



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:49 AM UTC

PDB ID : 4AT7 / pdb_00004at7
Title : Crystal structure of the NF90-NF45 dimerisation domain complex
Authors : Wolkowicz, U.M.; Cook, A.G.
Deposited on : 2012-05-05
Resolution : 1.90 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

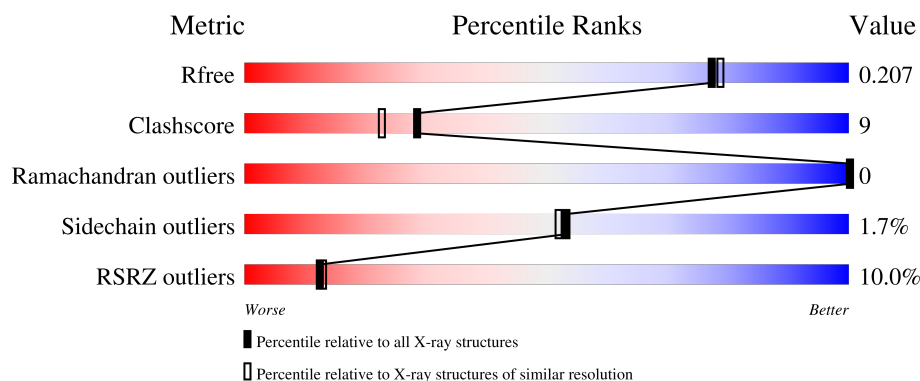
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	364	5% 80% 12% 8%
2	B	383	12% 72% 11% 15%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MLI	B	1375	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5773 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 INTERLEUKIN ENHANCER-BINDING FACTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	7	0
			2579	1657	434	478	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9CXY6
A	0	SER	-	expression tag	UNP Q9CXY6

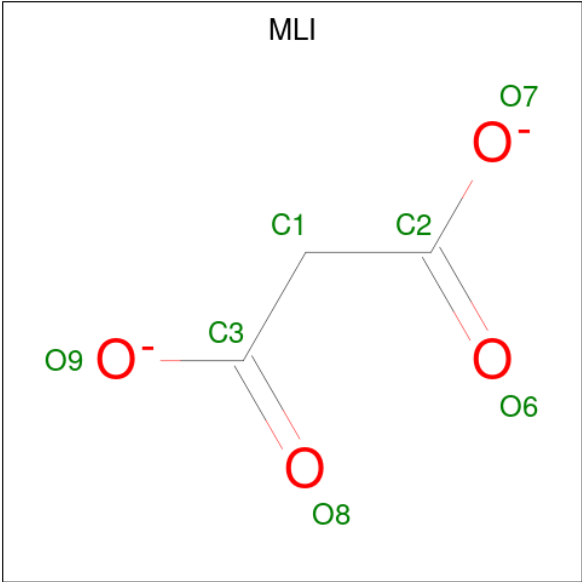
- Molecule 2 is a protein called INTERLEUKIN ENHANCER-BINDING FACTOR 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	324	Total	C	N	O	S	0	7	0
			2473	1562	427	468	16			

There are 2 discrepancies between the modelled and reference sequences:

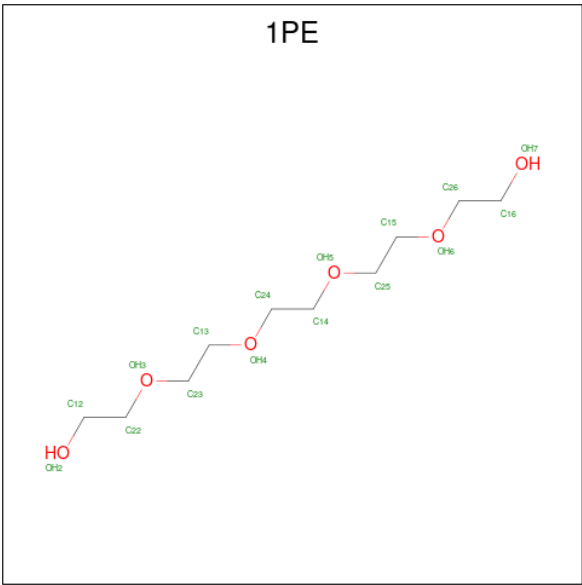
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP Q9Z1X4
B	0	HIS	-	expression tag	UNP Q9Z1X4

- Molecule 3 is MALONATE ION (CCD ID: MLI) (formula: C₃H₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	3	4		
3	A	1	Total	C	O	0	0
			7	3	4		
3	B	1	Total	C	O	0	0
			7	3	4		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	10	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

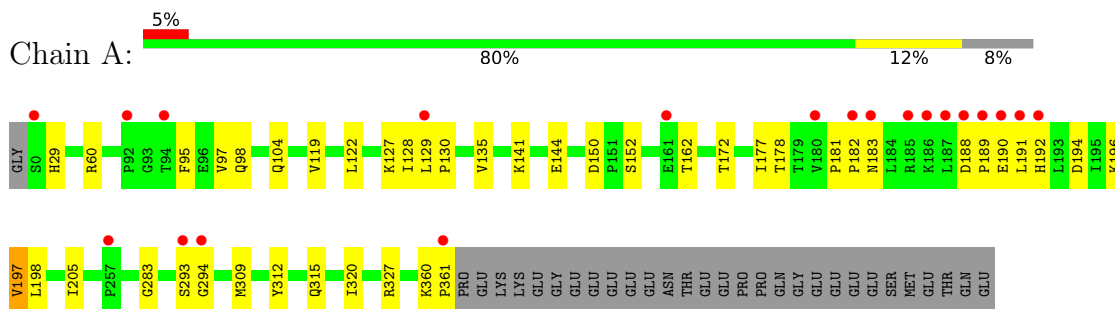
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	381	Total	O	0	0
			381	381		
6	B	273	Total	O	0	0
			273	273		

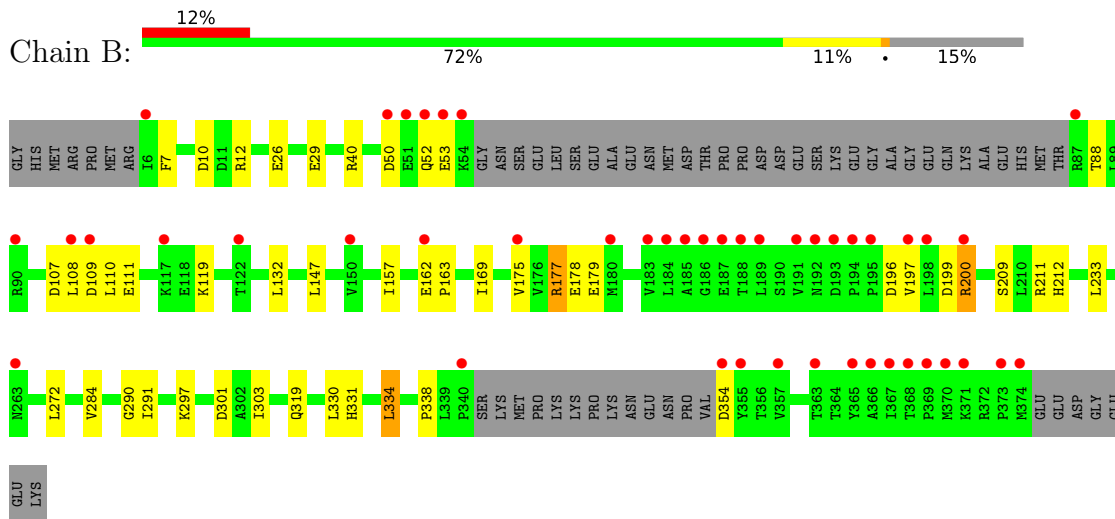
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: INTERLEUKIN ENHANCER-BINDING FACTOR 2



- Molecule 2: INTERLEUKIN ENHANCER-BINDING FACTOR 3



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.90Å 131.30Å 176.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.00 – 1.90 88.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (88.00-1.90) 98.7 (88.00-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.52 (at 1.90Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.185 , 0.210 0.182 , 0.207	Depositor DCC
R_{free} test set	3764 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.497	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5773	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, 1PE, MLI

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	0.51	0/2652	0.77	0/3618
2	B	0.48	0/2528	0.74	1/3441 (0.0%)
All	All	0.50	0/5180	0.75	1/7059 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	196	ASP	N-CA-C	5.05	116.92	110.61

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	2579	0	2622	45	0
2	B	2473	0	2475	45	0
3	A	14	0	4	0	0
3	B	7	0	2	3	0
4	A	32	0	44	4	0
5	A	7	0	10	0	0
5	B	7	0	10	2	0
6	A	381	0	0	21	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	273	0	0	16	2
All	All	5773	0	5167	90	2

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 9.

All (90) 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:183:ASN:ND2	6:A:2181:HOH:O	1.88	1.05
1:A:128:ILE:C	6:A:2181:HOH:O	2.07	0.96
2:B:52:GLN:C	6:B:2064:HOH:O	2.08	0.95
1:A:191:LEU:N	6:A:2235:HOH:O	2.04	0.90
1:A:150:ASP:OD1	6:A:2203:HOH:O	1.91	0.89
2:B:200:ARG:HG3	2:B:200:ARG:HH11	1.39	0.88
2:B:53:GLU:OE1	6:B:2063:HOH:O	1.93	0.87
1:A:294:GLY:O	6:A:2314:HOH:O	1.92	0.86
2:B:200:ARG:HH11	2:B:200:ARG:CG	1.89	0.84
1:A:190:GLU:N	6:A:2235:HOH:O	2.12	0.83
2:B:119:LYS:HE2	2:B:197:VAL:HG11	1.61	0.82
1:A:128:ILE:CA	6:A:2181:HOH:O	2.28	0.82
2:B:107:ASP:OD1	6:B:2101:HOH:O	1.97	0.82
1:A:135:VAL:HG22	1:A:177:ILE:HD13	1.60	0.82
2:B:52:GLN:O	6:B:2064:HOH:O	1.96	0.82
2:B:26:GLU:OE2	6:B:2034:HOH:O	1.99	0.80
1:A:189:PRO:C	6:A:2235:HOH:O	2.24	0.80
1:A:127:LYS:O	6:A:2181:HOH:O	1.99	0.80
2:B:179:GLU:OE2	6:B:2156:HOH:O	2.00	0.79
4:A:1364:1PE:OH7	6:A:2379:HOH:O	2.00	0.78
2:B:163:PRO:O	6:B:2147:HOH:O	2.02	0.77
1:A:327:ARG:NH1	6:A:2340:HOH:O	1.90	0.76
1:A:152:SER:OG	6:A:2203:HOH:O	2.04	0.75
2:B:50:ASP:OD1	6:B:2063:HOH:O	2.04	0.74
2:B:109:ASP:N	6:B:2103:HOH:O	2.17	0.74
1:A:127:LYS:C	6:A:2181:HOH:O	2.33	0.72
2:B:297:LYS:HG3	5:B:1376:PEG:H12	1.71	0.72
2:B:233:LEU:HD21	2:B:272[B]:LEU:HD11	1.72	0.71
2:B:354:ASP:CB	6:B:2260:HOH:O	2.39	0.70
1:A:190:GLU:C	6:A:2235:HOH:O	2.31	0.69
1:A:205:ILE:HG23	6:A:2246:HOH:O	1.97	0.65
1:A:128:ILE:O	6:A:2181:HOH:O	2.11	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:29:GLU:OE1	6:B:2038:HOH:O	2.15	0.63
1:A:98:GLN:HB3	1:A:127:LYS:HE3	1.81	0.61
2:B:200:ARG:CG	2:B:200:ARG:NH1	2.57	0.61
2:B:175:VAL:HA	2:B:178:GLU:OE1	2.03	0.59
1:A:188:ASP:O	6:A:2235:HOH:O	2.17	0.59
2:B:119:LYS:CE	2:B:197:VAL:HG11	2.36	0.54
1:A:128:ILE:N	6:A:2181:HOH:O	2.39	0.54
2:B:132:LEU:HD21	2:B:157:ILE:HD11	1.88	0.54
1:A:178:THR:HA	1:A:198:LEU:HD22	1.90	0.54
1:A:29:HIS:HB3	1:A:283:GLY:O	2.08	0.53
1:A:181:PRO:HD2	1:A:182:PRO:HD2	1.91	0.52
2:B:178:GLU:HA	6:B:2154:HOH:O	2.10	0.52
1:A:181:PRO:CD	1:A:182:PRO:HD2	2.41	0.51
1:A:194:ASP:OD2	1:A:196:LYS:HB2	2.11	0.50
2:B:119:LYS:HE2	2:B:197:VAL:CG1	2.38	0.50
2:B:211:ARG:NH2	6:B:2163:HOH:O	1.93	0.50
2:B:212:HIS:ND1	3:B:1375:MLI:H11	2.27	0.50
1:A:95:PHE:CE2	1:A:97:VAL:HB	2.47	0.50
1:A:309:MET:HA	1:A:312:TYR:CE2	2.46	0.50
1:A:144:GLU:HB2	4:A:1365:1PE:H122	1.94	0.49
2:B:53:GLU:OE2	2:B:88:THR:OG1	2.29	0.49
2:B:157:ILE:HD11	2:B:169:ILE:HD11	1.95	0.49
1:A:162:THR:HG22	1:A:197:VAL:HG22	1.95	0.48
1:A:181:PRO:O	1:A:182:PRO:C	2.57	0.47
2:B:291:ILE:HD12	2:B:303:ILE:CG2	2.45	0.47
2:B:175:VAL:O	2:B:179:GLU:HG3	2.14	0.47
1:A:60:ARG:HG2	6:A:2060:HOH:O	2.14	0.47
1:A:141:LYS:NZ	4:A:1365:1PE:H131	2.30	0.47
2:B:330:LEU:HG	2:B:334:LEU:HD22	1.96	0.47
2:B:178:GLU:CA	6:B:2154:HOH:O	2.63	0.47
1:A:188:ASP:C	1:A:190:GLU:H	2.23	0.46
2:B:40:ARG:NH2	6:B:2055:HOH:O	2.46	0.46
1:A:129:LEU:HD13	1:A:192:HIS:CE1	2.51	0.46
1:A:141:LYS:O	1:A:141:LYS:HD3	2.16	0.46
2:B:301:ASP:OD1	2:B:303:ILE:HG12	2.16	0.46
2:B:177:ARG:NH1	6:B:2153:HOH:O	2.48	0.45
1:A:129:LEU:HA	1:A:130[B]:PRO:HD3	1.82	0.45
1:A:129:LEU:HD22	1:A:192:HIS:CE1	2.52	0.44
1:A:104:GLN:HG2	1:A:122:LEU:CD2	2.48	0.44
1:A:144:GLU:CB	4:A:1365:1PE:H122	2.48	0.44
2:B:199:ASP:OD1	2:B:199:ASP:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:GLN:CD	2:B:319:GLN:HB3	2.43	0.43
1:A:152:SER:CB	6:A:2203:HOH:O	2.65	0.43
2:B:108:LEU:HD21	2:B:163:PRO:HG2	2.01	0.42
1:A:197:VAL:HG13	6:A:2226:HOH:O	2.19	0.42
2:B:284:VAL:HB	2:B:303:ILE:HD12	2.02	0.42
2:B:162:GLU:HA	2:B:163:PRO:HA	1.87	0.42
1:A:293:SER:HA	1:A:294:GLY:HA2	1.72	0.41
2:B:209[A]:SER:HB3	3:B:1375:MLI:H12	2.01	0.41
2:B:209[B]:SER:OG	3:B:1375:MLI:H12	2.20	0.41
2:B:290:GLY:HA2	2:B:303:ILE:HD11	2.02	0.41
2:B:297:LYS:CG	5:B:1376:PEG:H32	2.51	0.41
1:A:360:LYS:HA	1:A:361:PRO:HD3	1.85	0.41
2:B:331:HIS:CD2	2:B:338:PRO:HD3	2.55	0.41
1:A:119:VAL:HA	1:A:172:THR:O	2.21	0.41
2:B:291:ILE:HD12	2:B:303:ILE:HG23	2.04	0.40
2:B:7:PHE:HB3	2:B:10:ASP:HB2	2.03	0.40
1:A:181:PRO:N	1:A:182:PRO:HD2	2.35	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:2290:HOH:O	6:B:2204:HOH:O[3_655]	2.04	0.16
6:B:2028:HOH:O	6:B:2028:HOH:O[3_555]	2.04	0.16

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	339/364 (93%)	326 (96%)	13 (4%)	0	100	100
2	B	325/383 (85%)	319 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	664/747 (89%)	645 (97%)	19 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	282/317 (89%)	280 (99%)	2 (1%)	76	78
2	B	265/330 (80%)	258 (97%)	7 (3%)	40	35
All	All	547/647 (84%)	538 (98%)	9 (2%)	53	54

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	VAL
1	A	320	ILE
2	B	12	ARG
2	B	110	LEU
2	B	111	GLU
2	B	147	LEU
2	B	177	ARG
2	B	200	ARG
2	B	334	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	GLN
1	A	82	ASN
1	A	104	GLN
1	A	117	HIS
1	A	192	HIS
1	A	295	ASN

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Mol	Chain	Res	Type
2	B	331	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 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	$\# Z > 2$
5	PEG	A	1366	-	6,6,6	0.62	0	5,5,5	1.47	0
3	MLI	A	1362	-	6,6,6	1.18	0	7,7,7	1.47	1 (14%)
4	1PE	A	1365	-	15,15,15	0.70	0	14,14,14	1.53	0
5	PEG	B	1376	-	6,6,6	0.52	0	5,5,5	1.53	0
4	1PE	A	1364	-	15,15,15	0.56	0	14,14,14	1.18	0
3	MLI	A	1363	-	6,6,6	1.40	0	7,7,7	1.01	0
3	MLI	B	1375	-	6,6,6	1.51	1 (16%)	7,7,7	0.90	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	A	1366	-	-	2/4/4/4	-
3	MLI	A	1362	-	-	2/4/4/4	-
4	1PE	A	1365	-	-	3/13/13/13	-
5	PEG	B	1376	-	-	2/4/4/4	-
4	1PE	A	1364	-	-	12/13/13/13	-
3	MLI	A	1363	-	-	0/4/4/4	-
3	MLI	B	1375	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1375	MLI	C1-C2	-2.05	1.47	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1362	MLI	C3-C1-C2	2.20	120.71	112.95

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1364	1PE	C25-C15-OH6-C26
4	A	1365	1PE	OH4-C13-C23-OH3
5	A	1366	PEG	O1-C1-C2-O2
4	A	1364	1PE	OH5-C14-C24-OH4
4	A	1364	1PE	OH7-C16-C26-OH6
5	A	1366	PEG	O2-C3-C4-O4
4	A	1365	1PE	OH5-C14-C24-OH4
4	A	1364	1PE	C23-C13-OH4-C24
4	A	1364	1PE	OH4-C13-C23-OH3
4	A	1364	1PE	OH6-C15-C25-OH5
5	B	1376	PEG	C4-C3-O2-C2
4	A	1364	1PE	C13-C23-OH3-C22
4	A	1364	1PE	C15-C25-OH5-C14
4	A	1365	1PE	C13-C23-OH3-C22
3	A	1362	MLI	C3-C1-C2-O6
4	A	1364	1PE	C12-C22-OH3-C23
4	A	1364	1PE	C16-C26-OH6-C15
4	A	1364	1PE	OH2-C12-C22-OH3
3	B	1375	MLI	C3-C1-C2-O6

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Mol	Chain	Res	Type	Atoms
5	B	1376	PEG	C1-C2-O2-C3
4	A	1364	1PE	C14-C24-OH4-C13
3	A	1362	MLI	C3-C1-C2-O7

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1365	1PE	3	0
5	B	1376	PEG	2	0
4	A	1364	1PE	1	0
3	B	1375	MLI	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	334/364 (91%)	0.07	20 (5%) 27 29	11, 24, 51, 68	7 (2%)
2	B	324/383 (84%)	0.53	46 (14%) 6 6	10, 28, 60, 84	9 (2%)
All	All	658/747 (88%)	0.30	66 (10%) 12 13	10, 26, 54, 84	16 (2%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	184	LEU	5.9
2	B	368	THR	5.7
2	B	188	THR	4.9
2	B	369	PRO	4.8
2	B	191	VAL	4.8
1	A	187	LEU	4.4
2	B	6	ILE	4.2
2	B	194	PRO	4.2
2	B	195	PRO	4.2
1	A	191	LEU	4.1
2	B	192	ASN	4.1
1	A	361	PRO	3.8
2	B	374	MET	3.8
2	B	355	TYR	3.8
2	B	87	ARG	3.7
2	B	183	VAL	3.5
1	A	294	GLY	3.5
2	B	90	ARG	3.4
2	B	366	ALA	3.3
1	A	180	VAL	3.2
1	A	0	SER	3.1
2	B	354	ASP	3.1
1	A	189	PRO	3.1
2	B	108	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	340	PRO	3.1
1	A	182	PRO	2.9
2	B	197	VAL	2.9
2	B	189	LEU	2.8
2	B	367	ILE	2.8
2	B	122	THR	2.8
1	A	190	GLU	2.8
2	B	185	ALA	2.8
2	B	53	GLU	2.8
1	A	257	PRO	2.8
2	B	187	GLU	2.7
1	A	183	ASN	2.7
2	B	186	GLY	2.7
1	A	188	ASP	2.7
2	B	109	ASP	2.7
1	A	185	ARG	2.6
1	A	161	GLU	2.6
2	B	180	MET	2.6
2	B	175	VAL	2.6
2	B	193	ASP	2.5
2	B	198	LEU	2.5
2	B	150	VAL	2.5
2	B	162	GLU	2.4
1	A	129	LEU	2.4
1	A	94	THR	2.4
2	B	200	ARG	2.4
1	A	92	PRO	2.3
1	A	293	SER	2.3
2	B	52	GLN	2.3
2	B	357	VAL	2.2
2	B	54	LYS	2.2
2	B	50	ASP	2.2
2	B	263	ASN	2.2
2	B	370	MET	2.2
2	B	117	LYS	2.2
2	B	371	LYS	2.2
2	B	373	PRO	2.2
1	A	186	LYS	2.2
2	B	365	TYR	2.1
1	A	192	HIS	2.1
2	B	363	THR	2.0
2	B	51	GLU	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	MLI	A	1362	7/7	0.71	0.19	29,51,59,60	0
4	1PE	A	1364	16/16	0.74	0.19	40,47,62,64	0
5	PEG	B	1376	7/7	0.79	0.20	41,44,54,56	0
4	1PE	A	1365	16/16	0.80	0.19	46,61,73,78	0
3	MLI	B	1375	7/7	0.85	0.15	30,33,44,56	0
5	PEG	A	1366	7/7	0.87	0.14	41,46,56,57	0
3	MLI	A	1363	7/7	0.92	0.10	27,37,45,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.