1	C	274	GLN	3.1
1	D	274	GLN	3.1
1	D	278	ARG	2.9
1	B	136	PRO	2.9
1	C	279	SER	2.9
1	A	43	TRP	2.8
1	A	279	SER	2.8
1	C	373	GLY	2.7
1	B	135	GLY	2.7
1	C	136	PRO	2.6
1	C	375	ALA	2.6
1	C	135	GLY	2.6
1	C	277	GLY	2.6
1	C	255	LYS	2.5
1	D	22	LYS	2.5
1	D	259	GLU	2.5
1	D	33	ASP	2.5
1	B	272	LEU	2.5
1	A	277	GLY	2.4
1	A	134	ARG	2.3
1	C	300	PRO	2.3
1	C	259	GLU	2.3
1	B	271	ALA	2.2
1	C	379	VAL	2.2
1	D	138	MET	2.1
1	C	275	LYS	2.1
1	A	382	ASP	2.1
1	C	347	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	243	ASP	2.1
1	C	346	ASP	2.1
1	A	274	GLN	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
2	ZN	D	501	1/1	0.95	0.06	-0.87	59,59,59,59	0
2	ZN	A	503	1/1	0.76	0.08	-1.18	100,100,100,100	0
2	ZN	C	501	1/1	0.97	0.05	-2.41	65,65,65,65	0
2	ZN	A	502	1/1	0.98	0.05	-2.85	41,41,41,41	0
2	ZN	B	503	1/1	0.98	0.04	-2.96	76,76,76,76	0
2	ZN	C	505	1/1	0.92	0.07	-	99,99,99,99	0
2	ZN	B	502	1/1	0.97	0.03	-	50,50,50,50	0
2	ZN	B	505	1/1	0.92	0.07	-	65,65,65,65	0
2	ZN	C	502	1/1	0.97	0.03	-	44,44,44,44	0
2	ZN	B	501	1/1	0.99	0.03	-	28,28,28,28	0
2	ZN	C	503	1/1	0.87	0.09	-	100,100,100,100	0
2	ZN	A	501	1/1	0.98	0.04	-	86,86,86,86	0
2	ZN	D	502	1/1	0.94	0.06	-	43,43,43,43	0
2	ZN	C	504	1/1	0.99	0.06	-	67,67,67,67	0
2	ZN	B	504	1/1	0.96	0.06	-	61,61,61,61	0
2	ZN	A	504	1/1	0.97	0.09	-	70,70,70,70	0
2	ZN	D	503	1/1	0.99	0.04	-	28,28,28,28	0

6.5 Other polymers

There are no such residues in this entry.