



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:02 PM UTC

PDB ID : 3ZO5 / pdb_00003zo5
Title : Structure of SENP2-Loop1 in complex with preSUMO-2
Authors : Alegre, K.O.; Reverter, D.
Deposited on : 2013-02-20
Resolution : 2.15 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

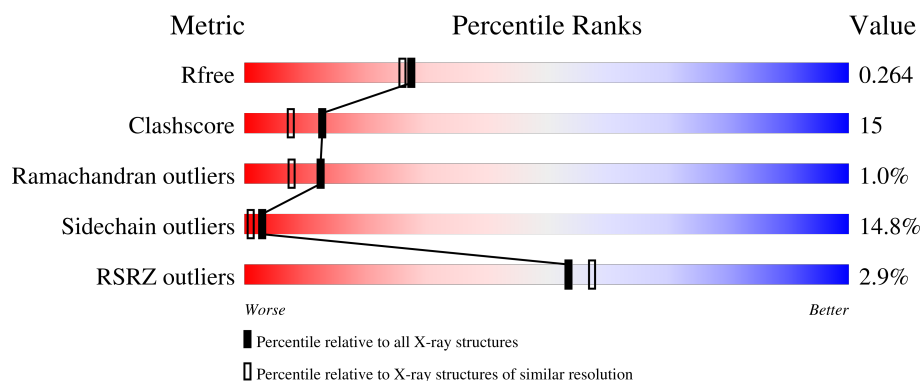
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	238	3% 58% 29% 7% • •
2	B	89	2% 54% 29% 8% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2595 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 SENTRIN-SPECIFIC PROTEASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1898	1219	332	337	10			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	358	GLY	-	expression tag	UNP Q9HC62
A	359	SER	-	expression tag	UNP Q9HC62
A	360	HIS	-	expression tag	UNP Q9HC62
A	361	MET	-	expression tag	UNP Q9HC62
A	362	ALA	-	expression tag	UNP Q9HC62
A	393	PRO	-	insertion	UNP Q9HC62
A	394	PRO	-	insertion	UNP Q9HC62
A	395	PRO	-	insertion	UNP Q9HC62
A	396	PRO	-	insertion	UNP Q9HC62
A	397	ALA	-	insertion	UNP Q9HC62
A	398	LYS	-	insertion	UNP Q9HC62
A	399	GLY	-	insertion	UNP Q9HC62
A	400	GLY	-	insertion	UNP Q9HC62
A	554	SER	CYS	engineered mutation	UNP Q9HC62

- Molecule 2 is a protein called SMALL UBIQUITIN-RELATED MODIFIER 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	81	Total	C	N	O	S	0	0	0
			652	406	116	126	4			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	13	MET	-	expression tag	UNP P61956
B	14	ALA	-	expression tag	UNP P61956

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Chain	Residue	Modelled	Actual	Comment	Reference
B	15	ASN	-	expression tag	UNP P61956
B	96	LEU	-	expression tag	UNP P61956
B	97	GLU	-	expression tag	UNP P61956
B	98	HIS	-	expression tag	UNP P61956
B	99	HIS	-	expression tag	UNP P61956
B	100	HIS	-	expression tag	UNP P61956
B	101	HIS	-	expression tag	UNP P61956

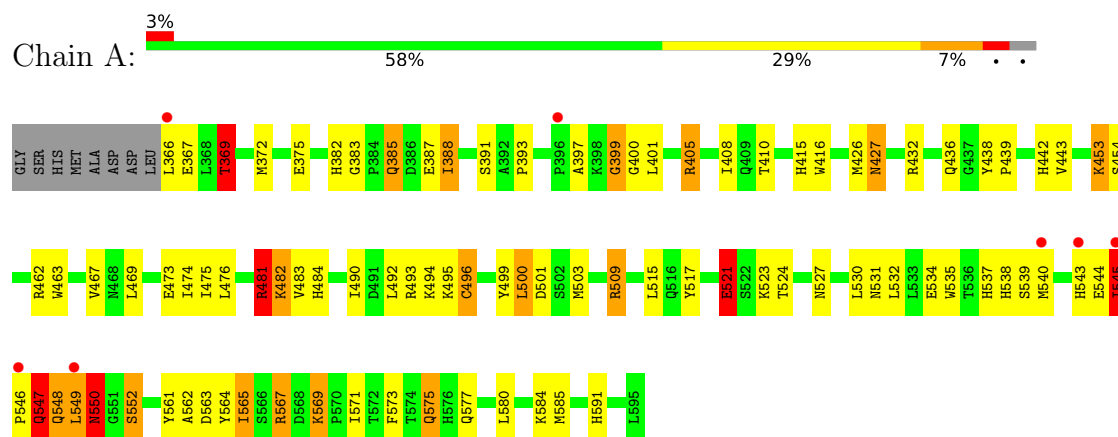
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total	O	0	0
			39	39		
3	B	6	Total	O	0	0
			6	6		

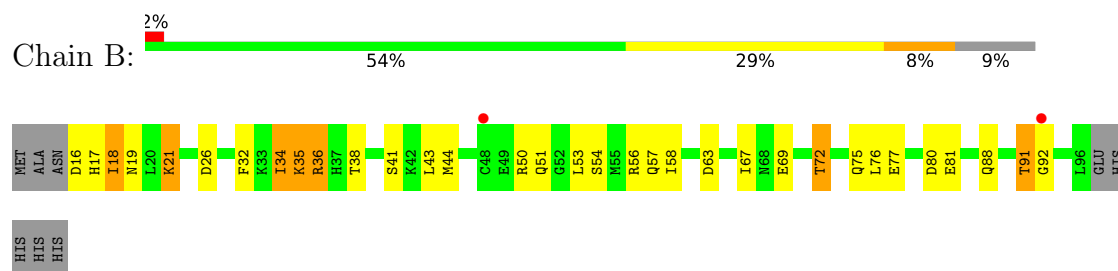
3 Residue-property plots [i](#)

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: SENTRIN-SPECIFIC PROTEASE 2



• Molecule 2: SMALL UBIQUITIN-RELATED MODIFIER 2



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	145.52Å 145.52Å 104.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	80.52 – 2.15 80.52 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (80.52-2.15) 99.8 (80.52-2.15)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.188 , 0.236 (Not available) , 0.264	Depositor DCC
R_{free} test set	1193 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	55.1	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2595	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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

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	1.52	16/1947 (0.8%)	1.42	12/2627 (0.5%)
2	B	1.17	2/662 (0.3%)	1.33	1/889 (0.1%)
All	All	1.44	18/2609 (0.7%)	1.40	13/3516 (0.4%)

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
1	A	0	1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	415	HIS	CG-CD2	7.84	1.44	1.35
1	A	415	HIS	ND1-CE1	7.45	1.40	1.32
2	B	58	ILE	C-O	-6.37	1.16	1.23
1	A	427	ASN	CB-CG	-6.33	1.36	1.52
1	A	567	ARG	CD-NE	-6.30	1.37	1.46
1	A	427	ASN	N-CA	-6.23	1.38	1.46
1	A	401	LEU	N-CA	6.03	1.53	1.45
1	A	552	SER	N-CA	5.99	1.53	1.46
1	A	547	GLN	CA-C	5.86	1.59	1.53
1	A	524	THR	C-O	-5.81	1.17	1.24
1	A	484	HIS	ND1-CE1	5.52	1.38	1.32
2	B	92	GLY	C-O	5.34	1.30	1.23
1	A	463	TRP	NE1-CE2	-5.32	1.31	1.37
1	A	442	HIS	N-CA	5.31	1.52	1.46
1	A	546	PRO	CA-C	5.21	1.59	1.52
1	A	388	ILE	CA-CB	5.17	1.60	1.54
1	A	439	PRO	CA-C	5.12	1.58	1.52
1	A	585	MET	C-O	-5.01	1.17	1.24

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	550	ASN	N-CA-C	9.61	127.26	107.37
1	A	521	GLU	CB-CA-C	-7.04	99.83	110.88
1	A	545	ILE	N-CA-C	6.47	122.86	108.88
1	A	369	THR	N-CA-CB	-6.25	101.42	110.36
1	A	543	HIS	N-CA-CB	-6.23	101.57	110.79
1	A	543	HIS	CB-CA-C	-5.91	102.92	111.14
1	A	539	SER	N-CA-C	-5.77	100.78	109.95
1	A	427	ASN	N-CA-CB	-5.74	101.66	110.16
1	A	569	LYS	CB-CA-C	5.66	116.14	109.47
1	A	388	ILE	CA-CB-CG2	5.28	119.48	110.50
2	B	91	THR	CB-CA-C	-5.20	100.96	109.80
1	A	427	ASN	CB-CA-C	-5.19	102.03	110.85
1	A	481	ARG	N-CA-C	-5.18	101.77	109.96

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	405	ARG	Sidechain

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	1898	0	1911	55	0
2	B	652	0	641	26	0
3	A	39	0	0	0	0
3	B	6	0	0	0	0
All	All	2595	0	2552	77	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 15.

All (77) 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)
2:B:72:THR:HG22	2:B:75:GLN:H	1.15	1.09
1:A:369:THR:HG22	1:A:372:MET:H	1.16	1.05
1:A:547:GLN:HE22	1:A:549:LEU:HD12	1.34	0.91
1:A:547:GLN:NE2	1:A:549:LEU:HD12	1.86	0.89
1:A:547:GLN:OE1	1:A:550:ASN:N	2.11	0.83
1:A:426:MET:HB3	1:A:443:VAL:HG11	1.62	0.81
1:A:545:ILE:HD11	1:A:573:PHE:O	1.81	0.79
1:A:369:THR:HG22	1:A:372:MET:N	1.96	0.76
2:B:54:SER:HB3	2:B:57:GLN:HE21	1.49	0.76
2:B:72:THR:CG2	2:B:75:GLN:H	1.98	0.73
2:B:72:THR:HG22	2:B:75:GLN:N	1.98	0.70
2:B:18:ILE:HG12	2:B:80:ASP:HA	1.75	0.67
1:A:385:GLN:OE1	2:B:56:ARG:NH1	2.28	0.66
1:A:462:ARG:NH1	2:B:63:ASP:OD1	2.29	0.66
1:A:462:ARG:NH1	2:B:63:ASP:OD2	2.29	0.65
1:A:495:LYS:HD3	1:A:534:GLU:HG3	1.79	0.65
1:A:548:GLN:N	1:A:548:GLN:OE1	2.31	0.63
1:A:462:ARG:NH1	2:B:63:ASP:CG	2.57	0.62
1:A:432:ARG:NH2	1:A:567:ARG:HD2	2.14	0.62
2:B:80:ASP:O	2:B:81:GLU:CB	2.48	0.61
1:A:481:ARG:O	1:A:482:LYS:C	2.42	0.61
2:B:35:LYS:HB2	2:B:38:THR:OG1	2.01	0.60
1:A:547:GLN:HE21	1:A:575:GLN:CD	2.09	0.60
2:B:44:MET:HE1	2:B:67:ILE:HG22	1.83	0.60
2:B:44:MET:CE	2:B:67:ILE:HG22	2.31	0.60
1:A:547:GLN:O	1:A:547:GLN:HG3	2.01	0.59
2:B:43:LEU:HD23	2:B:43:LEU:C	2.28	0.59
1:A:563:ASP:O	1:A:567:ARG:HD3	2.03	0.58
2:B:16:ASP:HB2	2:B:36:ARG:HD3	1.86	0.56
1:A:580:LEU:C	1:A:580:LEU:HD13	2.30	0.56
1:A:494:LYS:HG3	1:A:496:CYS:HB3	1.88	0.55
1:A:476:LEU:HD13	1:A:562:ALA:HB1	1.90	0.53
2:B:19:ASN:HA	2:B:32:PHE:O	2.08	0.53
1:A:531:ASN:O	1:A:534:GLU:HG2	2.08	0.53
1:A:375:GLU:CD	1:A:591:HIS:HE2	2.18	0.52
1:A:495:LYS:HG2	1:A:535:TRP:CE2	2.45	0.51
1:A:547:GLN:OE1	1:A:549:LEU:HB2	2.11	0.51
1:A:473:GLU:HB3	1:A:493:ARG:HD3	1.93	0.50
1:A:475:ILE:HB	1:A:490:ILE:HB	1.95	0.49
1:A:515:LEU:HG	1:A:532:LEU:HD22	1.95	0.49
2:B:19:ASN:N	2:B:80:ASP:OD1	2.37	0.49
1:A:393:PRO:HB2	1:A:397:ALA:CB	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:54:SER:HB3	2:B:57:GLN:NE2	2.23	0.48
1:A:500:LEU:HD11	1:A:565:ILE:HD11	1.95	0.48
1:A:523:LYS:O	1:A:527:ASN:HA	2.15	0.47
1:A:410:THR:HB	1:A:416:TRP:O	2.15	0.47
1:A:537:HIS:O	1:A:538:HIS:HD2	1.97	0.46
2:B:76:LEU:C	2:B:77:GLU:HG2	2.39	0.46
1:A:432:ARG:CZ	1:A:567:ARG:HD2	2.45	0.46
1:A:499:TYR:CE2	1:A:501:ASP:HB2	2.50	0.46
1:A:564:TYR:CD2	1:A:569:LYS:HG2	2.50	0.46
1:A:369:THR:HB	1:A:372:MET:SD	2.56	0.45
1:A:436:GLN:HB2	1:A:438:TYR:CD2	2.51	0.45
1:A:426:MET:CB	1:A:443:VAL:HG11	2.40	0.45
2:B:80:ASP:O	2:B:81:GLU:HB3	2.16	0.45
2:B:34:ILE:HG13	2:B:35:LYS:N	2.32	0.44
2:B:41:SER:HB3	2:B:69:GLU:HB3	1.97	0.44
1:A:500:LEU:N	1:A:500:LEU:HD23	2.33	0.44
1:A:545:ILE:CD1	1:A:573:PHE:O	2.59	0.44
2:B:51:GLN:HB2	2:B:53:LEU:HG	1.98	0.43
1:A:399:GLY:HA2	1:A:400:GLY:HA3	1.83	0.43
2:B:19:ASN:O	2:B:81:GLU:N	2.44	0.43
1:A:549:LEU:H	1:A:549:LEU:HG	1.65	0.43
2:B:50:ARG:HD3	2:B:51:GLN:OE1	2.19	0.43
1:A:387:GLU:OE1	1:A:405:ARG:NH2	2.51	0.43
1:A:517:TYR:CZ	1:A:521:GLU:HG2	2.54	0.42
1:A:565:ILE:HD12	1:A:571:ILE:HD11	2.01	0.42
1:A:565:ILE:CD1	1:A:571:ILE:HD11	2.49	0.42
1:A:474:ILE:HD13	1:A:474:ILE:HG21	1.81	0.42
1:A:453:LYS:NZ	1:A:509:ARG:NH1	2.68	0.42
1:A:545:ILE:HG12	1:A:545:ILE:O	2.20	0.42
1:A:383:GLY:HA3	1:A:405:ARG:HH21	1.85	0.42
1:A:545:ILE:HG21	1:A:561:TYR:HE1	1.85	0.41
2:B:21:LYS:HE2	2:B:21:LYS:HB2	1.95	0.41
1:A:494:LYS:HE2	1:A:494:LYS:HB3	1.79	0.41
1:A:492:LEU:HD23	1:A:535:TRP:HH2	1.85	0.40
1:A:500:LEU:HD11	1:A:565:ILE:CD1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	228/238 (96%)	220 (96%)	6 (3%)	2 (1%)	14	9
2	B	79/89 (89%)	74 (94%)	4 (5%)	1 (1%)	9	5
All	All	307/327 (94%)	294 (96%)	10 (3%)	3 (1%)	12	8

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	545	ILE
1	A	399	GLY
2	B	26	ASP

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	211/217 (97%)	178 (84%)	33 (16%)	2	1
2	B	72/79 (91%)	63 (88%)	9 (12%)	4	2
All	All	283/296 (96%)	241 (85%)	42 (15%)	3	1

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	366	LEU
1	A	367	GLU
1	A	369	THR

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Mol	Chain	Res	Type
1	A	382	HIS
1	A	385	GLN
1	A	388	ILE
1	A	391	SER
1	A	408	ILE
1	A	427	ASN
1	A	453	LYS
1	A	454	SER
1	A	467	VAL
1	A	469	LEU
1	A	481	ARG
1	A	482	LYS
1	A	483	VAL
1	A	496	CYS
1	A	500	LEU
1	A	503	MET
1	A	509	ARG
1	A	521	GLU
1	A	530	LEU
1	A	540	MET
1	A	544	GLU
1	A	547	GLN
1	A	548	GLN
1	A	549	LEU
1	A	550	ASN
1	A	552	SER
1	A	565	ILE
1	A	575	GLN
1	A	577	GLN
1	A	584	LYS
2	B	17	HIS
2	B	18	ILE
2	B	21	LYS
2	B	34	ILE
2	B	35	LYS
2	B	36	ARG
2	B	72	THR
2	B	88	GLN
2	B	91	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	GLN
1	A	413	ASN
1	A	415	HIS
1	A	442	HIS
1	A	516	GLN
1	A	538	HIS
2	B	17	HIS
2	B	57	GLN
2	B	75	GLN
2	B	89	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	230/238 (96%)	0.18	7 (3%) 52 56	26, 42, 74, 100	0
2	B	81/89 (91%)	0.34	2 (2%) 58 62	32, 44, 63, 79	0
All	All	311/327 (95%)	0.22	9 (2%) 53 57	26, 42, 73, 100	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	366	LEU	3.2
1	A	546	PRO	2.9
1	A	540	MET	2.8
2	B	48	CYS	2.5
1	A	545	ILE	2.3
1	A	543	HIS	2.3
1	A	549	LEU	2.3
2	B	92	GLY	2.2
1	A	396	PRO	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 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.