Full wwPDB X-ray Structure Validation Report ⓘ

Aug 24, 2023 – 04:12 PM JST

PDB ID	:	7Y4F
Title	:	bacterial DPP4
Authors	:	Hang, J.; Jiang, C.; Wang, K.; Zhang, Z.; Guo, F.; Liu, J.; Wang, G.; Lei, X.; Gonzalez, F.; Qiao, J.
Deposited on	:	2022-06-14
Resolution	:	1.92 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:

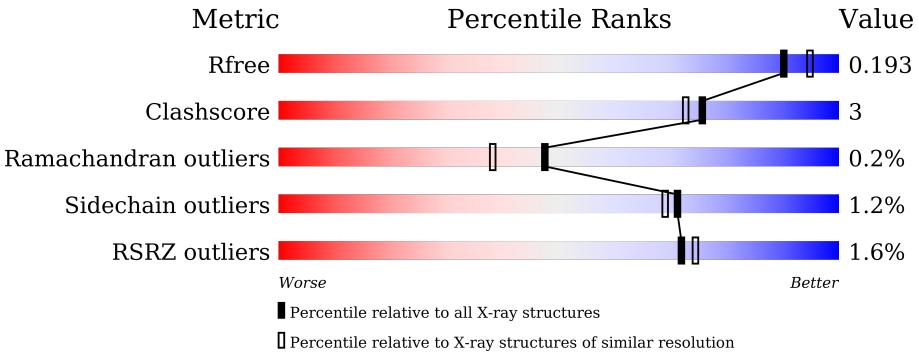
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 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}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 <=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	736	90% 6%
1	B	736	2% 91% 6%
1	C	736	90% 7%
1	D	736	3% 89% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 25882 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 Dipeptidyl peptidase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	714	Total	C	N	O	S	0	0	0
			5770	3688	960	1096	26			
1	B	714	Total	C	N	O	S	0	0	0
			5770	3688	960	1096	26			
1	C	714	Total	C	N	O	S	0	0	0
			5770	3688	960	1096	26			
1	D	714	Total	C	N	O	S	0	0	0
			5770	3688	960	1096	26			

- Molecule 2 is water.

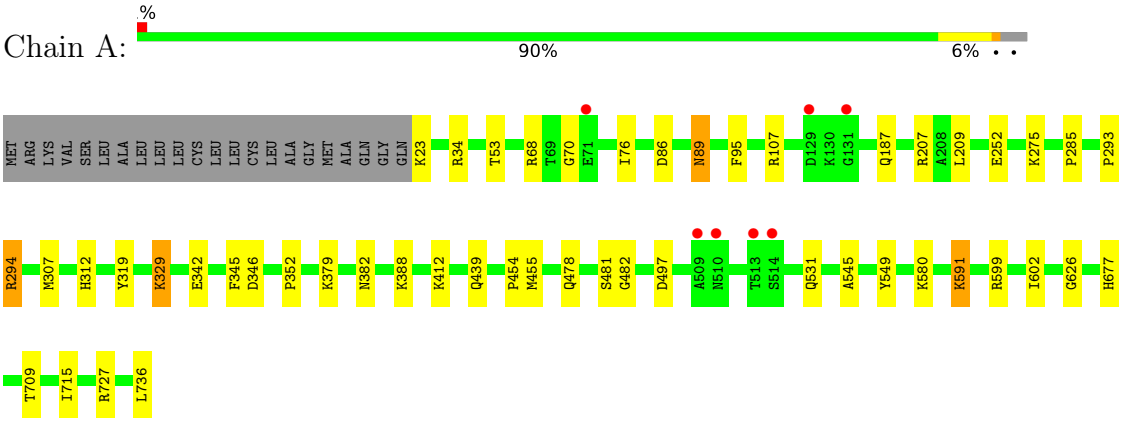
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	757	Total	O	0	0
			757	757		
2	B	725	Total	O	0	0
			725	725		
2	C	748	Total	O	0	0
			748	748		
2	D	572	Total	O	0	0
			572	572		

3 Residue-property plots (i)

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.

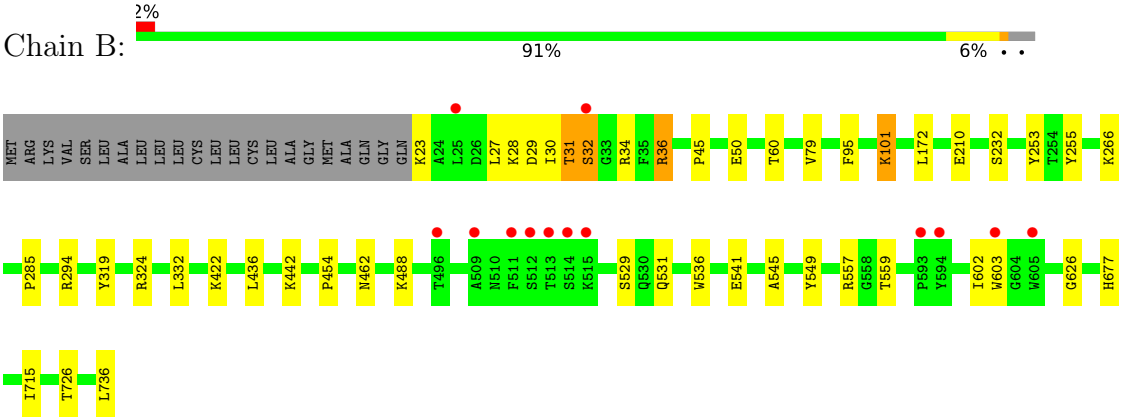
• Molecule 1: Dipeptidyl peptidase IV

Chain A:



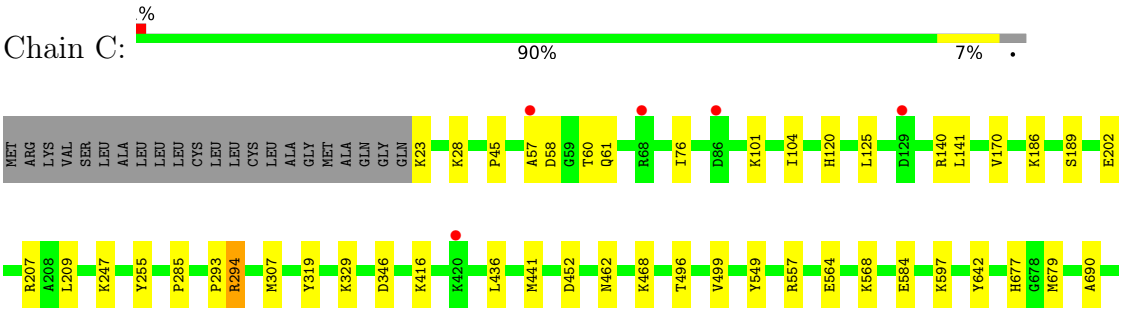
• Molecule 1: Dipeptidyl peptidase IV

Chain B:



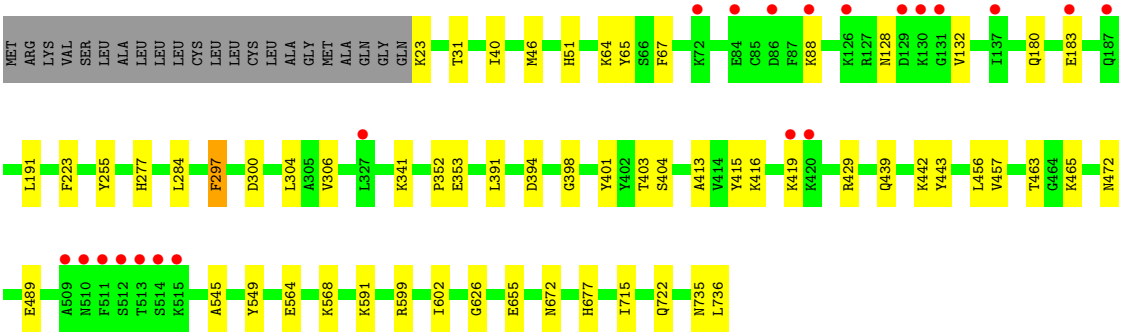
• Molecule 1: Dipeptidyl peptidase IV

Chain C:



• Molecule 1: Dipeptidyl peptidase IV

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	95.80Å 148.86Å 137.12Å 90.00° 104.02° 90.00°	Depositor
Resolution (Å)	46.36 – 1.92 46.36 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.36-1.92) 99.4 (46.36-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.168 , 0.193 0.168 , 0.193	Depositor DCC
R_{free} test set	14255 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	27.6	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 45.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	25882	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.41	0/5918	0.59	2/8008 (0.0%)
1	B	0.40	0/5918	0.58	1/8008 (0.0%)
1	C	0.41	0/5918	0.59	1/8008 (0.0%)
1	D	0.37	0/5918	0.57	0/8008
All	All	0.40	0/23672	0.58	4/32032 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	294	ARG	NE-CZ-NH2	-7.06	116.77	120.30
1	C	294	ARG	NE-CZ-NH2	-6.24	117.18	120.30
1	A	294	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	B	332	LEU	CA-CB-CG	5.14	127.13	115.30

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	5770	0	5599	39	0
1	B	5770	0	5599	37	0
1	C	5770	0	5599	31	0
1	D	5770	0	5599	35	0
2	A	757	0	0	16	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	725	0	0	13	0
2	C	748	0	0	9	1
2	D	572	0	0	11	0
All	All	25882	0	22396	141	1

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 3.

All (141) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:655:GLU:OE1	2:D:801:HOH:O	1.83	0.96
1:B:210:GLU:OE1	2:B:801:HOH:O	1.85	0.94
1:B:541:GLU:OE2	1:B:603:TRP:HZ2	1.50	0.93
1:C:101:LYS:NZ	2:C:801:HOH:O	2.08	0.85
1:D:394:ASP:OD2	2:D:802:HOH:O	1.93	0.84
1:A:107:ARG:NH1	2:A:807:HOH:O	2.12	0.81
1:A:293:PRO:O	1:A:294:ARG:HG3	1.79	0.81
1:B:541:GLU:OE2	1:B:603:TRP:CZ2	2.33	0.81
1:C:247:LYS:NZ	2:C:803:HOH:O	2.14	0.79
1:A:89:ASN:OD1	2:A:802:HOH:O	2.02	0.77
1:D:46:MET:HE3	1:D:51:HIS:HB2	1.66	0.77
1:A:352:PRO:O	2:A:803:HOH:O	2.02	0.76
1:C:23:LYS:N	2:C:804:HOH:O	2.18	0.75
1:D:489:GLU:OE1	2:D:804:HOH:O	2.04	0.75
1:B:23:LYS:N	2:B:805:HOH:O	2.20	0.74
1:A:497:ASP:OD1	2:A:804:HOH:O	2.05	0.74
1:A:454:PRO:O	2:A:805:HOH:O	2.07	0.72
1:C:23:LYS:NZ	2:C:805:HOH:O	2.19	0.71
1:A:252:GLU:OE1	2:A:806:HOH:O	2.07	0.71
1:D:46:MET:HE1	1:D:64:LYS:HG3	1.71	0.71
1:A:709:THR:HG21	1:C:690:ALA:O	1.91	0.71
1:D:463:THR:O	2:D:805:HOH:O	2.09	0.70
1:D:46:MET:CE	1:D:51:HIS:HB2	2.21	0.69
1:A:294:ARG:HG3	1:A:294:ARG:HH11	1.57	0.68
1:B:50:GLU:OE2	2:B:803:HOH:O	2.10	0.68
1:D:599:ARG:NH1	2:D:803:HOH:O	2.03	0.68
1:B:442:LYS:HA	1:B:462:ASN:HD21	1.59	0.68
1:C:441:MET:O	1:C:462:ASN:ND2	2.19	0.68
1:C:23:LYS:NZ	2:C:807:HOH:O	2.27	0.66
1:D:429:ARG:NH1	2:D:810:HOH:O	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:36:ARG:NH2	2:B:807:HOH:O	2.28	0.65
1:D:31:THR:HG22	2:D:1282:HOH:O	1.96	0.65
1:A:70:GLY:O	2:A:808:HOH:O	2.15	0.65
1:C:60:THR:HG23	1:C:61:GLN:HG3	1.81	0.61
1:D:51:HIS:HB3	1:D:65:TYR:O	2.00	0.61
1:A:294:ARG:HD2	1:A:345:PHE:HB3	1.82	0.61
1:D:341:LYS:NZ	2:D:812:HOH:O	2.30	0.61
1:A:599:ARG:HH11	1:A:736:LEU:HD22	1.64	0.61
1:B:23:LYS:N	2:B:812:HOH:O	2.34	0.60
1:B:488:LYS:NZ	2:B:810:HOH:O	2.33	0.60
1:A:388:LYS:HE3	1:A:412:LYS:HD3	1.83	0.59
1:A:23:LYS:HB3	1:A:482:GLY:O	2.03	0.59
1:B:442:LYS:HA	1:B:462:ASN:ND2	2.18	0.57
1:B:531:GLN:NE2	2:B:802:HOH:O	2.08	0.56
1:B:27:LEU:HB3	1:B:30:ILE:HD12	1.87	0.56
1:B:101:LYS:HD2	1:B:172:LEU:CD2	2.36	0.56
1:D:284:LEU:HD11	1:D:306:VAL:HG11	1.88	0.55
1:A:531:GLN:NE2	2:A:801:HOH:O	2.02	0.55
1:A:68:ARG:NH2	2:A:820:HOH:O	2.39	0.55
1:D:564:GLU:HG3	1:D:568:LYS:HD2	1.88	0.54
1:B:101:LYS:HD2	1:B:172:LEU:HD23	1.89	0.54
1:A:599:ARG:NH1	1:A:736:LEU:HD22	2.23	0.53
1:D:180:GLN:NE2	1:D:183:GLU:HG2	2.24	0.53
1:C:329:LYS:HD2	2:C:1341:HOH:O	2.09	0.53
1:A:329:LYS:N	1:A:329:LYS:HE3	2.24	0.53
1:D:442:LYS:HD2	1:D:443:TYR:CE2	2.44	0.53
1:C:293:PRO:HD2	1:C:307:MET:O	2.09	0.52
1:D:300:ASP:OD2	2:D:806:HOH:O	2.19	0.52
1:D:456:LEU:HD12	1:D:472:ASN:HA	1.91	0.52
1:A:207:ARG:NH1	1:A:209:LEU:O	2.44	0.51
1:A:53:THR:HG21	1:A:95:PHE:CZ	2.47	0.49
1:B:30:ILE:HG23	1:B:34:ARG:HD3	1.94	0.49
1:C:597:LYS:HD2	2:C:1471:HOH:O	2.12	0.49
1:B:30:ILE:HD13	1:B:34:ARG:HH11	1.78	0.49
1:C:58:ASP:OD1	1:C:60:THR:HG22	2.13	0.49
1:B:101:LYS:NZ	2:B:821:HOH:O	2.45	0.49
1:B:557:ARG:NE	2:B:824:HOH:O	2.46	0.48
1:A:478:GLN:O	1:A:481:SER:OG	2.28	0.48
1:B:324:ARG:NH1	2:B:822:HOH:O	2.46	0.48
1:B:45:PRO:HD3	1:B:436:LEU:HD21	1.96	0.47
1:C:285:PRO:HG2	1:C:319:TYR:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:HIS:HA	2:A:1080:HOH:O	2.14	0.47
1:C:564:GLU:HG3	1:C:568:LYS:HD2	1.97	0.47
1:D:191:LEU:HB2	1:D:223:PHE:HB2	1.97	0.47
1:D:23:LYS:N	2:D:837:HOH:O	2.47	0.47
1:B:232:SER:HA	1:B:253:TYR:O	2.14	0.47
1:B:31:THR:HG22	1:B:31:THR:O	2.14	0.46
1:D:549:TYR:HE2	1:D:736:LEU:HD23	1.80	0.46
1:C:293:PRO:O	1:C:294:ARG:HG3	2.16	0.46
1:B:266:LYS:NZ	2:B:819:HOH:O	2.44	0.46
1:C:294:ARG:NE	1:C:346:ASP:OD1	2.47	0.46
1:D:391:LEU:HD11	1:D:403:THR:HG23	1.96	0.46
1:A:53:THR:OG1	1:A:95:PHE:CE2	2.66	0.46
1:D:40:ILE:HD12	1:D:457:VAL:HG11	1.97	0.46
1:B:557:ARG:CZ	2:B:824:HOH:O	2.64	0.46
1:B:602:ILE:O	1:B:626:GLY:HA2	2.15	0.46
1:D:128:ASN:HB2	1:D:132:VAL:O	2.15	0.46
1:B:285:PRO:HG2	1:B:319:TYR:CZ	2.51	0.45
1:A:727:ARG:HD2	2:A:972:HOH:O	2.16	0.45
1:C:207:ARG:NH1	1:C:209:LEU:O	2.47	0.45
1:D:297:PHE:CE1	1:D:304:LEU:HB2	2.52	0.45
1:B:549:TYR:CE2	1:B:736:LEU:HD23	2.52	0.45
1:D:591:LYS:NZ	2:D:841:HOH:O	2.49	0.45
1:A:545:ALA:HA	1:A:549:TYR:O	2.17	0.45
1:C:496:THR:HG23	1:C:584:GLU:OE1	2.17	0.45
1:A:285:PRO:HG2	1:A:319:TYR:CE2	2.52	0.45
1:A:293:PRO:HD2	1:A:307:MET:O	2.17	0.45
1:B:454:PRO:HA	1:B:536:TRP:CG	2.52	0.44
1:A:602:ILE:O	1:A:626:GLY:HA2	2.18	0.44
1:A:412:LYS:NZ	2:A:819:HOH:O	2.38	0.44
1:C:499:VAL:HG21	1:C:557:ARG:NH1	2.31	0.44
1:A:379:LYS:HE2	1:A:382:ASN:HB3	2.00	0.43
1:A:187:GLN:NE2	2:A:839:HOH:O	2.49	0.43
1:B:30:ILE:C	1:B:32:SER:H	2.21	0.43
1:B:28:LYS:NZ	1:B:726:THR:OG1	2.51	0.43
1:B:32:SER:HB3	2:B:811:HOH:O	2.19	0.43
1:B:285:PRO:HG2	1:B:319:TYR:CE2	2.54	0.43
1:B:28:LYS:HE3	1:B:28:LYS:HB3	1.50	0.43
1:C:57:ALA:HB3	2:C:815:HOH:O	2.19	0.43
1:D:715:ILE:HG22	1:D:715:ILE:O	2.19	0.43
1:D:31:THR:HG21	1:D:722:GLN:HB2	2.02	0.42
1:C:186:LYS:HB3	1:C:189:SER:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:LYS:HG3	2:A:1225:HOH:O	2.20	0.42
1:A:294:ARG:NE	1:A:346:ASP:OD1	2.29	0.42
1:A:342:GLU:OE1	2:A:809:HOH:O	2.21	0.42
1:A:86:ASP:OD1	1:A:86:ASP:N	2.50	0.42
1:C:76:ILE:HG23	1:C:125:LEU:HD22	2.02	0.42
1:D:545:ALA:HA	1:D:549:TYR:O	2.20	0.42
1:C:549:TYR:OH	1:C:733:LEU:HD23	2.20	0.42
1:A:76:ILE:HD13	1:A:76:ILE:HA	1.87	0.41
1:C:285:PRO:HG2	1:C:319:TYR:CZ	2.55	0.41
1:A:53:THR:OG1	1:A:95:PHE:HE2	2.03	0.41
1:B:529:SER:O	1:B:559:THR:HB	2.20	0.41
1:C:140:ARG:NH2	2:C:836:HOH:O	2.49	0.41
1:C:104:ILE:O	1:C:120:HIS:HA	2.20	0.41
1:C:202:GLU:CD	1:C:642:TYR:HB2	2.41	0.41
1:C:141:LEU:CD1	1:C:170:VAL:HG21	2.51	0.41
1:D:413:ALA:HB3	1:D:415:TYR:CE1	2.56	0.41
1:D:602:ILE:O	1:D:626:GLY:HA2	2.21	0.41
1:D:401:TYR:CE1	1:D:416:LYS:HD3	2.56	0.41
1:B:549:TYR:HE2	1:B:736:LEU:HD23	1.86	0.41
1:C:329:LYS:HE2	1:C:329:LYS:HB2	1.93	0.41
1:D:398:GLY:HA3	1:D:419:LYS:HE2	2.02	0.41
1:D:672:ASN:ND2	1:D:735:ASN:OD1	2.51	0.41
1:C:45:PRO:HD3	1:C:436:LEU:HD11	2.02	0.41
1:A:591:LYS:HB3	1:A:591:LYS:HE2	1.69	0.40
1:B:545:ALA:HA	1:B:549:TYR:O	2.21	0.40
1:B:60:THR:HB	1:B:79:VAL:HG22	2.02	0.40
1:C:679:MET:HG3	1:C:707:VAL:CG1	2.51	0.40
1:D:352:PRO:O	1:D:353:GLU:HB2	2.22	0.40
1:A:388:LYS:HE2	2:A:841:HOH:O	2.21	0.40

All (1) 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)
2:A:1475:HOH:O	2:C:1498:HOH:O[1_455]	2.06	0.14

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	712/736 (97%)	689 (97%)	21 (3%)	2 (0%)	41	31
1	B	712/736 (97%)	686 (96%)	24 (3%)	2 (0%)	41	31
1	C	712/736 (97%)	692 (97%)	19 (3%)	1 (0%)	51	42
1	D	712/736 (97%)	688 (97%)	24 (3%)	0	100	100
All	All	2848/2944 (97%)	2755 (97%)	88 (3%)	5 (0%)	47	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	715	ILE
1	A	715	ILE
1	A	455	MET
1	B	31	THR
1	B	715	ILE

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	626/643 (97%)	619 (99%)	7 (1%)	73	72
1	B	626/643 (97%)	617 (99%)	9 (1%)	67	63
1	C	626/643 (97%)	620 (99%)	6 (1%)	76	75
1	D	626/643 (97%)	617 (99%)	9 (1%)	67	63
All	All	2504/2572 (97%)	2473 (99%)	31 (1%)	71	69

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	89	ASN
1	A	329	LYS
1	A	439	GLN
1	A	580	LYS
1	A	591	LYS
1	A	677	HIS
1	B	29	ASP
1	B	32	SER
1	B	36	ARG
1	B	95	PHE
1	B	101	LYS
1	B	255	TYR
1	B	294	ARG
1	B	422	LYS
1	B	677	HIS
1	C	28	LYS
1	C	255	TYR
1	C	416	LYS
1	C	452	ASP
1	C	468	LYS
1	C	677	HIS
1	D	67	PHE
1	D	88	LYS
1	D	255	TYR
1	D	277	HIS
1	D	297	PHE
1	D	404	SER
1	D	439	GLN
1	D	465	LYS
1	D	677	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95^{th} 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	714/736 (97%)	-0.28	7 (0%) 82 84	19, 29, 46, 66	0
1	B	714/736 (97%)	-0.27	13 (1%) 68 71	21, 30, 47, 65	0
1	C	714/736 (97%)	-0.28	5 (0%) 87 89	18, 30, 47, 62	0
1	D	714/736 (97%)	-0.17	21 (2%) 51 55	21, 35, 56, 74	0
All	All	2856/2944 (97%)	-0.25	46 (1%) 72 74	18, 31, 49, 74	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	25	LEU	4.0
1	D	419	LYS	3.9
1	D	187	GLN	3.8
1	A	514	SER	3.6
1	D	509	ALA	3.5
1	D	86	ASP	3.5
1	C	86	ASP	3.3
1	D	420	LYS	3.1
1	D	513	THR	3.1
1	D	129	ASP	3.1
1	D	512	SER	3.1
1	A	513	THR	2.9
1	D	131	GLY	2.9
1	A	129	ASP	2.8
1	B	514	SER	2.7
1	D	514	SER	2.7
1	B	509	ALA	2.6
1	B	32	SER	2.6
1	A	510	ASN	2.5
1	A	509	ALA	2.5
1	C	420	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	515	LYS	2.4
1	B	515	LYS	2.4
1	B	496	THR	2.4
1	B	593	PRO	2.4
1	D	510	ASN	2.4
1	D	130	LYS	2.4
1	B	512	SER	2.4
1	C	129	ASP	2.4
1	C	68	ARG	2.3
1	A	71	GLU	2.3
1	D	126	LYS	2.3
1	B	511	PHE	2.3
1	D	88	LYS	2.3
1	D	183	GLU	2.2
1	B	513	THR	2.2
1	D	72	LYS	2.2
1	D	327	LEU	2.1
1	A	131	GLY	2.1
1	B	605	TRP	2.1
1	C	57	ALA	2.1
1	D	84	GLU	2.1
1	D	137	ILE	2.1
1	B	594	TYR	2.1
1	B	603	TRP	2.1
1	D	511	PHE	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.