



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:44 pm GMT

PDB ID : 2HWG
Title : Structure of phosphorylated Enzyme I of the phosphoenolpyruvate:sugar phosphotransferase system
Authors : Lim, K.; Teplyakov, A.; Herzberg, O.
Deposited on : 2006-08-01
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

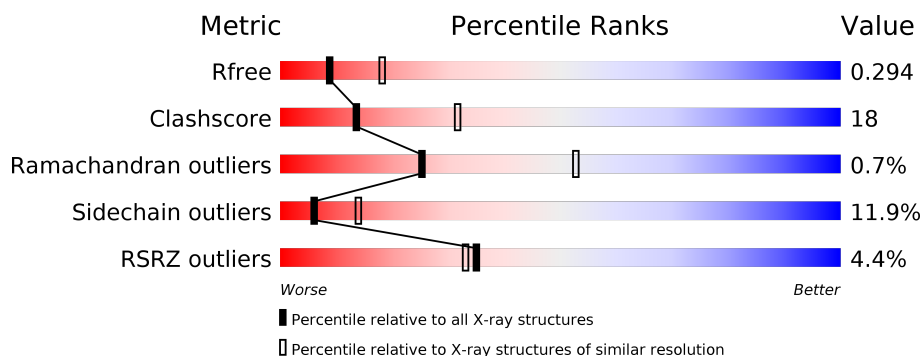
1 Overall quality at a glance

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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (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 $\leq 5\%$. 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	575	
1	B	575	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9102 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 Phosphoenolpyruvate-protein phosphotransferase.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	572	Total	C	N	O	P	S	Se	0	0	0
			4437	2785	756	875	1	3	17			
1	B	572	Total	C	N	O	P	S	Se	0	0	0
			4437	2785	756	875	1	3	17			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	78	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	98	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	189	NEP	HIS	MODIFIED RESIDUE	UNP P08839
A	193	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	239	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	302	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	334	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	345	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	364	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	389	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	392	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	429	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	469	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	477	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	501	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	518	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	525	MSE	MET	MODIFIED RESIDUE	UNP P08839
A	562	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	1	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	78	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	98	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	189	NEP	HIS	MODIFIED RESIDUE	UNP P08839
B	193	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	239	MSE	MET	MODIFIED RESIDUE	UNP P08839

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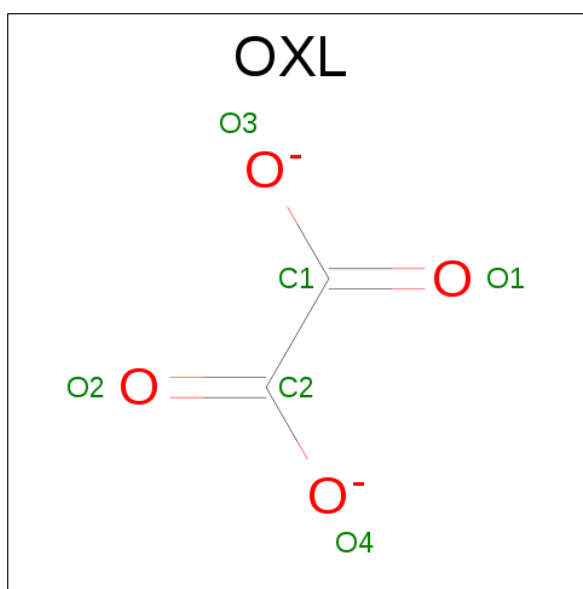
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Chain	Residue	Modelled	Actual	Comment	Reference
B	302	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	334	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	345	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	364	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	389	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	392	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	429	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	469	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	477	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	501	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	518	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	525	MSE	MET	MODIFIED RESIDUE	UNP P08839
B	562	MSE	MET	MODIFIED RESIDUE	UNP P08839

- 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 OXALATE ION (three-letter code: OXL) (formula: C₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 6	C 2	O 4	0	0
3	B	1	Total 6	C 2	O 4	0	0

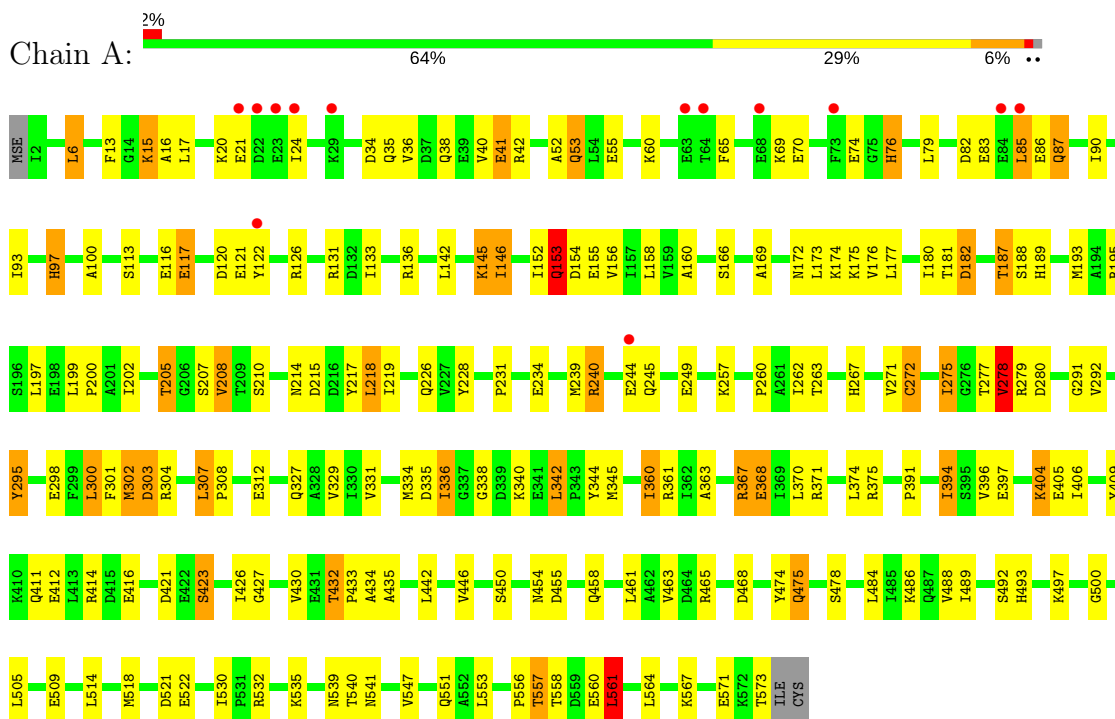
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total 110	O 110	0	0
4	B	104	Total 104	O 104	0	0

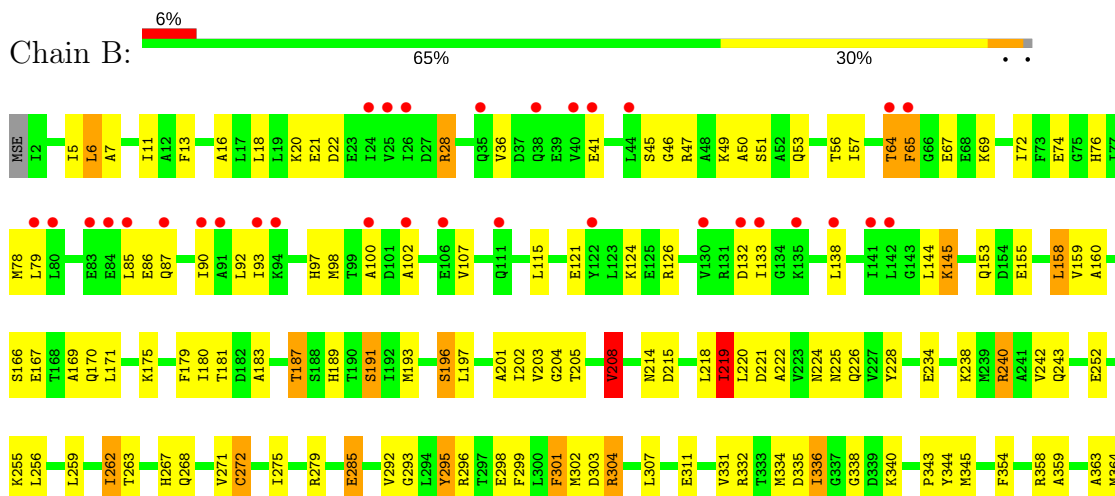
3 Residue-property plots

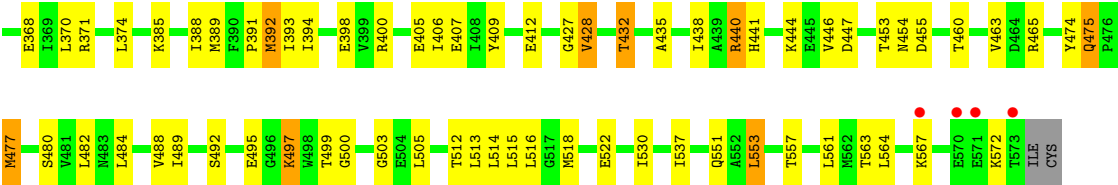
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Phosphoenolpyruvate-protein phosphotransferase



• Molecule 1: Phosphoenolpyruvate-protein phosphotransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.49Å 94.08Å 161.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 47.04 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.70) 99.5 (47.04-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 2.69Å)	Xtriage
Refinement program	CNS, REFMAC	Depositor
R, R_{free}	0.204 , 0.284 0.223 , 0.294	Depositor DCC
R_{free} test set	1798 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9102	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.02% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OXL, MG, NEP

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	0.84	2/4457 (0.0%)	0.90	6/5982 (0.1%)
1	B	0.81	2/4457 (0.0%)	0.87	4/5982 (0.1%)
All	All	0.82	4/8914 (0.0%)	0.88	10/11964 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	285	GLU	CG-CD	7.15	1.62	1.51
1	A	60	LYS	CE-NZ	6.19	1.64	1.49
1	B	272	CYS	CB-SG	-5.56	1.72	1.81
1	A	272	CYS	CB-SG	-5.24	1.73	1.81

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	561	LEU	CA-CB-CG	10.50	139.44	115.30
1	B	262	ILE	CG1-CB-CG2	-7.79	94.27	111.40
1	B	219	ILE	CG1-CB-CG2	-6.35	97.42	111.40
1	B	208	VAL	CB-CA-C	-5.57	100.83	111.40
1	A	182	ASP	CB-CG-OD1	5.49	123.24	118.30
1	A	278	VAL	CB-CA-C	-5.46	101.03	111.40
1	A	300	LEU	CA-CB-CG	5.32	127.54	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	414	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	B	400	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	338	GLY	N-CA-C	-5.04	100.50	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	338	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4437	0	4492	171	0
1	B	4437	0	4492	151	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
4	A	110	0	0	12	0
4	B	104	0	0	5	0
All	All	9102	0	8984	319	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 18.

All (319) 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:A:345:MSE:CE	1:A:345:MSE:SE	2.14	1.46
1:A:169:ALA:HA	1:A:193:MSE:HE1	1.25	1.09
1:A:342:LEU:HD13	1:A:345:MSE:HG2	1.38	1.05
1:B:432:THR:HG22	1:B:435:ALA:H	1.22	1.04
1:B:440:ARG:CD	1:B:440:ARG:H	1.71	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:ARG:HD2	1:B:440:ARG:H	0.89	1.02
1:B:22:ASP:HB2	1:B:145:LYS:NZ	1.73	1.02
1:B:440:ARG:N	1:B:440:ARG:HD2	1.73	1.02
1:A:432:THR:HG22	1:A:435:ALA:H	1.25	1.01
1:B:393:ILE:HG13	1:B:428:VAL:HG22	1.44	1.00
1:A:20:LYS:HG3	1:A:145:LYS:HG3	1.43	0.99
1:A:153:GLN:OE1	1:A:154:ASP:HB2	1.64	0.97
1:A:277:THR:HG22	1:A:279:ARG:H	1.27	0.95
1:A:20:LYS:HG3	1:A:145:LYS:CG	1.99	0.92
1:A:16:ALA:HB2	1:A:218:LEU:HD11	1.51	0.89
1:B:187:THR:CG2	1:B:465:ARG:HD3	2.02	0.89
1:B:205:THR:CG2	1:B:208:VAL:HG22	2.02	0.89
1:A:307:LEU:HD23	1:A:308:PRO:HD2	1.51	0.88
1:A:169:ALA:CA	1:A:193:MSE:HE1	2.03	0.88
1:A:87:GLN:OE1	1:A:87:GLN:HA	1.73	0.87
1:B:205:THR:HG21	1:B:208:VAL:HG22	1.57	0.85
1:A:219:ILE:HD12	1:A:239:MSE:HG3	1.57	0.84
1:B:392:MSE:HA	1:B:392:MSE:HE3	1.60	0.84
1:A:169:ALA:HA	1:A:193:MSE:CE	2.08	0.84
1:A:226:GLN:HB3	4:A:1028:HOH:O	1.80	0.82
1:A:342:LEU:H	1:A:342:LEU:HD12	1.43	0.81
1:B:22:ASP:HB2	1:B:145:LYS:HZ1	1.42	0.81
1:B:363:ALA:HB1	1:B:370:LEU:HB2	1.62	0.79
1:B:262:ILE:HG12	1:B:268:GLN:HG3	1.65	0.79
1:B:393:ILE:HG13	1:B:428:VAL:CG2	2.12	0.79
1:B:514:LEU:O	1:B:518:MSE:HG3	1.84	0.78
1:A:493:HIS:HE1	1:A:521:ASP:OD2	1.67	0.78
1:B:11:ILE:HD13	1:B:243:GLN:HA	1.67	0.77
1:A:394:ILE:HG13	1:A:432:THR:HG21	1.67	0.77
1:B:5:ILE:HD12	1:B:204:GLY:HA3	1.67	0.76
1:A:406:ILE:HD13	1:A:426:ILE:HD13	1.68	0.76
1:B:371:ARG:NH1	1:B:412:GLU:OE1	2.18	0.76
1:B:98:MSE:HE2	1:B:102:ALA:HB1	1.67	0.76
1:A:567:LYS:O	1:A:571:GLU:HG3	1.86	0.75
1:B:187:THR:HG22	1:B:465:ARG:HD3	1.66	0.75
1:B:28:ARG:HG3	1:B:28:ARG:HH11	1.52	0.74
1:A:226:GLN:NE2	1:A:228:TYR:OH	2.21	0.73
1:A:267:HIS:HE1	4:A:1010:HOH:O	1.71	0.72
1:A:342:LEU:CD1	1:A:345:MSE:HG2	2.20	0.71
1:B:385:LYS:HE2	4:B:1159:HOH:O	1.90	0.71
1:A:82:ASP:O	1:A:85:LEU:HD23	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:GLN:O	1:B:57:ILE:HG13	1.90	0.70
1:A:360:ILE:HD13	1:A:391:PRO:HD2	1.73	0.70
1:A:6:LEU:CD2	1:A:6:LEU:H	2.05	0.69
1:A:117:GLU:HA	1:A:117:GLU:OE1	1.92	0.69
1:A:187:THR:HG21	1:A:474:TYR:OH	1.93	0.68
1:A:277:THR:HG22	1:A:279:ARG:N	2.05	0.67
1:B:22:ASP:HB2	1:B:145:LYS:HZ2	1.57	0.67
1:A:486:LYS:HD2	1:A:553:LEU:HD13	1.75	0.67
1:A:219:ILE:HG13	1:A:228:TYR:HD2	1.59	0.66
1:A:136:ARG:HG3	1:A:136:ARG:HH11	1.60	0.66
1:B:187:THR:HG22	1:B:465:ARG:HB2	1.78	0.66
1:B:563:THR:HG23	1:B:567:LYS:HE2	1.77	0.66
1:A:489:ILE:O	1:A:492:SER:HB2	1.95	0.65
1:A:298:GLU:HG2	1:A:335:ASP:O	1.95	0.65
1:B:432:THR:CG2	1:B:435:ALA:H	2.05	0.65
1:B:6:LEU:HD21	1:B:222:ALA:O	1.97	0.65
1:A:87:GLN:CA	1:A:87:GLN:OE1	2.44	0.65
1:B:144:LEU:HB3	1:B:145:LYS:NZ	2.13	0.64
1:B:193:MSE:HE3	1:B:299:PHE:CD1	2.32	0.64
1:B:371:ARG:HG3	1:B:409:TYR:CE1	2.32	0.64
1:A:298:GLU:HG3	1:A:335:ASP:H	1.62	0.64
1:A:153:GLN:HE22	1:A:154:ASP:HB3	1.62	0.63
1:B:298:GLU:HG2	1:B:335:ASP:O	1.98	0.63
1:A:514:LEU:O	1:A:518:MSE:HG3	1.97	0.63
1:A:13:PHE:CD1	1:A:219:ILE:HG22	2.34	0.63
1:B:187:THR:CG2	1:B:187:THR:O	2.47	0.63
1:B:50:ALA:HA	1:B:53:GLN:OE1	1.99	0.63
1:B:79:LEU:HB2	1:B:133:ILE:HD13	1.81	0.62
1:A:173:LEU:HD22	4:A:1181:HOH:O	1.98	0.62
1:A:187:THR:HG21	1:A:474:TYR:CZ	2.33	0.62
1:B:301:PHE:HD1	1:B:301:PHE:H	1.47	0.62
1:A:219:ILE:HG13	1:A:228:TYR:CD2	2.35	0.62
1:A:432:THR:CG2	1:A:434:ALA:HB3	2.30	0.62
1:A:421:ASP:OD1	1:A:423:SER:HB2	1.99	0.61
1:A:218:LEU:HD12	1:A:218:LEU:N	2.14	0.61
1:B:20:LYS:C	1:B:20:LYS:HD3	2.22	0.61
1:B:219:ILE:HG13	1:B:228:TYR:CD2	2.36	0.61
1:A:412:GLU:O	1:A:416:GLU:HG3	2.01	0.60
1:B:86:GLU:O	1:B:90:ILE:HB	2.01	0.60
1:A:363:ALA:HB1	1:A:370:LEU:HB2	1.81	0.60
1:B:196:SER:HB3	4:B:1006:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:THR:HG21	1:B:474:TYR:OH	2.02	0.60
1:A:535:LYS:O	1:A:539:ASN:ND2	2.34	0.60
1:A:153:GLN:CD	1:A:154:ASP:HB2	2.23	0.59
1:A:336:ILE:HG12	1:A:342:LEU:HG	1.84	0.59
1:B:22:ASP:CB	1:B:145:LYS:NZ	2.58	0.59
1:A:17:LEU:HD23	1:A:156:VAL:HG21	1.83	0.59
1:A:189:NEP:CG	1:A:340:LYS:HE3	2.33	0.59
1:A:219:ILE:HD12	1:A:239:MSE:CG	2.28	0.59
1:B:343:PRO:O	1:B:345:MSE:N	2.35	0.59
1:A:307:LEU:HD23	1:A:308:PRO:CD	2.29	0.59
1:B:275:ILE:HG12	1:B:292:VAL:HG11	1.83	0.59
1:A:20:LYS:HG3	1:A:145:LYS:HG2	1.82	0.58
1:A:405:GLU:HG3	1:A:409:TYR:CE2	2.38	0.58
1:B:93:ILE:HD11	1:B:100:ALA:HA	1.85	0.58
1:B:205:THR:CB	1:B:208:VAL:HG22	2.33	0.58
1:A:271:VAL:CG1	1:A:530:ILE:HG23	2.33	0.58
1:A:36:VAL:O	1:A:40:VAL:HG23	2.03	0.58
1:B:240:ARG:HE	1:B:243:GLN:HE22	1.51	0.57
1:B:187:THR:HG22	1:B:465:ARG:CD	2.34	0.57
1:B:187:THR:O	1:B:187:THR:HG23	2.05	0.57
1:B:279:ARG:HD2	4:B:1031:HOH:O	2.05	0.57
1:B:475:GLN:OE1	1:B:477:MSE:N	2.30	0.57
1:A:189:NEP:CD2	1:A:340:LYS:HE3	2.35	0.56
1:A:342:LEU:HD13	1:A:345:MSE:CG	2.25	0.56
1:A:557:THR:HB	1:A:560:GLU:OE1	2.05	0.56
1:B:5:ILE:H	1:B:204:GLY:H	1.54	0.56
1:A:342:LEU:HD12	1:A:342:LEU:N	2.11	0.56
1:A:113:SER:HA	1:A:116:GLU:OE1	2.05	0.55
1:A:557:THR:HG22	1:A:560:GLU:H	1.69	0.55
1:B:167:GLU:O	1:B:171:LEU:HD13	2.06	0.55
1:B:392:MSE:CE	1:B:392:MSE:HA	2.35	0.55
1:A:475:GLN:O	1:A:478:SER:OG	2.24	0.55
1:B:69:LYS:HA	1:B:72:ILE:HD12	1.89	0.55
1:A:509:GLU:CG	4:A:1036:HOH:O	2.55	0.54
1:A:173:LEU:HD21	1:A:197:LEU:HD13	1.89	0.54
1:B:205:THR:HB	1:B:208:VAL:HG22	1.88	0.54
1:A:40:VAL:HG13	1:A:90:ILE:HG12	1.88	0.54
1:B:7:ALA:HB1	1:B:191:SER:HB3	1.90	0.53
1:B:394:ILE:HG22	1:B:432:THR:HG21	1.89	0.53
1:A:295:TYR:HB3	1:A:331:VAL:HA	1.90	0.53
1:A:371:ARG:HG3	1:A:409:TYR:CE1	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:LYS:HE2	1:B:145:LYS:N	2.23	0.53
1:A:275:ILE:HB	1:A:280:ASP:HB2	1.91	0.53
1:B:179:PHE:O	1:B:201:ALA:HA	2.08	0.53
1:B:454:ASN:HB3	1:B:465:ARG:CZ	2.38	0.53
1:A:432:THR:HG22	1:A:435:ALA:N	2.09	0.53
1:A:6:LEU:H	1:A:6:LEU:HD23	1.73	0.53
1:B:189:NEP:P	1:B:465:ARG:HH22	2.31	0.53
1:B:447:ASP:O	1:B:497:LYS:HG3	2.09	0.53
1:A:160:ALA:O	1:A:181:THR:HA	2.09	0.53
1:B:13:PHE:CE2	1:B:219:ILE:HG21	2.43	0.53
1:A:397:GLU:OE2	1:B:557:THR:HB	2.09	0.53
1:A:145:LYS:CD	1:A:145:LYS:H	2.21	0.53
1:A:540:THR:HG22	1:A:541:ASN:N	2.24	0.53
1:B:121:GLU:HA	1:B:121:GLU:OE1	2.08	0.53
1:B:432:THR:HG22	1:B:435:ALA:N	2.07	0.53
1:A:475:GLN:NE2	1:A:558:THR:HG21	2.24	0.53
1:A:153:GLN:NE2	1:A:154:ASP:CB	2.72	0.52
1:B:499:THR:HG22	1:B:500:GLY:O	2.09	0.52
1:B:220:LEU:C	1:B:220:LEU:HD23	2.30	0.52
1:A:219:ILE:CG1	1:A:228:TYR:HB2	2.40	0.52
1:A:360:ILE:CD1	1:A:391:PRO:HD2	2.39	0.52
1:A:375:ARG:HH22	1:A:416:GLU:CD	2.12	0.52
1:B:13:PHE:CD2	1:B:219:ILE:HG22	2.45	0.52
1:B:221:ASP:OD2	1:B:224:ASN:HB2	2.10	0.52
1:B:271:VAL:HG11	1:B:530:ILE:HG23	1.91	0.52
1:B:18:LEU:HA	1:B:159:VAL:O	2.10	0.52
1:A:226:GLN:CB	4:A:1028:HOH:O	2.49	0.51
1:A:13:PHE:CD1	1:A:240:ARG:NH1	2.78	0.51
1:B:22:ASP:CB	1:B:145:LYS:HZ2	2.20	0.51
1:B:271:VAL:HG12	1:B:271:VAL:O	2.10	0.51
1:B:453:THR:OG1	1:B:503:GLY:HA3	2.11	0.51
1:A:146:ILE:HD12	1:A:146:ILE:H	1.76	0.51
1:B:453:THR:H	1:B:503:GLY:HA3	1.76	0.51
1:B:512:THR:O	1:B:516:LEU:HB2	2.11	0.51
1:A:245:GLN:O	1:A:249:GLU:HG3	2.11	0.50
1:A:463:VAL:HG22	1:A:474:TYR:HD1	1.76	0.50
1:A:272:CYS:HB3	1:A:291:GLY:O	2.12	0.50
1:B:307:LEU:HD12	1:B:345:MSE:SE	2.62	0.50
1:A:298:GLU:O	1:A:301:PHE:HB2	2.12	0.50
1:B:13:PHE:CD2	1:B:219:ILE:CG2	2.95	0.50
1:B:477:MSE:CE	1:B:514:LEU:HD12	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:441:HIS:O	1:B:444:LYS:HB2	2.12	0.50
1:B:144:LEU:HB3	1:B:145:LYS:HZ1	1.77	0.49
1:B:22:ASP:HB2	1:B:145:LYS:CE	2.41	0.49
1:A:454:ASN:HA	1:A:474:TYR:OH	2.12	0.49
1:B:298:GLU:HB3	1:B:336:ILE:CD1	2.42	0.49
1:A:486:LYS:N	1:A:518:MSE:HE1	2.27	0.49
1:A:484:LEU:O	1:A:488:VAL:HG23	2.12	0.49
1:A:153:GLN:NE2	1:A:154:ASP:HB3	2.25	0.49
1:A:509:GLU:HG3	4:A:1036:HOH:O	2.12	0.49
1:A:136:ARG:HG3	1:A:136:ARG:NH1	2.24	0.49
1:B:65:PHE:HB3	1:B:69:LYS:HG3	1.95	0.49
1:A:93:ILE:HD11	1:A:100:ALA:HA	1.94	0.49
1:A:121:GLU:OE1	1:A:121:GLU:HA	2.13	0.49
1:B:343:PRO:C	1:B:345:MSE:H	2.17	0.48
1:B:67:GLU:O	1:B:67:GLU:HG2	2.13	0.48
1:B:302:MSE:O	1:B:304:ARG:N	2.46	0.48
1:B:28:ARG:NH1	1:B:28:ARG:HG3	2.25	0.48
1:A:155:GLU:HA	1:A:175:LYS:O	2.12	0.48
1:A:182:ASP:O	1:A:205:THR:O	2.32	0.48
1:A:298:GLU:O	1:A:302:MSE:HG3	2.14	0.48
1:A:468:ASP:OD1	1:A:468:ASP:N	2.47	0.47
1:B:158:LEU:HB2	1:B:179:PHE:HB3	1.96	0.47
1:B:374:LEU:HD12	1:B:409:TYR:HE2	1.78	0.47
1:A:120:ASP:OD1	1:A:122:TYR:HB3	2.14	0.47
1:B:295:TYR:HB3	1:B:331:VAL:HA	1.96	0.47
1:B:389:MSE:HA	1:B:427:GLY:O	2.14	0.47
1:A:547:VAL:O	1:A:551:GLN:HG3	2.14	0.47
1:A:455:ASP:O	1:A:458:GLN:HB3	2.14	0.47
1:B:513:LEU:HD21	1:B:572:LYS:NZ	2.30	0.47
1:A:16:ALA:CB	1:A:218:LEU:HD11	2.34	0.47
1:A:24:ILE:HG13	1:A:24:ILE:H	1.50	0.47
1:A:153:GLN:HE22	1:A:154:ASP:CB	2.26	0.47
1:B:187:THR:O	1:B:465:ARG:HD2	2.15	0.47
1:B:238:LYS:O	1:B:242:VAL:HG23	2.14	0.46
1:B:495:GLU:O	1:B:497:LYS:HD3	2.15	0.46
1:B:205:THR:HG21	1:B:208:VAL:CG2	2.37	0.46
1:B:214:ASN:O	1:B:215:ASP:HB2	2.15	0.46
1:B:296:ARG:HD3	1:B:299:PHE:CE2	2.50	0.46
1:B:518:MSE:HE3	1:B:553:LEU:HD11	1.97	0.46
1:A:42:ARG:NH1	4:A:1097:HOH:O	2.49	0.46
1:A:6:LEU:HD23	1:A:6:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:489:ILE:O	1:B:492:SER:HB3	2.16	0.46
1:A:6:LEU:CD2	1:A:6:LEU:N	2.76	0.46
1:B:93:ILE:O	1:B:97:HIS:HA	2.15	0.46
1:A:217:TYR:O	1:A:231:PRO:HD2	2.16	0.46
1:A:430:VAL:HG11	1:A:488:VAL:HG21	1.98	0.46
1:B:484:LEU:O	1:B:488:VAL:HG23	2.16	0.46
1:A:117:GLU:HB3	4:A:1123:HOH:O	2.16	0.46
1:B:183:ALA:O	1:B:203:VAL:O	2.34	0.46
1:B:279:ARG:CD	4:B:1031:HOH:O	2.61	0.46
1:B:145:LYS:CE	1:B:145:LYS:H	2.29	0.45
1:B:477:MSE:HE1	1:B:514:LEU:HD12	1.97	0.45
1:A:394:ILE:HD11	1:A:432:THR:OG1	2.16	0.45
1:B:358:ARG:HD3	1:B:392:MSE:HG2	1.99	0.45
1:A:205:THR:CB	1:A:208:VAL:HG22	2.46	0.45
1:A:292:VAL:HB	1:A:329:VAL:HG22	1.98	0.45
1:B:115:LEU:HD13	1:B:126:ARG:HB2	1.98	0.45
1:A:475:GLN:HE21	1:A:558:THR:HG21	1.82	0.45
1:B:256:LEU:HD23	1:B:259:LEU:HD12	1.99	0.45
1:A:116:GLU:OE2	1:A:131:ARG:NH1	2.41	0.45
1:A:486:LYS:HB2	1:A:518:MSE:HE3	1.98	0.45
1:B:406:ILE:HG22	1:B:407:GLU:OE2	2.16	0.45
1:B:428:VAL:HB	1:B:446:VAL:HG11	1.99	0.45
1:B:455:ASP:CG	1:B:465:ARG:HH21	2.19	0.45
1:A:187:THR:HG22	1:A:465:ARG:HB3	1.99	0.44
1:A:461:LEU:HB2	1:A:463:VAL:HG13	1.99	0.44
1:B:180:ILE:HA	1:B:202:ILE:O	2.17	0.44
1:B:561:LEU:HD23	1:B:561:LEU:C	2.36	0.44
1:A:432:THR:CG2	1:A:435:ALA:H	2.14	0.44
1:A:486:LYS:HA	1:A:518:MSE:CE	2.47	0.44
1:B:267:HIS:HE1	4:B:1043:HOH:O	2.01	0.44
1:A:13:PHE:HB3	1:A:217:TYR:OH	2.16	0.44
1:A:195:ARG:NH1	4:A:1048:HOH:O	2.50	0.44
1:A:556:PRO:HB3	1:B:441:HIS:ND1	2.33	0.44
1:A:169:ALA:CB	1:A:193:MSE:HE1	2.47	0.44
1:A:361:ARG:HH21	1:A:394:ILE:HD13	1.83	0.44
1:A:404:LYS:HE2	1:A:404:LYS:HB3	1.66	0.44
1:A:83:GLU:HA	1:A:86:GLU:HB3	1.99	0.44
1:A:271:VAL:HG11	1:A:530:ILE:HG23	2.00	0.44
1:B:74:GLU:OE1	1:B:78:MSE:HE3	2.18	0.44
1:B:92:LEU:HD12	1:B:107:VAL:HG23	1.99	0.44
1:A:69:LYS:HE2	1:A:312:GLU:OE2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:MSE:HE1	1:B:398:GLU:HG2	1.99	0.43
1:B:477:MSE:HE2	1:B:477:MSE:HB3	1.89	0.43
1:A:15:LYS:HE3	1:A:15:LYS:HB2	1.78	0.43
1:A:219:ILE:HG12	1:A:228:TYR:HB2	2.00	0.43
1:B:160:ALA:O	1:B:181:THR:HA	2.18	0.43
1:A:433:PRO:HD2	1:B:460:THR:O	2.18	0.43
1:B:272:CYS:HB3	1:B:293:GLY:H	1.84	0.43
1:A:152:ILE:O	1:A:175:LYS:HG3	2.17	0.43
1:B:301:PHE:CD1	1:B:301:PHE:N	2.82	0.43
1:B:46:GLY:HA2	1:B:49:LYS:HE3	1.98	0.43
1:A:405:GLU:HG3	1:A:409:TYR:CZ	2.53	0.43
1:A:396:VAL:HG22	1:A:442:LEU:HD23	2.00	0.43
1:A:93:ILE:O	1:A:97:HIS:HA	2.19	0.43
1:B:145:LYS:HE2	1:B:145:LYS:O	2.18	0.43
1:A:189:NEP:CE1	1:A:340:LYS:HE3	2.49	0.43
1:A:218:LEU:H	1:A:218:LEU:HD12	1.80	0.43
1:A:342:LEU:HD22	1:A:344:TYR:CE1	2.54	0.43
1:B:189:NEP:CE1	1:B:340:LYS:HE3	2.49	0.43
1:B:76:HIS:HA	1:B:133:ILE:HD11	2.01	0.43
1:A:540:THR:HG22	1:A:541:ASN:O	2.19	0.43
1:B:11:ILE:N	1:B:11:ILE:HD12	2.34	0.43
1:B:153:GLN:OE1	1:B:153:GLN:HA	2.16	0.43
1:B:16:ALA:HB2	1:B:218:LEU:HD11	2.01	0.42
1:A:207:SER:HB3	1:A:210:SER:OG	2.18	0.42
1:B:155:GLU:HA	1:B:175:LYS:O	2.19	0.42
1:A:153:GLN:O	1:A:175:LYS:HE3	2.19	0.42
1:A:79:LEU:HD21	1:A:126:ARG:HD3	2.01	0.42
1:A:53:GLN:HA	4:A:1158:HOH:O	2.20	0.42
1:A:486:LYS:CA	1:A:518:MSE:CE	2.98	0.42
1:B:166:SER:O	1:B:169:ALA:HB3	2.20	0.42
1:A:20:LYS:CG	1:A:145:LYS:HG3	2.32	0.42
1:A:187:THR:HG23	1:A:187:THR:O	2.20	0.42
1:A:427:GLY:HA2	1:A:446:VAL:HB	2.00	0.42
1:A:24:ILE:HG23	1:A:142:LEU:CD1	2.49	0.42
1:A:262:ILE:HG22	1:A:263:THR:O	2.20	0.42
1:A:561:LEU:HA	1:A:564:LEU:HD23	2.02	0.42
1:B:279:ARG:HH11	1:B:279:ARG:HG2	1.85	0.42
1:A:180:ILE:HA	1:A:202:ILE:O	2.20	0.41
1:A:327:GLN:HG3	4:A:1173:HOH:O	2.19	0.41
1:A:461:LEU:HD12	1:A:475:GLN:H	1.84	0.41
1:B:11:ILE:CD1	1:B:243:GLN:HA	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:LEU:HD12	1:B:561:LEU:HD11	2.01	0.41
1:B:193:MSE:HE3	1:B:299:PHE:CE1	2.55	0.41
1:B:302:MSE:C	1:B:304:ARG:H	2.23	0.41
1:A:24:ILE:HG23	1:A:142:LEU:HD12	2.02	0.41
1:A:260:PRO:HB2	1:A:262:ILE:HG13	2.02	0.41
1:B:13:PHE:CE2	1:B:219:ILE:CG2	3.03	0.41
1:B:359:ALA:HB1	1:B:391:PRO:HG2	2.01	0.41
1:B:298:GLU:HG3	1:B:335:ASP:H	1.84	0.41
1:A:153:GLN:CD	1:A:154:ASP:CB	2.88	0.41
1:B:516:LEU:HD21	1:B:537:ILE:HG23	2.02	0.41
1:A:52:ALA:O	1:A:55:GLU:HB2	2.21	0.41
1:B:262:ILE:HG22	1:B:263:THR:N	2.35	0.41
1:A:65:PHE:HZ	1:A:303:ASP:O	2.04	0.41
1:A:374:LEU:HD23	1:A:374:LEU:HA	1.96	0.41
1:A:76:HIS:CB	1:A:133:ILE:HD11	2.51	0.41
1:A:41:GLU:CD	4:A:1113:HOH:O	2.58	0.41
1:B:564:LEU:HD23	1:B:564:LEU:HA	1.89	0.41
1:B:515:LEU:HD23	1:B:515:LEU:HA	1.85	0.41
1:B:516:LEU:HD12	1:B:516:LEU:HA	1.90	0.41
1:A:76:HIS:HB3	1:A:133:ILE:HD11	2.02	0.40
1:A:450:SER:HA	1:A:500:GLY:O	2.20	0.40
1:A:177:LEU:O	1:A:200:PRO:HD2	2.21	0.40
1:B:332:ARG:HD3	1:B:389:MSE:HE3	2.03	0.40
1:A:199:LEU:HA	1:A:199:LEU:HD12	1.58	0.40
1:B:41:GLU:O	1:B:45:SER:HB3	2.22	0.40
1:A:301:PHE:HB3	1:A:342:LEU:HD23	2.02	0.40
1:A:367:ARG:O	1:A:368:GLU:C	2.60	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	569/575 (99%)	533 (94%)	31 (5%)	5 (1%)	20	46
1	B	569/575 (99%)	531 (93%)	35 (6%)	3 (0%)	32	60
All	All	1138/1150 (99%)	1064 (94%)	66 (6%)	8 (1%)	25	53

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	344	TYR
1	A	35	GLN
1	A	172	ASN
1	A	278	VAL
1	B	303	ASP
1	A	257	LYS
1	B	64	THR
1	A	153	GLN

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	472/457 (103%)	414 (88%)	58 (12%)	5	13
1	B	472/457 (103%)	418 (89%)	54 (11%)	7	15
All	All	944/914 (103%)	832 (88%)	112 (12%)	6	14

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	15	LYS
1	A	21	GLU
1	A	34	ASP
1	A	38	GLN
1	A	41	GLU
1	A	53	GLN
1	A	70	GLU

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Mol	Chain	Res	Type
1	A	74	GLU
1	A	76	HIS
1	A	85	LEU
1	A	87	GLN
1	A	97	HIS
1	A	117	GLU
1	A	145	LYS
1	A	146	ILE
1	A	153	GLN
1	A	158	LEU
1	A	166	SER
1	A	174	LYS
1	A	176	VAL
1	A	187	THR
1	A	188	SER
1	A	205	THR
1	A	208	VAL
1	A	214	ASN
1	A	215	ASP
1	A	218	LEU
1	A	234	GLU
1	A	240	ARG
1	A	244	GLU
1	A	275	ILE
1	A	278	VAL
1	A	295	TYR
1	A	300	LEU
1	A	302	MSE
1	A	303	ASP
1	A	304	ARG
1	A	307	LEU
1	A	334	MSE
1	A	336	ILE
1	A	342	LEU
1	A	360	ILE
1	A	367	ARG
1	A	368	GLU
1	A	394	ILE
1	A	404	LYS
1	A	411	GLN
1	A	423	SER
1	A	432	THR

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Mol	Chain	Res	Type
1	A	475	GLN
1	A	497	LYS
1	A	505	LEU
1	A	522	GLU
1	A	532	ARG
1	A	557	THR
1	A	561	LEU
1	A	573	THR
1	B	6	LEU
1	B	21	GLU
1	B	28	ARG
1	B	36	VAL
1	B	47	ARG
1	B	51	SER
1	B	56	THR
1	B	64	THR
1	B	65	PHE
1	B	85	LEU
1	B	87	GLN
1	B	124	LYS
1	B	132	ASP
1	B	138	LEU
1	B	145	LYS
1	B	158	LEU
1	B	170	GLN
1	B	187	THR
1	B	191	SER
1	B	196	SER
1	B	197	LEU
1	B	208	VAL
1	B	219	ILE
1	B	225	ASN
1	B	226	GLN
1	B	234	GLU
1	B	240	ARG
1	B	252	GLU
1	B	255	LYS
1	B	285	GLU
1	B	295	TYR
1	B	301	PHE
1	B	304	ARG
1	B	311	GLU

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Mol	Chain	Res	Type
1	B	334	MSE
1	B	336	ILE
1	B	354	PHE
1	B	368	GLU
1	B	388	ILE
1	B	392	MSE
1	B	405	GLU
1	B	428	VAL
1	B	432	THR
1	B	438	ILE
1	B	440	ARG
1	B	463	VAL
1	B	475	GLN
1	B	477	MSE
1	B	480	SER
1	B	497	LYS
1	B	505	LEU
1	B	522	GLU
1	B	551	GLN
1	B	553	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	HIS
1	A	111	GLN
1	A	153	GLN
1	A	214	ASN
1	A	226	GLN
1	A	245	GLN
1	A	267	HIS
1	A	268	GLN
1	A	411	GLN
1	A	493	HIS
1	A	555	GLN
1	B	225	ASN
1	B	226	GLN
1	B	243	GLN
1	B	267	HIS
1	B	411	GLN
1	B	539	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	NEP	A	189	1,2	11,14,15	1.68	4 (36%)	7,20,22	2.12	2 (28%)
1	NEP	B	189	1,2	11,14,15	2.08	3 (27%)	7,20,22	2.37	3 (42%)

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
1	NEP	A	189	1,2	-	0/4/12/14	0/1/1/1
1	NEP	B	189	1,2	-	0/4/12/14	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	189	NEP	CD2-NE2	-3.33	1.33	1.39
1	B	189	NEP	CD2-NE2	-2.77	1.34	1.39
1	A	189	NEP	P-O1P	-2.66	1.49	1.54
1	B	189	NEP	P-O1P	-2.44	1.49	1.54
1	A	189	NEP	P-O2P	-2.13	1.50	1.54
1	A	189	NEP	CD2-CG	2.45	1.39	1.36
1	B	189	NEP	P-O3P	5.12	1.51	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	NEP	CG-CD2-NE2	-5.08	102.17	108.96
1	A	189	NEP	CG-CD2-NE2	-4.59	102.82	108.96
1	B	189	NEP	CB-CA-N	-2.30	103.50	112.54
1	B	189	NEP	O2P-P-O1P	2.13	115.04	106.64
1	A	189	NEP	O2P-P-O1P	2.41	116.12	106.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	189	NEP	3	0
1	B	189	NEP	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	OXL	A	903	2	0,5,5	0.00	-	0,6,6	0.00	-
3	OXL	B	904	2	0,5,5	0.00	-	0,6,6	0.00	-

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	OXL	A	903	2	-	0/0/4/4	0/0/0/0
3	OXL	B	904	2	-	0/0/4/4	0/0/0/0

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	554/575 (96%)	-0.03	13 (2%) 61 61	10, 27, 63, 84	0
1	B	554/575 (96%)	0.06	36 (6%) 20 17	10, 26, 67, 85	0
All	All	1108/1150 (96%)	0.02	49 (4%) 35 33	10, 26, 66, 85	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	65	PHE	4.2
1	A	24	ILE	4.1
1	B	85	LEU	4.1
1	B	573	THR	4.1
1	B	26	ILE	3.9
1	A	23	GLU	3.7
1	B	93	ILE	3.5
1	B	90	ILE	3.4
1	A	68	GLU	3.3
1	B	100	ALA	3.3
1	B	41	GLU	3.3
1	B	38	GLN	3.3
1	B	40	VAL	3.2
1	B	25	VAL	3.2
1	B	133	ILE	3.1
1	B	44	LEU	3.0
1	B	132	ASP	2.9
1	B	84	GLU	2.8
1	B	571	GLU	2.7
1	B	24	ILE	2.7
1	B	94	LYS	2.7
1	B	130	VAL	2.6
1	B	567	LYS	2.6
1	B	83	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	21	GLU	2.5
1	B	91	ALA	2.4
1	B	138	LEU	2.4
1	A	73	PHE	2.4
1	A	64	THR	2.3
1	A	84	GLU	2.3
1	B	122	TYR	2.3
1	A	22	ASP	2.3
1	B	64	THR	2.3
1	A	85	LEU	2.3
1	B	87	GLN	2.2
1	A	63	GLU	2.2
1	B	111	GLN	2.2
1	B	80	LEU	2.2
1	B	102	ALA	2.2
1	B	106	GLU	2.2
1	B	570	GLU	2.2
1	B	142	LEU	2.2
1	A	29	LYS	2.1
1	B	79	LEU	2.1
1	B	141	ILE	2.1
1	B	35	GLN	2.1
1	A	244	GLU	2.1
1	B	135	LYS	2.1
1	A	122	TYR	2.0

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

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
1	NEP	B	189	14/15	0.99	0.15	-	9,15,18,18	0
1	NEP	A	189	14/15	0.99	0.15	-	20,21,22,23	0

6.3 Carbohydrates ⓘ

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
3	OXL	B	904	6/6	0.97	0.18	0.97	27,29,29,30	0
2	MG	B	902	1/1	0.98	0.13	-1.50	25,25,25,25	0
3	OXL	A	903	6/6	0.98	0.14	-1.54	18,19,21,23	0
2	MG	A	901	1/1	0.98	0.13	-1.69	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.