



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:04 PM UTC

PDB ID : 2PFL / pdb_00002pfl
Title : CRYSTAL STRUCTURE OF PFL FROM E.COLI
Authors : Becker, A.; Fritz-Wolf, K.; Kabsch, W.; Knappe, J.; Schultz, S.; Wagner, A.F.V.
Deposited on : 1999-05-26
Resolution : 2.90 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
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

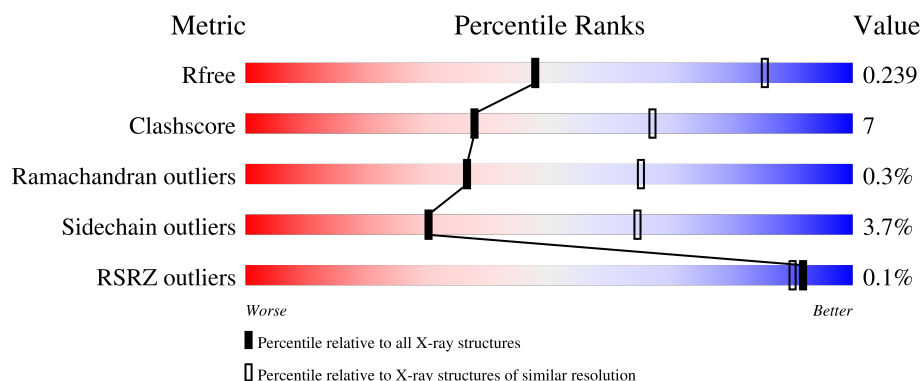
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	759	 81% 18% .
1	B	759	 79% 19% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12751 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 (PYRUVATE FORMATE-LYASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	759	Total	C	N	O	S	0	1	0
			5997	3789	1025	1147	36			
1	B	759	Total	C	N	O	S	0	2	0
			6008	3795	1029	1148	36			

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	B	1	Total	Na	0	0
			1	1		

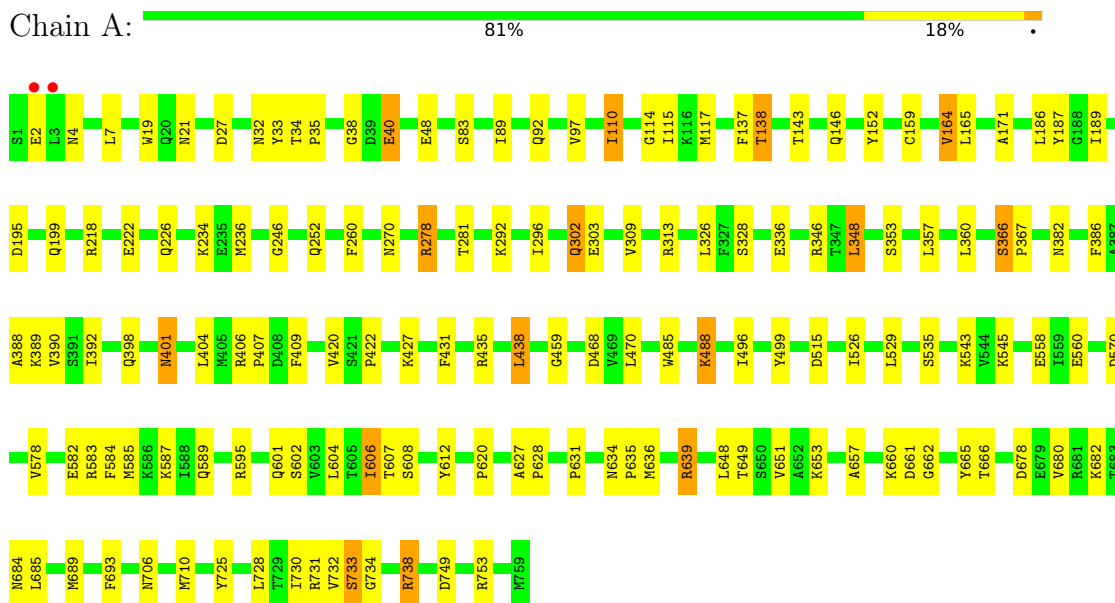
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	398	Total	O	0	0
			398	398		
4	B	344	Total	O	0	0
			344	344		

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: PROTEIN (PYRUVATE FORMATE-LYASE)





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	159.02Å 159.02Å 160.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90 15.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (15.00-2.90) 97.8 (15.00-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.91Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.202 , 0.242 0.202 , 0.239	Depositor DCC
R_{free} test set	2176 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	64.3	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for -h,l,k 0.000 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12751	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: NA, CL

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	0.46	0/6118	0.95	21/8265 (0.3%)
1	B	0.46	0/6129	0.95	25/8279 (0.3%)
All	All	0.46	0/12247	0.95	46/16544 (0.3%)

There are no bond length outliers.

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ILE	N-CA-C	-7.59	103.53	111.58
1	B	89	ILE	N-CA-C	-7.48	103.65	111.58
1	B	32	ASN	N-CA-C	6.78	122.45	114.04
1	B	732	VAL	N-CA-C	6.57	119.97	113.53
1	A	83	SER	N-CA-C	6.45	118.31	111.28
1	B	401	ASN	N-CA-C	6.45	118.94	108.63
1	A	138	THR	N-CA-C	-6.39	107.33	114.62
1	B	138	THR	N-CA-C	-6.38	107.34	114.62
1	A	732	VAL	N-CA-C	6.38	119.78	113.53
1	A	32	ASN	N-CA-C	6.32	122.46	114.31
1	B	83	SER	N-CA-C	6.29	118.14	111.28
1	B	187	TYR	N-CA-C	6.21	120.93	113.23
1	A	366	SER	CA-C-N	6.20	125.61	118.85
1	A	366	SER	C-N-CA	6.20	125.61	118.85
1	A	401	ASN	N-CA-C	6.12	118.42	108.63
1	A	246	GLY	CA-C-N	6.08	125.99	119.85
1	A	246	GLY	C-N-CA	6.08	125.99	119.85
1	A	187	TYR	N-CA-C	6.02	120.91	113.50
1	B	499	TYR	N-CA-C	-5.84	104.99	111.36
1	B	137	PHE	N-CA-C	5.81	119.13	112.97
1	A	328	SER	N-CA-C	5.75	118.12	110.53
1	A	570	ASP	CA-C-N	5.72	125.58	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	570	ASP	C-N-CA	5.72	125.58	119.28
1	B	366	SER	CA-C-N	5.69	125.06	118.85
1	B	366	SER	C-N-CA	5.69	125.06	118.85
1	B	97	VAL	N-CA-C	5.67	117.34	109.29
1	B	328	SER	N-CA-C	5.61	117.93	110.53
1	A	110	ILE	CA-C-N	5.60	125.22	119.56
1	A	110	ILE	C-N-CA	5.60	125.22	119.56
1	A	97	VAL	N-CA-C	5.58	117.21	109.29
1	A	137	PHE	N-CA-C	5.49	118.79	112.97
1	B	559	ILE	N-CA-C	5.41	115.65	107.75
1	A	499	TYR	N-CA-C	-5.40	105.47	111.36
1	B	246	GLY	CA-C-N	5.40	125.69	119.92
1	B	246	GLY	C-N-CA	5.40	125.69	119.92
1	B	110	ILE	CA-C-N	5.31	124.92	119.56
1	B	110	ILE	C-N-CA	5.31	124.92	119.56
1	A	738	ARG	N-CA-C	-5.30	102.43	110.28
1	B	738	ARG	N-CA-C	-5.16	102.64	110.28
1	B	375	TRP	N-CA-C	5.14	117.89	110.28
1	B	639	ARG	N-CA-C	5.12	117.59	111.71
1	B	71	VAL	N-CA-C	-5.08	105.58	110.72
1	A	639	ARG	N-CA-C	5.05	117.52	111.71
1	B	111	PRO	N-CA-C	5.05	120.17	113.86
1	B	721	ASN	CA-C-N	5.04	124.21	118.97
1	B	721	ASN	C-N-CA	5.04	124.21	118.97

There are no chirality outliers.

There are no planarity outliers.

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	5997	0	5921	80	0
1	B	6008	0	5933	88	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	398	0	0	7	0
4	B	344	0	0	8	0
All	All	12751	0	11854	166	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 7.

All (166) 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:710:MET:HE1	1:A:730:ILE:HG22	1.62	0.79
1:B:602:SER:HB3	1:B:661:ASP:HB3	1.64	0.79
1:A:602:SER:HB3	1:A:661:ASP:HB3	1.63	0.79
1:B:40:GLU:HG2	1:B:386:PHE:CD1	2.18	0.78
1:A:40:GLU:HG2	1:A:386:PHE:CD1	2.20	0.76
1:B:666:THR:HA	1:B:706:ASN:HB2	1.71	0.72
1:A:389:LYS:HG2	1:A:682:LYS:HD3	1.71	0.72
1:A:666:THR:HA	1:A:706:ASN:HB2	1.70	0.71
1:B:710:MET:HE1	1:B:730:ILE:HG22	1.73	0.69
1:B:389:LYS:HG2	1:B:682:LYS:HD3	1.73	0.69
1:A:685:LEU:HD23	1:A:689:MET:HE2	1.77	0.66
1:B:159:CYS:HB3	1:B:164:VAL:HG12	1.77	0.66
1:A:34:THR:HG23	4:A:2377:HOH:O	1.97	0.65
1:B:545:LYS:HB3	1:B:558:GLU:HB2	1.77	0.65
1:A:115:ILE:HG22	4:A:2233:HOH:O	1.95	0.64
1:B:578:VAL:HG13	1:B:655:PRO:HD3	1.79	0.64
1:A:159:CYS:HB3	1:A:164:VAL:HG12	1.78	0.64
1:B:110:ILE:HG22	4:B:2202:HOH:O	1.98	0.62
1:B:278:ARG:HD2	4:B:2033:HOH:O	1.99	0.61
1:A:278:ARG:HD2	4:A:2162:HOH:O	2.00	0.60
1:B:685:LEU:HG	1:B:689:MET:HE2	1.84	0.60
1:A:543:LYS:HB3	1:A:560:GLU:HB3	1.84	0.60
1:B:4:ASN:HB3	1:B:7:LEU:HG	1.84	0.60
1:A:420:VAL:HG23	1:A:662:GLY:HA3	1.84	0.59
1:B:606:ILE:HG22	1:B:607:THR:H	1.68	0.58
1:A:438:LEU:HG	1:A:526:ILE:HD12	1.86	0.57
1:B:438:LEU:HG	1:B:526:ILE:HD12	1.86	0.57
1:B:546:PRO:HB2	1:B:548:ARG:HE	1.68	0.57
1:A:143:THR:H	1:A:146[B]:GLN:HE21	1.50	0.57
1:A:4:ASN:HB3	1:A:7:LEU:HG	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:VAL:HG13	1:B:711:ASN:HD21	1.69	0.57
1:B:420:VAL:HG23	1:B:662:GLY:HA3	1.86	0.57
1:B:40:GLU:HG2	1:B:386:PHE:CG	2.41	0.56
1:A:2:GLU:HG2	1:A:21:ASN:HA	1.89	0.55
1:A:302:GLN:HG2	4:A:2139:HOH:O	2.05	0.55
1:A:606:ILE:HG22	1:A:607:THR:H	1.71	0.55
1:A:678:ASP:O	1:A:682:LYS:HG3	2.05	0.55
1:A:636:MET:HB2	1:A:639:ARG:HD2	1.88	0.55
1:B:636:MET:HB2	1:B:639:ARG:HD2	1.88	0.55
1:B:143:THR:OG1	1:B:146[B]:GLN:HG2	2.07	0.55
1:B:678:ASP:O	1:B:682:LYS:HG3	2.07	0.54
1:A:40:GLU:HG2	1:A:386:PHE:CG	2.42	0.54
1:A:33:TYR:CE1	1:A:35:PRO:HG3	2.43	0.54
1:A:189:ILE:HG21	1:A:234:LYS:HG3	1.89	0.54
1:B:189:ILE:HG21	1:B:234:LYS:HG3	1.92	0.52
1:A:409:PHE:HE2	1:A:422:PRO:HB2	1.75	0.51
1:A:657:ALA:HA	1:A:660:LYS:HE3	1.92	0.51
1:B:367:PRO:HG2	1:B:738:ARG:HG3	1.93	0.51
1:B:657:ALA:HA	1:B:660:LYS:HE3	1.92	0.51
1:B:749:ASP:O	1:B:753:ARG:HG3	2.10	0.51
1:A:367:PRO:HG2	1:A:738:ARG:HG3	1.92	0.51
1:A:545:LYS:HG3	1:A:558:GLU:HB2	1.92	0.51
1:A:406:ARG:HB3	1:A:407:PRO:HD3	1.93	0.51
1:B:507:GLU:HG2	4:B:2162:HOH:O	2.11	0.50
1:B:583:ARG:O	1:B:587:LYS:HG3	2.10	0.50
1:B:33:TYR:CE1	1:B:35:PRO:HG3	2.46	0.50
1:A:680:VAL:HG12	1:A:684:ASN:ND2	2.27	0.50
1:B:680:VAL:HG12	1:B:684:ASN:ND2	2.27	0.49
1:B:406:ARG:HB3	1:B:407:PRO:HD3	1.95	0.49
1:B:623:ARG:NH1	1:B:627:ALA:O	2.46	0.49
1:B:115:ILE:HG21	1:B:138:THR:CG2	2.42	0.49
1:B:409:PHE:HE2	1:B:422:PRO:HB2	1.77	0.49
1:B:446:ILE:HA	1:B:465:ILE:HD13	1.95	0.49
1:B:648:LEU:HD23	1:B:665:TYR:HE2	1.78	0.49
1:A:401:ASN:ND2	1:A:404:LEU:HB2	2.29	0.48
1:A:601:GLN:HG2	1:A:602:SER:N	2.29	0.48
1:B:670:VAL:HG13	1:B:711:ASN:ND2	2.28	0.48
1:A:114:GLY:HA3	1:A:117:MET:HE1	1.95	0.48
1:A:635:PRO:HD2	4:A:2151:HOH:O	2.14	0.48
1:A:115:ILE:HG21	1:A:138:THR:CG2	2.44	0.48
1:A:648:LEU:HD23	1:A:665:TYR:HE2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:481:HIS:HB2	4:B:2119:HOH:O	2.14	0.48
1:B:706:ASN:HD21	1:B:734:GLY:N	2.12	0.48
1:B:110:ILE:HG13	1:B:270:ASN:HB3	1.96	0.47
1:B:601:GLN:HG2	1:B:602:SER:N	2.29	0.47
1:B:725:TYR:HB3	1:B:728:LEU:HB2	1.96	0.47
1:A:386:PHE:O	1:A:390:VAL:HG23	2.14	0.47
1:A:92:GLN:NE2	1:A:92:GLN:H	2.11	0.47
1:B:346:ARG:NH2	4:B:2079:HOH:O	2.48	0.47
1:A:110:ILE:HG13	1:A:270:ASN:HB3	1.97	0.47
1:A:583:ARG:O	1:A:587:LYS:HG3	2.14	0.47
1:B:649:THR:O	1:B:653:LYS:HG3	2.15	0.47
1:A:117:MET:HE3	1:A:171:ALA:HA	1.96	0.47
1:B:401:ASN:ND2	1:B:404:LEU:HB2	2.30	0.47
1:B:578:VAL:O	1:B:582:GLU:HG3	2.14	0.47
1:B:195:ASP:O	1:B:199:GLN:HG3	2.14	0.47
1:B:386:PHE:O	1:B:390:VAL:HG23	2.15	0.46
1:B:651:VAL:HG11	1:B:665:TYR:HB2	1.97	0.46
1:B:92:GLN:NE2	1:B:92:GLN:H	2.12	0.46
1:A:459:GLY:HA2	1:A:485:TRP:CZ2	2.50	0.46
1:A:706:ASN:HD21	1:A:734:GLY:N	2.13	0.46
1:B:313:ARG:CZ	1:B:366:SER:HB2	2.46	0.46
1:B:526:ILE:HD11	1:B:584:PHE:CD2	2.51	0.46
1:A:353:SER:O	1:A:357:LEU:HD13	2.14	0.46
1:A:749:ASP:O	1:A:753:ARG:HG3	2.16	0.46
1:A:651:VAL:HG11	1:A:665:TYR:HB2	1.97	0.46
1:B:353:SER:O	1:B:357:LEU:HD13	2.15	0.46
1:A:195:ASP:O	1:A:199:GLN:HG3	2.16	0.45
1:B:116:LYS:HB2	1:B:117:MET:HE3	1.99	0.45
1:B:566:PHE:O	1:B:635:PRO:HB3	2.17	0.45
1:A:604:LEU:HD12	4:A:2020:HOH:O	2.17	0.45
1:A:526:ILE:HD11	1:A:584:PHE:CD2	2.52	0.45
1:A:725:TYR:HB3	1:A:728:LEU:HB2	1.97	0.45
1:B:19:TRP:HB3	1:B:27:ASP:HB3	1.99	0.45
1:A:4:ASN:H	1:A:7:LEU:HD12	1.82	0.45
1:B:565:GLN:C	1:B:573:VAL:HG11	2.42	0.44
1:B:218:ARG:O	1:B:222:GLU:HG3	2.17	0.44
1:B:222:GLU:O	1:B:226:GLN:HG3	2.17	0.44
1:B:649:THR:HG22	1:B:653:LYS:HE2	2.00	0.44
1:A:159:CYS:HB3	1:A:165:LEU:HB2	1.98	0.44
1:B:236:MET:HE1	1:B:260:PHE:O	2.17	0.44
1:A:38:GLY:C	1:A:382:ASN:HD22	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:MET:HE1	1:A:260:PHE:O	2.18	0.44
1:A:606:ILE:HG22	1:A:607:THR:N	2.32	0.44
1:A:218:ARG:O	1:A:222:GLU:HG3	2.18	0.44
1:A:19:TRP:HB3	1:A:27:ASP:HB3	1.99	0.43
1:A:488:LYS:HE2	1:B:208:GLU:HB3	1.98	0.43
1:B:605:THR:O	1:B:608:SER:HB2	2.18	0.43
1:B:606:ILE:HG22	1:B:607:THR:N	2.32	0.43
1:A:631:PRO:O	1:A:634:ASN:HB2	2.19	0.43
1:A:401:ASN:HB2	1:A:693:PHE:CD2	2.54	0.43
1:A:313:ARG:CZ	1:A:366:SER:HB2	2.49	0.43
1:B:281:THR:HG21	1:B:348:LEU:HD12	2.01	0.42
1:B:627:ALA:HA	1:B:628:PRO:HD3	1.88	0.42
1:B:680:VAL:HG12	1:B:684:ASN:HD21	1.84	0.42
1:A:496:ILE:HD11	1:B:207:LEU:HD21	2.00	0.42
1:B:420:VAL:O	1:B:422:PRO:HD3	2.19	0.42
1:A:398:GLN:HB3	1:A:731:ARG:NH2	2.34	0.42
1:A:535:SER:HB3	1:A:620:PRO:HB2	2.01	0.42
1:B:186:LEU:HD13	1:B:187:TYR:CE1	2.54	0.42
1:B:631:PRO:O	1:B:634:ASN:HB2	2.20	0.42
1:B:113:GLY:N	4:B:2202:HOH:O	2.52	0.42
1:B:115:ILE:HG21	1:B:138:THR:HG23	2.02	0.42
1:A:117:MET:HE3	1:A:171:ALA:C	2.44	0.42
1:A:281:THR:HG21	1:A:348:LEU:HD12	2.01	0.42
1:A:427:LYS:HG2	1:A:515:ASP:OD1	2.20	0.42
1:A:608:SER:O	1:A:612:TYR:HB2	2.20	0.42
1:B:117:MET:HE3	1:B:117:MET:N	2.34	0.42
1:B:322:GLU:CD	4:B:2134:HOH:O	2.61	0.42
1:A:680:VAL:HG12	1:A:684:ASN:HD21	1.83	0.42
1:B:585:MET:O	1:B:589:GLN:HB2	2.20	0.42
1:B:670:VAL:HG13	1:B:671:PRO:HD2	2.01	0.42
1:A:222:GLU:O	1:A:226:GLN:HG3	2.20	0.41
1:B:295:LYS:O	1:B:296:ILE:HD12	2.20	0.41
1:B:388:ALA:O	1:B:392:ILE:HG13	2.19	0.41
1:B:535:SER:HB3	1:B:620:PRO:HB2	2.01	0.41
1:A:303:GLU:HA	4:A:2131:HOH:O	2.20	0.41
1:A:406:ARG:HG2	1:A:406:ARG:HH11	1.86	0.41
1:A:420:VAL:O	1:A:422:PRO:HD3	2.19	0.41
1:A:627:ALA:HA	1:A:628:PRO:HD3	1.86	0.41
1:A:115:ILE:HG21	1:A:138:THR:HG23	2.02	0.41
1:B:312:LEU:HB2	1:B:369:PRO:HG3	2.03	0.41
1:A:388:ALA:O	1:A:392:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:465:ILE:N	1:B:465:ILE:HD12	2.36	0.41
1:B:628:PRO:HG3	4:B:2063:HOH:O	2.20	0.41
1:B:656:PHE:CD1	1:B:703:GLN:HG3	2.56	0.41
1:A:585:MET:O	1:A:589:GLN:HB2	2.20	0.41
1:A:649:THR:O	1:A:653:LYS:HG3	2.22	0.40
1:B:176:ARG:HB3	1:B:430:GLN:HB2	2.03	0.40
1:A:366:SER:HA	1:A:367:PRO:HD3	1.83	0.40
1:A:578:VAL:O	1:A:582:GLU:HG3	2.21	0.40
1:B:565:GLN:O	1:B:573:VAL:HG11	2.21	0.40
1:B:251:ALA:HA	1:B:286:TYR:HB3	2.04	0.40
1:B:604:LEU:HD13	1:B:664:SER:HB2	2.03	0.40
1:A:309:VAL:O	1:A:313:ARG:HG3	2.21	0.40
1:B:427:LYS:HG2	1:B:515:ASP:OD1	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	758/759 (100%)	716 (94%)	40 (5%)	2 (0%)	36	65
1	B	759/759 (100%)	716 (94%)	40 (5%)	3 (0%)	30	59
All	All	1517/1518 (100%)	1432 (94%)	80 (5%)	5 (0%)	36	65

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	ILE
1	A	733	SER
1	B	606	ILE
1	B	733	SER
1	B	550	GLU

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	639/638 (100%)	615 (96%)	24 (4%)	29	64
1	B	640/638 (100%)	617 (96%)	23 (4%)	31	65
All	All	1279/1276 (100%)	1232 (96%)	47 (4%)	30	64

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLU
1	A	48	GLU
1	A	152	TYR
1	A	164	VAL
1	A	186	LEU
1	A	252	GLN
1	A	278	ARG
1	A	292	LYS
1	A	296	ILE
1	A	302	GLN
1	A	326	LEU
1	A	336	GLU
1	A	346	ARG
1	A	348	LEU
1	A	360	LEU
1	A	431	PHE
1	A	435	ARG
1	A	438	LEU
1	A	468	ASP
1	A	470	LEU
1	A	488	LYS
1	A	529	LEU
1	A	595	ARG
1	A	733	SER
1	B	5	GLU
1	B	40	GLU
1	B	75	THR

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Mol	Chain	Res	Type
1	B	117	MET
1	B	152	TYR
1	B	157	LEU
1	B	164	VAL
1	B	186	LEU
1	B	278	ARG
1	B	296	ILE
1	B	336	GLU
1	B	346	ARG
1	B	348	LEU
1	B	360	LEU
1	B	431	PHE
1	B	435	ARG
1	B	438	LEU
1	B	454	LEU
1	B	468	ASP
1	B	488	LYS
1	B	529	LEU
1	B	595	ARG
1	B	733	SER

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

Mol	Chain	Res	Type
1	A	92	GLN
1	A	302	GLN
1	A	358	ASN
1	A	382	ASN
1	A	748	GLN
1	B	92	GLN
1	B	382	ASN
1	B	410	ASN
1	B	471	ASN
1	B	684	ASN
1	B	711	ASN
1	B	748	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	759/759 (100%)	-0.52	2 (0%) 90 87	22, 64, 87, 100	1 (0%)
1	B	759/759 (100%)	-0.39	0 100 100	28, 67, 99, 100	2 (0%)
All	All	1518/1518 (100%)	-0.46	2 (0%) 92 90	22, 65, 95, 100	3 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	GLU	4.9
1	A	3	LEU	2.4

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(Å ²)	Q<0.9
3	NA	A	2001	1/1	0.82	0.12	69,69,69,69	0
3	NA	B	2002	1/1	0.85	0.10	90,90,90,90	0
2	CL	A	1001	1/1	0.88	0.16	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CL	B	1002	1/1	0.91	0.16	77,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.