



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:33 AM UTC

PDB ID : 6H4J / pdb_00006h4j
Title : Usp25 catalytic domain
Authors : Klemm, T.A.; Sauer, F.; Kisker, C.
Deposited on : 2018-07-21
Resolution : 3.07 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

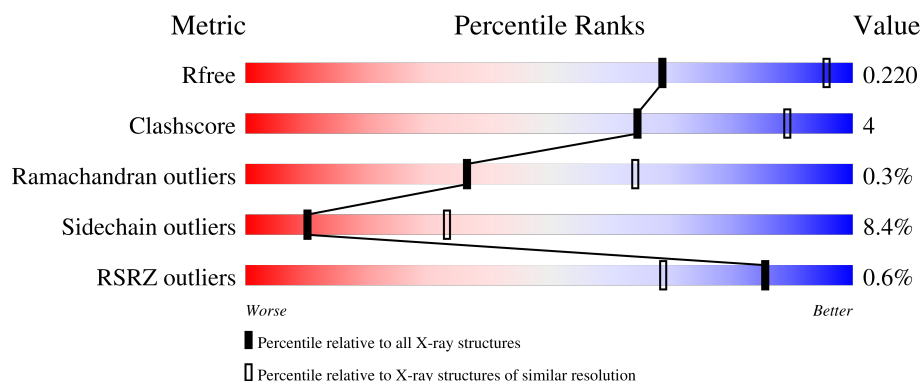
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.07 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	552	
1	B	552	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7588 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 Ubiquitin carboxyl-terminal hydrolase 25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	0	0
			3931	2504	681	730	16			
1	B	464	Total	C	N	O	S	0	1	0
			3625	2317	617	677	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	155	GLY	-	expression tag	UNP Q9UHP3
A	156	PRO	-	expression tag	UNP Q9UHP3
B	155	GLY	-	expression tag	UNP Q9UHP3
B	156	PRO	-	expression tag	UNP Q9UHP3

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

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

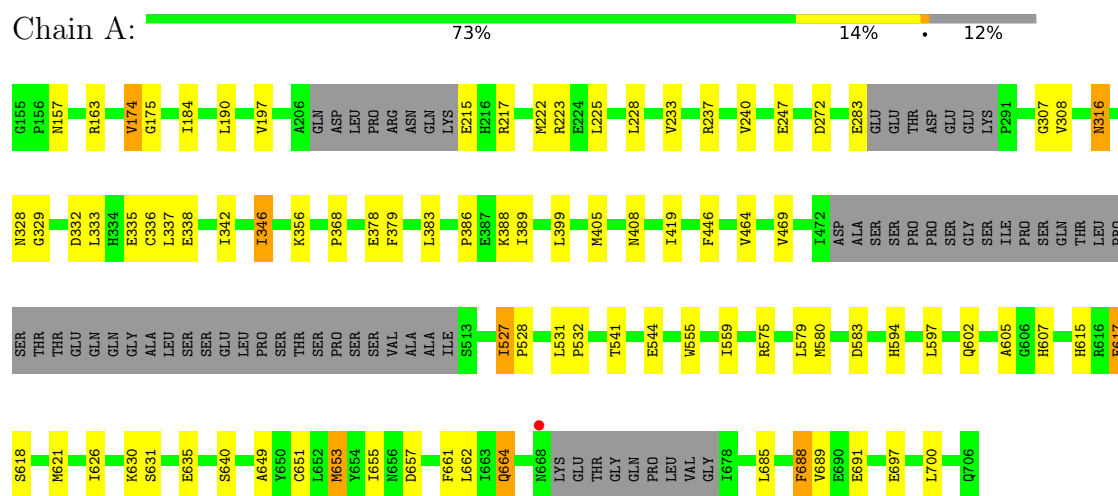
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	18	Total	O	0	0
			18	18		

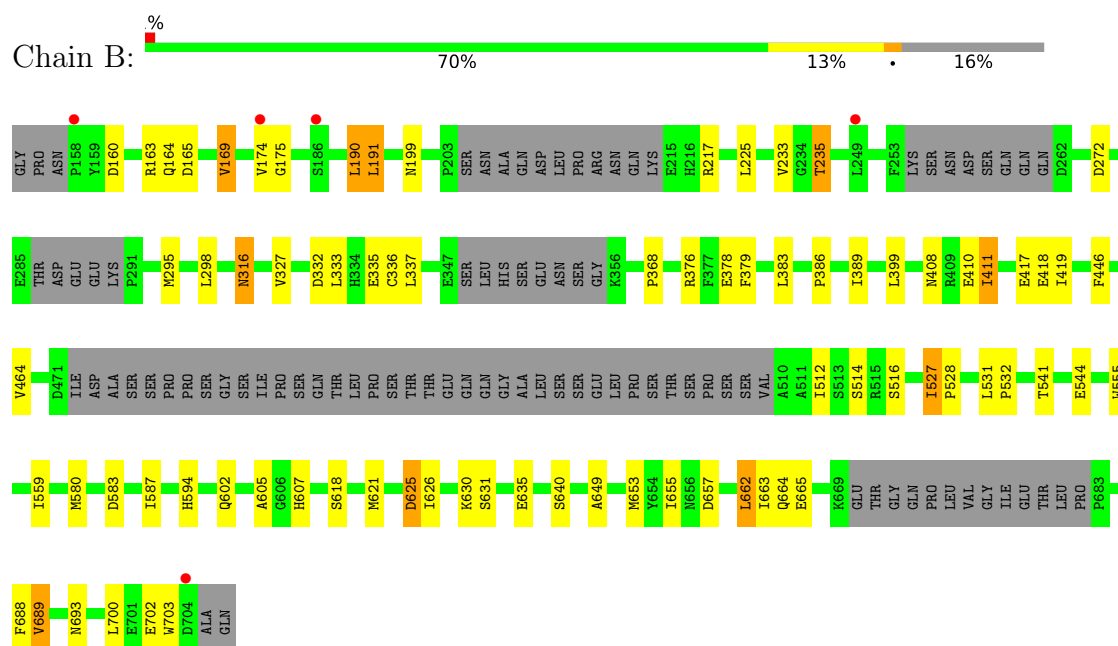
3 Residue-property plots

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: Ubiquitin carboxyl-terminal hydrolase 25



• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 25



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	81.94Å 202.63Å 169.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.54 – 3.07 48.54 – 3.07	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.54-3.07) 92.7 (48.54-3.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.181 , 0.230 (Not available) , 0.220	Depositor DCC
R_{free} test set	1365 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	86.6	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 91.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7588	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: 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	0.86	1/4031 (0.0%)	1.34	20/5466 (0.4%)
1	B	0.85	1/3718 (0.0%)	1.33	18/5059 (0.4%)
All	All	0.86	2/7749 (0.0%)	1.34	38/10525 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	174	VAL	CA-C	5.34	1.59	1.52
1	B	689	VAL	CA-C	5.28	1.59	1.52

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	335	GLU	CA-C-N	7.82	130.61	120.44
1	A	335	GLU	C-N-CA	7.82	130.61	120.44
1	A	175	GLY	CA-C-N	7.65	133.23	122.36
1	A	175	GLY	C-N-CA	7.65	133.23	122.36
1	B	335	GLU	CA-C-N	7.17	130.11	120.65
1	B	335	GLU	C-N-CA	7.17	130.11	120.65
1	A	688	PHE	CA-C-N	7.06	130.13	120.46
1	A	688	PHE	C-N-CA	7.06	130.13	120.46
1	A	469	VAL	CA-C-N	6.88	133.82	123.23
1	A	469	VAL	C-N-CA	6.88	133.82	123.23
1	A	272	ASP	CA-CB-CG	6.53	119.13	112.60
1	A	583	ASP	CA-C-N	6.40	129.72	120.38
1	A	583	ASP	C-N-CA	6.40	129.72	120.38
1	B	272	ASP	CA-CB-CG	6.37	118.97	112.60
1	B	233	VAL	N-CA-C	-6.36	106.60	112.96
1	B	272	ASP	CA-C-N	6.12	128.80	120.54
1	B	272	ASP	C-N-CA	6.12	128.80	120.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	GLU	CB-CG-CD	6.08	122.93	112.60
1	B	217	ARG	CA-C-N	6.03	128.65	120.44
1	B	217	ARG	C-N-CA	6.03	128.65	120.44
1	B	378	GLU	CB-CG-CD	5.99	122.78	112.60
1	B	688	PHE	CA-C-N	5.97	132.72	121.97
1	B	688	PHE	C-N-CA	5.97	132.72	121.97
1	B	410	GLU	CB-CG-CD	5.85	122.54	112.60
1	A	688	PHE	CA-CB-CG	5.79	119.59	113.80
1	B	316	ASN	CA-CB-CG	5.75	118.35	112.60
1	A	617	GLU	CB-CG-CD	5.69	122.27	112.60
1	A	272	ASP	CA-C-N	5.64	128.16	120.54
1	A	272	ASP	C-N-CA	5.64	128.16	120.54
1	A	316	ASN	CA-CB-CG	5.45	118.05	112.60
1	B	175	GLY	CA-C-N	5.43	130.65	122.67
1	B	175	GLY	C-N-CA	5.43	130.65	122.67
1	A	157	ASN	CA-CB-CG	5.11	117.71	112.60
1	A	332	ASP	CA-C-N	5.09	127.10	120.28
1	A	332	ASP	C-N-CA	5.09	127.10	120.28
1	B	160	ASP	CA-CB-CG	5.07	117.67	112.60
1	B	332	ASP	CA-C-N	5.03	127.02	120.28
1	B	332	ASP	C-N-CA	5.03	127.02	120.28

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	3931	0	3699	31	0
1	B	3625	0	3302	25	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	0	0	0
3	B	18	0	0	0	0
All	All	7588	0	7001	56	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 4.

All (56) 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:328:ASN:CG	1:A:329:GLY:H	1.72	0.94
1:A:661:PHE:HA	1:A:664:GLN:HG2	1.66	0.78
1:A:328:ASN:CG	1:A:329:GLY:N	2.45	0.73
1:B:594:HIS:HD2	1:B:653:MET:HE3	1.56	0.71
1:A:594:HIS:HD2	1:A:653:MET:HE3	1.56	0.70
1:A:215:GLU:HG3	1:A:217:ARG:H	1.58	0.67
1:A:602:GLN:HB2	1:A:605:ALA:HB3	1.76	0.66
1:A:405:MET:HB2	1:A:408:ASN:HD22	1.62	0.65
1:A:419:ILE:HD11	1:A:580:MET:HG2	1.80	0.64
1:B:327:VAL:HG21	1:B:376:ARG:HG2	1.80	0.64
1:A:338:GLU:O	1:A:342:ILE:HG13	2.00	0.62
1:A:697:GLU:HA	1:A:700:LEU:HD12	1.83	0.60
1:B:169:VAL:HG22	1:B:235:THR:HG23	1.83	0.60
1:A:174:VAL:HG12	1:A:174:VAL:O	2.02	0.59
1:B:191:LEU:HD13	1:B:663:ILE:HG23	1.86	0.58
1:B:408:ASN:HA	1:B:411:ILE:HD13	1.87	0.56
1:B:327:VAL:CG2	1:B:376:ARG:HG2	2.35	0.56
1:B:555:TRP:O	1:B:559:ILE:HG12	2.06	0.55
1:B:419:ILE:HD11	1:B:580:MET:HG2	1.88	0.54
1:A:555:TRP:O	1:A:559:ILE:HG12	2.08	0.53
1:A:368:PRO:HB2	1:A:662:LEU:HD11	1.90	0.53
1:A:615:HIS:CE1	1:A:655:ILE:HD11	2.43	0.52
1:B:411:ILE:HD12	1:B:411:ILE:H	1.74	0.52
1:A:661:PHE:HA	1:A:664:GLN:CG	2.39	0.51
1:B:174:VAL:HG12	1:B:174:VAL:O	2.11	0.51
1:B:602:GLN:HB2	1:B:605:ALA:HB3	1.93	0.50
1:A:307:GLY:HA2	1:A:346:ILE:HD11	1.92	0.50
1:B:333:LEU:HD23	1:B:399:LEU:HD13	1.92	0.50
1:B:640:SER:HB3	1:B:649:ALA:HB2	1.93	0.50
1:A:197:VAL:HG13	1:A:222:MET:CE	2.41	0.50
1:A:640:SER:HB3	1:A:649:ALA:HB2	1.93	0.50
1:A:197:VAL:HG13	1:A:222:MET:HE1	1.94	0.49
1:A:328:ASN:ND2	1:A:329:GLY:H	2.11	0.48
1:B:625:ASP:O	1:B:626:ILE:HB	2.13	0.48
1:B:190:LEU:HD11	1:B:655:ILE:HD11	1.95	0.48
1:B:464:VAL:HG22	1:B:532:PRO:HB2	1.95	0.48
1:B:587:ILE:HG22	1:B:587:ILE:O	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:LEU:HD23	1:A:399:LEU:HD13	1.94	0.48
1:B:295:MET:HA	1:B:298:LEU:HD12	1.95	0.47
1:A:464:VAL:HG22	1:A:532:PRO:HB2	1.98	0.46
1:A:184:ILE:HD12	1:A:225:LEU:HD11	1.98	0.45
1:B:164:GLN:HG2	1:B:165:ASP:H	1.82	0.45
1:A:541:THR:HB	1:A:544:GLU:H	1.83	0.45
1:B:368:PRO:HB2	1:B:662:LEU:HD21	2.00	0.44
1:B:541:THR:HB	1:B:544:GLU:H	1.82	0.43
1:B:621:MET:HE1	1:B:630:LYS:HG2	2.00	0.43
1:A:163:ARG:HB2	1:A:237:ARG:O	2.19	0.43
1:A:419:ILE:HG13	1:A:580:MET:HE3	2.00	0.42
1:A:575:ARG:NE	1:A:579:LEU:HD11	2.35	0.42
1:A:597:LEU:HB2	1:A:651:CYS:HB3	2.02	0.42
1:B:379:PHE:HA	1:B:386:PRO:HA	2.02	0.41
1:A:379:PHE:HA	1:A:386:PRO:HA	2.03	0.41
1:B:621:MET:SD	1:B:630:LYS:HA	2.61	0.41
1:A:527:ILE:HA	1:A:528:PRO:HD3	1.93	0.41
1:B:527:ILE:HA	1:B:528:PRO:HD3	1.89	0.40
1:A:621:MET:SD	1:A:630:LYS:HA	2.62	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	478/552 (87%)	450 (94%)	28 (6%)	0	100	100
1	B	451/552 (82%)	420 (93%)	28 (6%)	3 (1%)	18	46
All	All	929/1104 (84%)	870 (94%)	56 (6%)	3 (0%)	36	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	625	ASP
1	B	235	THR
1	B	689	VAL

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	412/501 (82%)	380 (92%)	32 (8%)	11	36
1	B	361/501 (72%)	328 (91%)	33 (9%)	9	30
All	All	773/1002 (77%)	708 (92%)	65 (8%)	10	33

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	LEU
1	A	223	ARG
1	A	228	LEU
1	A	233	VAL
1	A	240	VAL
1	A	247	GLU
1	A	283	GLU
1	A	308	VAL
1	A	316	ASN
1	A	336	CYS
1	A	337	LEU
1	A	346	ILE
1	A	356	LYS
1	A	383	LEU
1	A	388	LYS
1	A	389	ILE
1	A	446	PHE
1	A	527	ILE
1	A	531	LEU
1	A	607	HIS
1	A	617	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	618	SER
1	A	626	ILE
1	A	631	SER
1	A	635	GLU
1	A	653	MET
1	A	657	ASP
1	A	664	GLN
1	A	685	LEU
1	A	688	PHE
1	A	689	VAL
1	A	691	GLU
1	B	163	ARG
1	B	169	VAL
1	B	190	LEU
1	B	191	LEU
1	B	199	ASN
1	B	225	LEU
1	B	316	ASN
1	B	336	CYS
1	B	337	LEU
1	B	383	LEU
1	B	389	ILE
1	B	411	ILE
1	B	417	GLU
1	B	418	GLU
1	B	446	PHE
1	B	512	ILE
1	B	514	SER
1	B	516	SER
1	B	527	ILE
1	B	531	LEU
1	B	583	ASP
1	B	607	HIS
1	B	618	SER
1	B	631	SER
1	B	635	GLU
1	B	657	ASP
1	B	662	LEU
1	B	664	GLN
1	B	665	GLU
1	B	693	ASN
1	B	700	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	702	GLU
1	B	703	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	173	ASN
1	A	185	GLN
1	A	261	GLN
1	A	350	HIS
1	A	359	GLN
1	A	408	ASN
1	A	624	ASN
1	A	664	GLN
1	B	322	GLN
1	B	594	HIS
1	B	624	ASN

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](#)

Of 3 ligands modelled in this entry, 3 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	488/552 (88%)	-0.45	1 (0%) 91 83	50, 92, 149, 182	0
1	B	464/552 (84%)	-0.20	5 (1%) 78 57	54, 109, 172, 202	1 (0%)
All	All	952/1104 (86%)	-0.33	6 (0%) 85 69	50, 99, 166, 202	1 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	174	VAL	4.5
1	B	158	PRO	2.9
1	B	186	SER	2.7
1	A	668	ASN	2.7
1	B	704	ASP	2.6
1	B	249	LEU	2.2

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
2	CL	A	801	1/1	0.92	0.07	111,111,111,111	0
2	CL	B	801	1/1	0.93	0.11	125,125,125,125	0
2	CL	A	802	1/1	0.98	0.15	104,104,104,104	0

6.5 Other polymers [i](#)

There are no such residues in this entry.