



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:06 AM GMT

PDB ID : 2PFL
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
<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

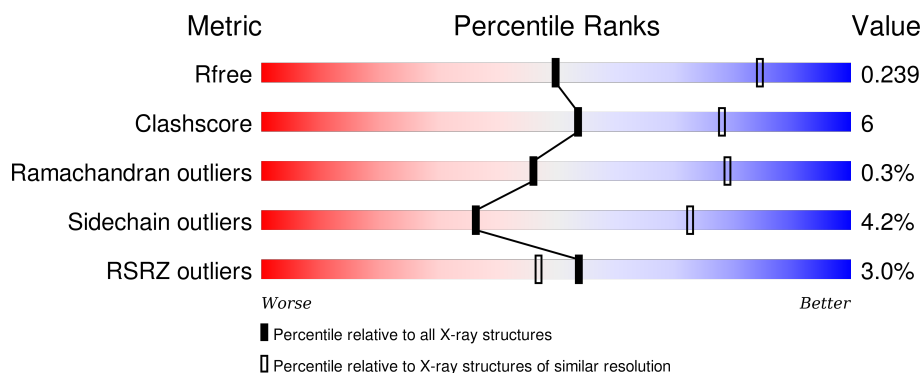
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	759	<div> <div>2%</div> <div>82%</div> <div>17%</div> </div>
1	B	759	<div> <div>4%</div> <div>81%</div> <div>18%</div> </div>

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 (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

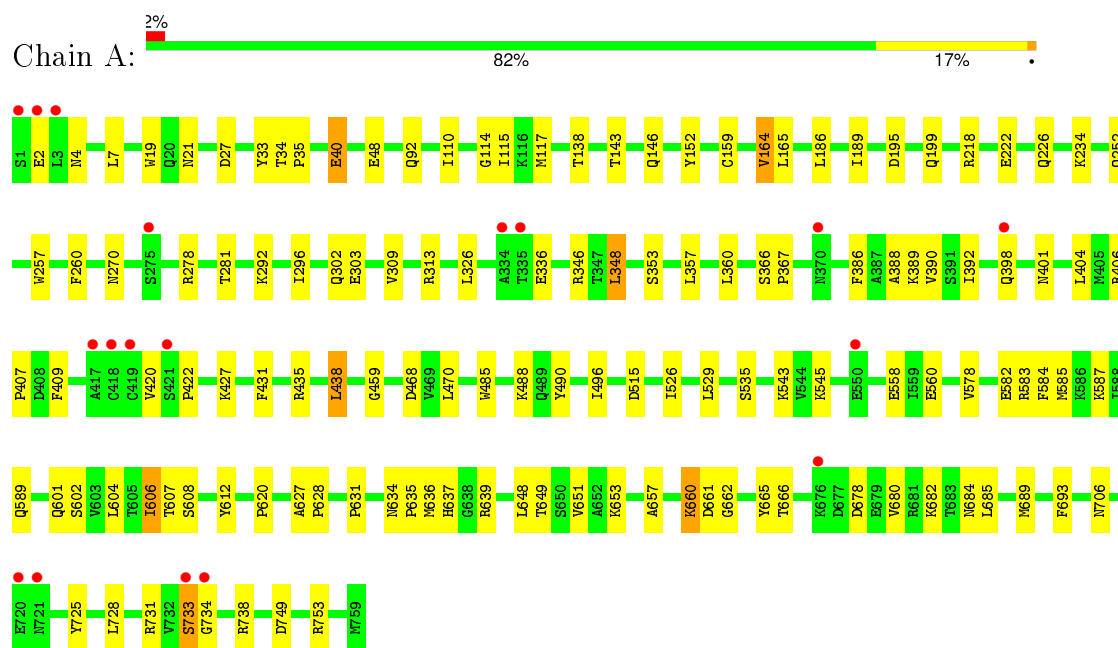
- Molecule 4 is water.

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

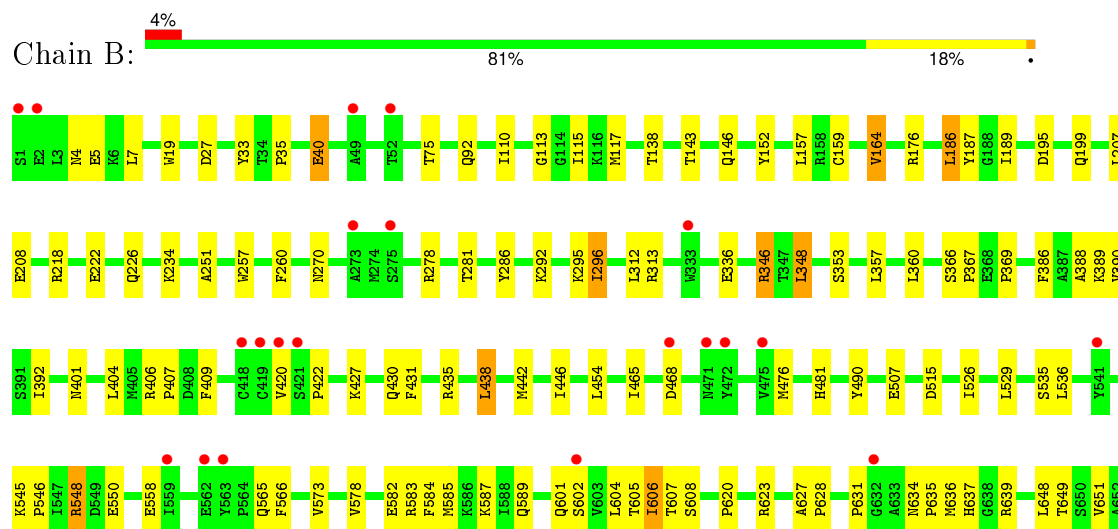
3 Residue-property plots

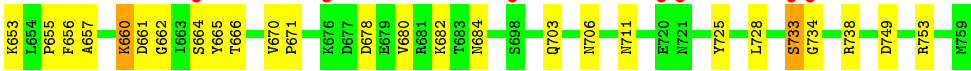
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: PROTEIN (PYRUVATE FORMATE-LYASE)



• 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 48.34 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.7 (15.00-2.90) 98.5 (48.34-2.90)	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 0.5	Depositor
R, R_{free}	0.202 , 0.242 0.202 , 0.239	Depositor DCC
R_{free} test set	2161 reflections (4.78%)	DCC
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 , 41.5	EDS
Estimated twinning fraction	0.010 for -h,l,k 0.000 for -l,-k,-h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 45503 reflections	Xtriage
F_o, F_c correlation	0.94	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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.37	0/6118	0.59	0/8265
1	B	0.38	0/6129	0.59	0/8279
All	All	0.37	0/12247	0.59	0/16544

There are no bond length outliers.

There are no bond angle outliers.

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	75	0
1	B	6008	0	5933	82	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	398	0	0	7	0
4	B	344	0	0	7	0
All	All	12751	0	11854	155	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 6.

All (155) 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: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:389:LYS:HG2	1:B:682:LYS:HD3	1.73	0.69
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:4:ASN:HB3	1:B:7:LEU:HG	1.84	0.60
1:A:543:LYS:HB3	1:A:560:GLU:HB3	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:B:670:VAL:HG13	1:B:711:ASN:HD21	1.69	0.57
1:A:4:ASN:HB3	1:A:7:LEU:HG	1.86	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:678:ASP:O	1:A:682:LYS:HG3	2.05	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:2:GLU:HG2	1:A:21:ASN:HA	1.89	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:189:ILE:HG21	1:A:234:LYS:HG3	1.89	0.54
1:A:33:TYR:CE1	1:A:35:PRO:HG3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:657:ALA:HA	1:B:660:LYS:HE3	1.92	0.51
1:B:367:PRO:HG2	1:B:738:ARG:HG3	1.93	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:409:PHE:HE2	1:B:422:PRO:HB2	1.77	0.49
1:B:115:ILE:HG21	1:B:138:THR:CG2	2.42	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:114:GLY:HA3	1:A:117:MET:HE1	1.95	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:401:ASN:ND2	1:A:404:LEU:HB2	2.29	0.48
1:A:635:PRO:HD2	4:A:2151:HOH:O	2.14	0.48
1:B:706:ASN:HD21	1:B:734:GLY:N	2.12	0.48
1:A:115:ILE:HG21	1:A:138:THR:CG2	2.44	0.48
1:B:481:HIS:HB2	4:B:2119:HOH:O	2.14	0.48
1:A:648:LEU:HD23	1:A:665:TYR:HE2	1.79	0.48
1:B:601:GLN:HG2	1:B:602:SER:N	2.29	0.47
1:B:110:ILE:HG13	1:B:270:ASN:HB3	1.96	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:685:LEU:HD23	1:A:689:MET:HE2	1.95	0.47
1:B:578:VAL:O	1:B:582:GLU:HG3	2.14	0.47
1:B:401:ASN:ND2	1:B:404:LEU:HB2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:A:459:GLY:HA2	1:A:485:TRP:CZ2	2.50	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: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:649:THR:HG22	1:B:653:LYS:HE2	2.00	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:A:159:CYS:HB3	1:A:165:LEU:HB2	1.98	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:B:606:ILE:HG22	1:B:607:THR:N	2.32	0.43
1:B:605:THR:O	1:B:608:SER:HB2	2.18	0.43
1:A:488:LYS:HE2	1:B:208:GLU:HB3	1.98	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:680:VAL:HG12	1:B:684:ASN:HD21	1.84	0.42
1:B:627:ALA:HA	1:B:628:PRO:HD3	1.88	0.42
1:B:281:THR:HG21	1:B:348:LEU:HD12	2.01	0.42
1:B:442:MET:HE1	1:B:536:LEU:HG	2.00	0.42
1:B:420:VAL:O	1:B:422:PRO:HD3	2.19	0.42
1:A:496:ILE:HD11	1:B:207:LEU:HD21	2.00	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:631:PRO:O	1:B:634:ASN:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:LEU:HD13	1:B:187:TYR:CE1	2.54	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:608:SER:O	1:A:612:TYR:HB2	2.20	0.42
1:A:427:LYS:HG2	1:A:515:ASP:OD1	2.20	0.42
1:A:281:THR:HG21	1:A:348:LEU:HD12	2.01	0.42
1:A:680:VAL:HG12	1:A:684:ASN:HD21	1.83	0.42
1:B:670:VAL:HG13	1:B:671:PRO:HD2	2.01	0.42
1:B:585:MET:O	1:B:589:GLN:HB2	2.20	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:535:SER:HB3	1:B:620:PRO:HB2	2.01	0.41
1:B:388:ALA:O	1:B:392:ILE:HG13	2.19	0.41
1:A:420:VAL:O	1:A:422:PRO:HD3	2.19	0.41
1:A:406:ARG:HH11	1:A:406:ARG:HG2	1.86	0.41
1:A:303:GLU:HA	4:A:2131:HOH:O	2.20	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:B:628:PRO:HG3	4:B:2063:HOH:O	2.20	0.41
1:B:465:ILE:N	1:B:465:ILE:HD12	2.36	0.41
1:B:656:PHE:CD1	1:B:703:GLN:HG3	2.56	0.41
1:A:388:ALA:O	1:A:392:ILE:HG13	2.20	0.41
1:A:585:MET:O	1:A:589:GLN:HB2	2.20	0.41
1:B:176:ARG:HB3	1:B:430:GLN:HB2	2.03	0.40
1:A:649:THR:O	1:A:653:LYS:HG3	2.22	0.40
1:A:366:SER:HA	1:A:367:PRO:HD3	1.83	0.40
1:B:565:GLN:O	1:B:573:VAL:HG11	2.21	0.40
1:A:578:VAL:O	1:A:582:GLU:HG3	2.21	0.40
1:B:604:LEU:HD13	1:B:664:SER:HB2	2.03	0.40
1:B:251:ALA:HA	1:B:286:TYR:HB3	2.04	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%)	46	79
1	B	759/759 (100%)	716 (94%)	40 (5%)	3 (0%)	39	74
All	All	1517/1518 (100%)	1432 (94%)	80 (5%)	5 (0%)	46	79

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 [i](#)

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%)	614 (96%)	25 (4%)	39	75
1	B	640/638 (100%)	612 (96%)	28 (4%)	35	70
All	All	1279/1276 (100%)	1226 (96%)	53 (4%)	36	73

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLU

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Mol	Chain	Res	Type
1	A	48	GLU
1	A	152	TYR
1	A	164	VAL
1	A	186	LEU
1	A	252	GLN
1	A	257	TRP
1	A	260	PHE
1	A	292	LYS
1	A	296	ILE
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	490	TYR
1	A	529	LEU
1	A	637	HIS
1	A	660	LYS
1	A	733	SER
1	B	5	GLU
1	B	40	GLU
1	B	75	THR
1	B	117	MET
1	B	152	TYR
1	B	157	LEU
1	B	164	VAL
1	B	186	LEU
1	B	257	TRP
1	B	260	PHE
1	B	292	LYS
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

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Mol	Chain	Res	Type
1	B	438	LEU
1	B	454	LEU
1	B	468	ASP
1	B	476	MET
1	B	490	TYR
1	B	529	LEU
1	B	548	ARG
1	B	637	HIS
1	B	660	LYS
1	B	733	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	358	ASN
1	A	382	ASN
1	A	748	GLN
1	B	92	GLN
1	B	358	ASN
1	B	382	ASN
1	B	711	ASN
1	B	748	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 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

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	759/759 (100%)	-0.15	18 (2%) 62 57	41, 64, 87, 100	0
1	B	759/759 (100%)	0.01	28 (3%) 45 38	39, 67, 99, 100	0
All	All	1518/1518 (100%)	-0.07	46 (3%) 54 47	39, 65, 95, 100	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	GLU	9.4
1	A	1	SER	7.3
1	A	3	LEU	5.3
1	B	419	CYS	5.0
1	B	2	GLU	4.9
1	B	1	SER	4.6
1	B	418	CYS	4.5
1	A	419	CYS	4.3
1	A	418	CYS	4.2
1	B	273	ALA	4.1
1	A	398	GLN	3.9
1	B	541	TYR	3.1
1	A	550	GLU	3.0
1	B	676	LYS	2.9
1	B	333	TRP	2.9
1	B	421	SER	2.8
1	A	335	THR	2.8
1	B	664	SER	2.8
1	A	421	SER	2.8
1	B	275	SER	2.6
1	A	720	GLU	2.6
1	B	475	VAL	2.6
1	B	468	ASP	2.6
1	A	733	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	676	LYS	2.5
1	A	721	ASN	2.5
1	B	49	ALA	2.5
1	B	698	SER	2.4
1	B	52	THR	2.4
1	A	417	ALA	2.4
1	B	602	SER	2.4
1	A	370	ASN	2.4
1	B	734	GLY	2.3
1	B	563	TYR	2.3
1	B	632	GLY	2.3
1	B	472	TYR	2.3
1	A	334	ALA	2.2
1	B	562	GLU	2.2
1	B	471	ASN	2.2
1	B	559	ILE	2.2
1	A	275	SER	2.2
1	B	721	ASN	2.2
1	A	734	GLY	2.1
1	B	720	GLU	2.1
1	B	420	VAL	2.0
1	B	733	SER	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(\AA^2)	Q<0.9
3	NA	A	2001	1/1	0.75	0.26	1.85	69,69,69,69	0
3	NA	B	2002	1/1	0.78	0.15	-0.39	90,90,90,90	0
2	CL	A	1001	1/1	0.83	0.17	-	79,79,79,79	0
2	CL	B	1002	1/1	0.89	0.27	-	77,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.