



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:37 AM UTC

PDB ID : 4FFV / pdb_00004ffv
Title : Crystal Structure of Dipeptidyl Peptidase IV (DPP4, DPP-IV, CD26) in Complex with 11A19 Fab
Authors : Wang, Z.; Sudom, A.; Walker, N.P.; Min, X.
Deposited on : 2012-06-01
Resolution : 2.40 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
Xtrriage (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

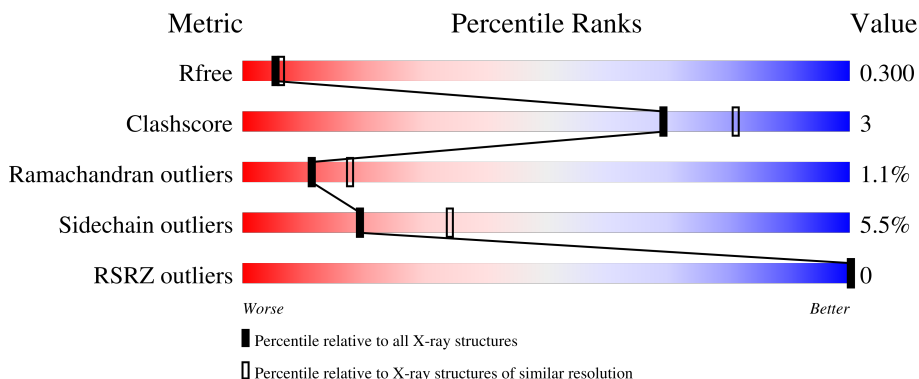
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	730	91% 8% .
1	B	730	87% 10% .
2	C	210	85% 12% ..
2	L	210	83% 14% ..
3	D	217	81% 12% . .

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Mol	Chain	Length	Quality of chain
3	H	217	 82% 11% . .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18423 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 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	727	Total 5921	C 3792	N 980	O 1123	S 26	0	0	0
1	B	729	Total 5940	C 3804	N 985	O 1125	S 26	0	0	0

- Molecule 2 is a protein called 11A19 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	207	Total 1579	C 982	N 269	O 321	S 7	0	0	0
2	L	207	Total 1579	C 982	N 269	O 321	S 7	0	0	0

- Molecule 3 is a protein called 11A19 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	209	Total 1596	C 1017	N 259	O 315	S 5	0	0	0
3	H	209	Total 1595	C 1016	N 259	O 315	S 5	0	0	0

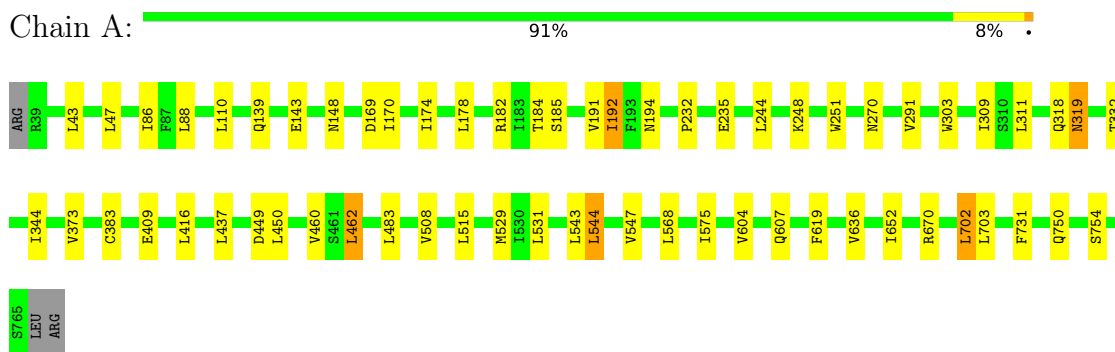
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	106	Total 106	O 106	0	0
4	B	100	Total 100	O 100	0	0
4	C	4	Total 4	O 4	0	0
4	D	3	Total 3	O 3	0	0

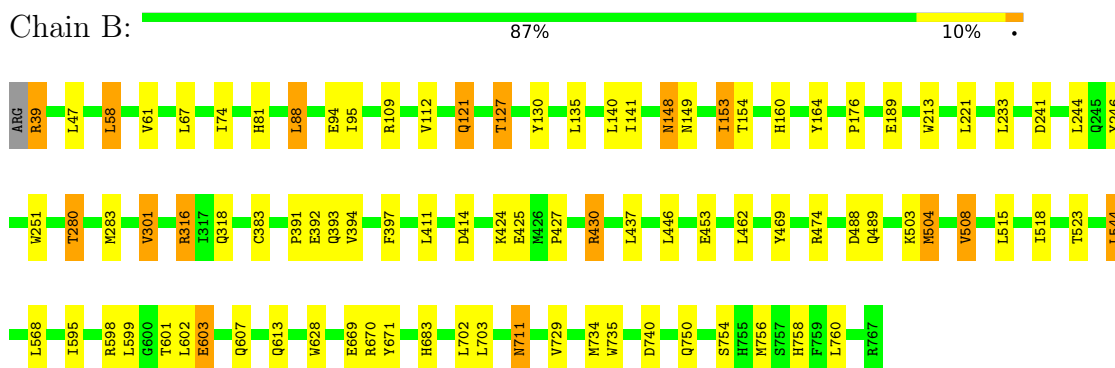
3 Residue-property plots

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.

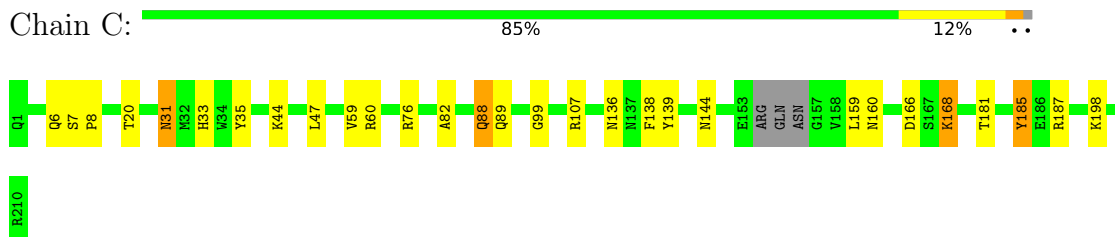
- Molecule 1: Dipeptidyl peptidase 4




- Molecule 1: Dipeptidyl peptidase 4

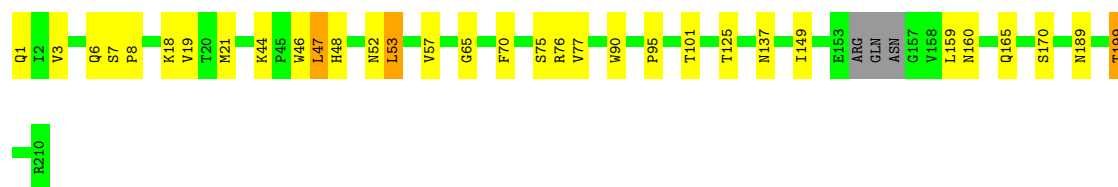


- Molecule 2: 11A19 Fab light chain




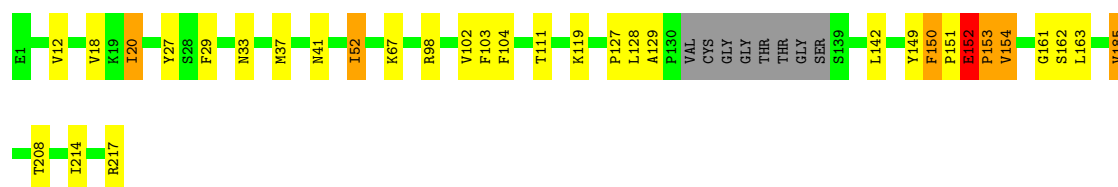
- Molecule 2: 11A19 Fab light chain

Chain L:  83% 14% ..




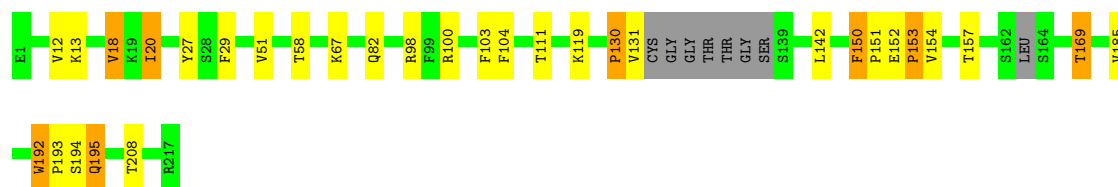
• Molecule 3: 11A19 Fab heavy chain

Chain D:  81% 12% ..



• Molecule 3: 11A19 Fab heavy chain

Chain H:  82% 11% ..



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.26Å 201.72Å 97.28Å 90.00° 93.71° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 30.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (30.00-2.40) 98.5 (30.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.271 , 0.301 0.272 , 0.300	Depositor DCC
R_{free} test set	7290 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtrriage
Anisotropy	0.141	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 17.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.477 for l,-k,h	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18423	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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](#)

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	0/6090	0.66	0/8280
1	B	0.42	1/6109 (0.0%)	0.68	1/8305 (0.0%)
2	C	0.45	0/1619	0.65	0/2201
2	L	0.47	0/1619	0.66	0/2201
3	D	0.44	0/1636	0.67	0/2234
3	H	0.45	0/1634	0.68	0/2230
All	All	0.43	1/18707 (0.0%)	0.67	1/25451 (0.0%)

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
2	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	121	GLN	CA-C	5.13	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	160	HIS	N-CA-C	5.85	119.62	111.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	99	GLY	Peptide

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	5921	0	5658	27	0
1	B	5940	0	5682	48	0
2	C	1579	0	1503	8	0
2	L	1579	0	1503	11	0
3	D	1596	0	1571	15	0
3	H	1595	0	1568	17	0
4	A	106	0	0	1	0
4	B	100	0	0	4	0
4	C	4	0	0	0	0
4	D	3	0	0	0	0
All	All	18423	0	17485	123	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 3.

All (123) 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:112:VAL:HG23	1:B:135:LEU:HD21	1.69	0.75
1:B:628:TRP:CE3	1:B:756:MET:HE1	2.25	0.71
3:H:150:PHE:HB3	3:H:151:PRO:HD3	1.74	0.69
1:A:191:VAL:HG12	1:A:192:ILE:HD12	1.73	0.69
1:A:607:GLN:NE2	4:A:849:HOH:O	2.29	0.64
1:A:529:MET:HE1	1:A:619:PHE:HE1	1.64	0.62
1:B:607:GLN:NE2	4:B:838:HOH:O	2.28	0.62
1:A:182:ARG:NH1	1:A:184:THR:O	2.33	0.61
1:A:170:ILE:H	1:A:184:THR:HG22	1.67	0.60
1:B:130:TYR:CZ	1:B:153:ILE:HD11	2.36	0.60
1:A:529:MET:HE1	1:A:619:PHE:CE1	2.36	0.60
3:H:51:VAL:HG22	3:H:58:THR:HG22	1.83	0.59
3:H:98:ARG:O	3:H:104:PHE:HA	2.03	0.59
1:B:67:LEU:HB3	1:B:74:ILE:HD11	1.84	0.59
1:B:503:LYS:O	1:B:504:MET:HB2	2.03	0.57
1:B:47:LEU:HD22	1:B:750:GLN:HA	1.86	0.57
1:B:518:ILE:HD12	1:B:613:GLN:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:GLU:OE1	3:D:33:ASN:ND2	2.38	0.56
2:C:35:TYR:HE1	2:C:88:GLN:HE21	1.52	0.56
1:B:121:GLN:NE2	4:B:897:HOH:O	2.38	0.56
1:A:47:LEU:HD22	1:A:750:GLN:HA	1.87	0.55
3:H:154:VAL:HG13	3:H:154:VAL:O	2.06	0.55
1:B:383:CYS:HB3	1:B:397:PHE:CD1	2.41	0.55
3:H:192:TRP:O	3:H:195:GLN:N	2.39	0.54
1:B:711:ASN:C	1:B:711:ASN:HD22	2.16	0.54
1:A:169:ASP:OD1	1:A:184:THR:HG23	2.07	0.54
1:B:601:THR:HG23	1:B:602:LEU:N	2.24	0.53
1:B:74:ILE:CG2	1:B:88:LEU:HB3	2.39	0.53
3:D:12:VAL:HG11	3:D:18:VAL:HG22	1.91	0.53
1:A:529:MET:HE3	1:A:575:ILE:HG21	1.90	0.52
1:B:127:THR:HG23	1:B:149:ASN:HA	1.91	0.52
1:B:503:LYS:O	1:B:504:MET:CB	2.57	0.52
1:B:544:LEU:HD12	1:B:568:LEU:HD13	1.90	0.52
2:L:46:TRP:CZ3	2:L:57:VAL:HG13	2.45	0.52
3:H:194:SER:C	3:H:195:GLN:HE21	2.18	0.52
3:H:169:THR:O	3:H:169:THR:CG2	2.59	0.51
3:D:20:ILE:HD12	3:D:111:THR:HB	1.93	0.51
1:B:427:PRO:O	1:B:430:ARG:NH2	2.44	0.50
1:A:731:PHE:CZ	1:B:734:MET:HE1	2.47	0.50
1:B:148:ASN:HB3	1:B:149:ASN:HD22	1.76	0.50
3:H:12:VAL:HG11	3:H:18:VAL:HG13	1.94	0.49
1:A:409:GLU:HG3	1:A:462:LEU:HD12	1.95	0.49
1:B:130:TYR:OH	1:B:153:ILE:HD11	2.12	0.49
1:B:233:LEU:HD13	1:B:251:TRP:CD1	2.48	0.49
1:A:544:LEU:HD12	1:A:568:LEU:HD13	1.94	0.49
3:D:12:VAL:HG21	3:D:18:VAL:CG2	2.43	0.49
3:D:151:PRO:O	3:D:152:GLU:HB2	2.13	0.49
3:H:130:PRO:O	3:H:131:VAL:HB	2.13	0.49
3:D:149:TYR:CE2	3:D:154:VAL:HG21	2.48	0.49
1:B:58:LEU:O	1:B:58:LEU:HD23	2.13	0.49
1:B:153:ILE:HG23	1:B:164:TYR:HB3	1.94	0.48
1:B:601:THR:HG23	1:B:602:LEU:HG	1.95	0.48
1:A:319:ASN:C	1:A:319:ASN:HD22	2.22	0.48
1:B:734:MET:HE3	1:B:735:TRP:O	2.15	0.47
1:B:141:ILE:HD13	1:B:176:PRO:HB2	1.95	0.47
2:L:165:GLN:HG2	2:L:170:SER:HA	1.96	0.47
1:A:182:ARG:NH1	1:A:185:SER:HA	2.30	0.47
1:A:449:ASP:O	1:A:450:LEU:C	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:VAL:HG23	1:B:135:LEU:CD2	2.40	0.46
3:D:163:LEU:HD23	3:D:185:VAL:HG21	1.97	0.46
1:B:462:LEU:HD23	1:B:469:TYR:HB3	1.98	0.46
2:C:33:HIS:HB2	2:C:88:GLN:HB3	1.99	0.45
3:D:27:TYR:CE2	3:D:29:PHE:HA	2.51	0.45
1:A:235:GLU:HG2	1:A:251:TRP:HB3	1.98	0.45
1:B:213:TRP:CE2	1:B:301:VAL:HG13	2.52	0.44
3:D:153:PRO:HA	3:D:154:VAL:HB	1.99	0.44
3:D:98:ARG:O	3:D:104:PHE:HA	2.17	0.44
2:L:47:LEU:CD2	2:L:53:LEU:HD23	2.48	0.44
1:B:595:ILE:HG21	1:B:603:GLU:HG3	2.00	0.44
1:A:184:THR:HG21	1:A:194:ASN:CB	2.46	0.44
3:H:20:ILE:HD12	3:H:111:THR:CB	2.48	0.44
2:C:31:ASN:HD22	2:C:31:ASN:HA	1.61	0.44
3:H:142:LEU:HD11	3:H:185:VAL:CG1	2.48	0.43
1:B:39:ARG:HD2	1:B:508:VAL:HG12	1.99	0.43
2:C:166:ASP:C	2:C:168:LYS:H	2.26	0.43
1:B:488:ASP:O	1:B:489:GLN:HB2	2.18	0.43
3:D:150:PHE:HB3	3:D:151:PRO:HD3	1.99	0.43
1:A:409:GLU:HG2	1:A:460:VAL:HG13	2.00	0.43
1:B:754:SER:O	1:B:758:HIS:ND1	2.51	0.43
1:B:318:GLN:OE1	1:B:670:ARG:HD3	2.19	0.43
2:L:7:SER:HA	2:L:8:PRO:HA	1.93	0.43
1:A:303:TRP:CE2	1:A:309:ILE:HD12	2.54	0.42
2:L:19:VAL:HG21	2:L:77:VAL:HG21	2.01	0.42
3:H:152:GLU:N	3:H:153:PRO:CD	2.82	0.42
1:B:74:ILE:HG23	1:B:88:LEU:HB3	2.00	0.42
2:L:47:LEU:HD22	2:L:53:LEU:HD23	2.01	0.42
1:A:318:GLN:OE1	1:A:670:ARG:HD3	2.20	0.42
1:A:409:GLU:CG	1:A:462:LEU:HD12	2.49	0.42
1:B:241:ASP:HB3	4:B:820:HOH:O	2.20	0.42
1:B:392:GLU:O	1:B:394:VAL:HG23	2.19	0.42
3:D:33:ASN:ND2	3:D:52:ILE:HG22	2.35	0.42
2:L:65:GLY:HA3	2:L:70:PHE:HA	2.01	0.42
2:C:89:GLN:CD	2:C:89:GLN:C	2.88	0.42
2:L:48:HIS:O	2:L:52:ASN:HB2	2.20	0.42
1:B:280:THR:HG22	4:B:821:HOH:O	2.20	0.41
2:C:181:THR:O	2:C:185:TYR:N	2.51	0.41
2:L:21:MET:HG3	2:L:101:THR:HG21	2.02	0.41
3:H:20:ILE:HD12	3:H:111:THR:HB	2.02	0.41
2:C:7:SER:HA	2:C:8:PRO:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:90:TRP:CG	2:L:95:PRO:HB3	2.56	0.41
2:L:159:LEU:HD23	2:L:160:ASN:N	2.35	0.41
2:C:159:LEU:HD23	2:C:160:ASN:N	2.35	0.41
3:H:169:THR:O	3:H:169:THR:HG22	2.21	0.41
1:B:316:ARG:HD3	1:B:669:GLU:OE1	2.20	0.41
1:B:599:LEU:HD13	1:B:671:TYR:HB3	2.01	0.41
1:A:529:MET:HE2	1:A:531:LEU:HD21	2.03	0.41
1:B:74:ILE:HG23	1:B:88:LEU:CB	2.51	0.41
1:A:547:VAL:HG21	1:A:636:VAL:HG11	2.02	0.41
3:D:142:LEU:HB2	3:D:214:ILE:HD13	2.03	0.41
1:A:652:ILE:HG23	1:A:702:LEU:HB3	2.03	0.41
1:B:598:ARG:HA	1:B:683:HIS:CD2	2.56	0.41
1:A:43:LEU:HD21	1:A:754:SER:HA	2.02	0.41
3:H:192:TRP:O	3:H:193:PRO:C	2.63	0.41
3:H:154:VAL:O	3:H:154:VAL:CG1	2.68	0.41
3:H:27:TYR:CE2	3:H:29:PHE:HA	2.57	0.40
3:D:129:ALA:O	3:D:217:ARG:NH2	2.54	0.40
1:B:153:ILE:CG2	1:B:164:TYR:HB3	2.52	0.40
1:B:601:THR:CG2	1:B:602:LEU:N	2.85	0.40
3:D:37:MET:HE1	3:D:104:PHE:CZ	2.57	0.40
1:A:232:PRO:HB2	1:B:246:TYR:CZ	2.56	0.40
1:B:58:LEU:HD23	1:B:58:LEU:C	2.47	0.40
1:A:344:ILE:N	1:A:344:ILE:HD12	2.37	0.40
1:B:740:ASP:OD1	1:B:740:ASP:C	2.65	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	725/730 (99%)	693 (96%)	32 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	727/730 (100%)	691 (95%)	31 (4%)	5 (1%)	18	28
2	C	203/210 (97%)	186 (92%)	14 (7%)	3 (2%)	8	12
2	L	203/210 (97%)	179 (88%)	20 (10%)	4 (2%)	6	7
3	D	205/217 (94%)	183 (89%)	12 (6%)	10 (5%)	1	1
3	H	203/217 (94%)	187 (92%)	12 (6%)	4 (2%)	6	7
All	All	2266/2314 (98%)	2119 (94%)	121 (5%)	26 (1%)	11	18

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	136	ASN
3	D	152	GLU
3	D	162	SER
1	B	393	GLN
1	B	504	MET
2	C	139	TYR
3	D	41	ASN
1	B	189	GLU
3	D	150	PHE
3	D	153	PRO
2	L	53	LEU
2	L	75	SER
2	L	199	THR
3	H	130	PRO
3	H	150	PHE
1	B	391	PRO
2	C	82	ALA
2	L	76	ARG
1	B	148	ASN
3	D	127	PRO
3	D	161	GLY
3	H	153	PRO
3	D	102	VAL
3	D	154	VAL
3	D	185	VAL
3	H	192	TRP

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	648/651 (100%)	619 (96%)	29 (4%)	24	42
1	B	650/651 (100%)	614 (94%)	36 (6%)	19	34
2	C	181/184 (98%)	165 (91%)	16 (9%)	9	15
2	L	181/184 (98%)	170 (94%)	11 (6%)	17	30
3	D	184/189 (97%)	176 (96%)	8 (4%)	26	44
3	H	184/189 (97%)	172 (94%)	12 (6%)	15	27
All	All	2028/2048 (99%)	1916 (94%)	112 (6%)	19	34

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

Mol	Chain	Res	Type
1	A	86	ILE
1	A	88	LEU
1	A	110	LEU
1	A	139	GLN
1	A	143	GLU
1	A	148	ASN
1	A	174	ILE
1	A	178	LEU
1	A	192	ILE
1	A	244	LEU
1	A	248	LYS
1	A	270	ASN
1	A	291	VAL
1	A	311	LEU
1	A	319	ASN
1	A	332	THR
1	A	373	VAL
1	A	383	CYS
1	A	416	LEU
1	A	437	LEU
1	A	462	LEU
1	A	483	LEU

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Mol	Chain	Res	Type
1	A	508	VAL
1	A	515	LEU
1	A	543	LEU
1	A	544	LEU
1	A	604	VAL
1	A	702	LEU
1	A	703	LEU
1	B	39	ARG
1	B	58	LEU
1	B	61	VAL
1	B	81	HIS
1	B	88	LEU
1	B	95	ILE
1	B	109	ARG
1	B	127	THR
1	B	140	LEU
1	B	153	ILE
1	B	154	THR
1	B	221	LEU
1	B	244	LEU
1	B	280	THR
1	B	283	MET
1	B	301	VAL
1	B	316	ARG
1	B	411	LEU
1	B	414	ASP
1	B	424	LYS
1	B	425	GLU
1	B	430	ARG
1	B	437	LEU
1	B	446	LEU
1	B	453	GLU
1	B	474	ARG
1	B	508	VAL
1	B	515	LEU
1	B	523	THR
1	B	544	LEU
1	B	603	GLU
1	B	702	LEU
1	B	703	LEU
1	B	711	ASN
1	B	729	VAL

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Mol	Chain	Res	Type
1	B	760	LEU
2	C	6	GLN
2	C	20	THR
2	C	31	ASN
2	C	44	LYS
2	C	47	LEU
2	C	59	VAL
2	C	60	ARG
2	C	76	ARG
2	C	88	GLN
2	C	107	ARG
2	C	138	PHE
2	C	144	ASN
2	C	168	LYS
2	C	185	TYR
2	C	187	ARG
2	C	198	LYS
3	D	20	ILE
3	D	52	ILE
3	D	67	LYS
3	D	103	PHE
3	D	119	LYS
3	D	128	LEU
3	D	152	GLU
3	D	208	THR
2	L	1	GLN
2	L	3	VAL
2	L	6	GLN
2	L	18	LYS
2	L	44	LYS
2	L	47	LEU
2	L	125	THR
2	L	137	ASN
2	L	149	ILE
2	L	189	ASN
2	L	199	THR
3	H	13	LYS
3	H	18	VAL
3	H	20	ILE
3	H	67	LYS
3	H	82	GLN
3	H	100	ARG

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Mol	Chain	Res	Type
3	H	103	PHE
3	H	119	LYS
3	H	157	THR
3	H	169	THR
3	H	195	GLN
3	H	208	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	121	GLN
1	A	149	ASN
1	A	177	HIS
1	A	227	ASN
1	A	270	ASN
1	A	319	ASN
1	A	336	ASN
1	A	341	GLN
1	A	436	GLN
1	A	442	ASN
1	A	484	HIS
1	B	121	GLN
1	B	149	ASN
1	B	181	HIS
1	B	261	ASN
1	B	343	HIS
1	B	361	HIS
1	B	386	GLN
1	B	456	GLN
1	B	484	HIS
1	B	489	GLN
1	B	528	GLN
1	B	596	ASN
1	B	613	GLN
1	B	686	ASN
1	B	711	ASN
2	C	31	ASN
2	C	88	GLN
2	C	93	HIS
2	C	136	ASN
2	C	197	HIS

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Mol	Chain	Res	Type
3	D	175	GLN
2	L	93	HIS
2	L	136	ASN
3	H	6	GLN
3	H	62	GLN
3	H	175	GLN
3	H	195	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 oligosaccharides 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 [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	727/730 (99%)	-1.38	0 100 100	14, 34, 58, 77	0
1	B	729/730 (99%)	-1.37	0 100 100	11, 34, 57, 80	1 (0%)
2	C	207/210 (98%)	-0.53	0 100 100	41, 90, 146, 162	0
2	L	207/210 (98%)	-0.55	0 100 100	38, 95, 146, 156	0
3	D	209/217 (96%)	-0.77	0 100 100	36, 80, 118, 132	0
3	H	209/217 (96%)	-0.79	0 100 100	38, 77, 117, 124	0
All	All	2288/2314 (98%)	-1.12	0 100 100	11, 43, 124, 162	1 (0%)

There are no RSRZ outliers to report.

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.