



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 9, 2026 – 09:23 PM UTC

PDB ID : 9WZK / pdb_00009wzk
Title : Crystal structure of the inactive mutant of rice protein disulfide isomerase-like protein OsPDIL2-3 a-b domains
Authors : Fujimoto, Z.; Sakurai, M.; Kishine, N.; Kawagoe, Y.
Deposited on : 2025-09-29
Resolution : 1.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

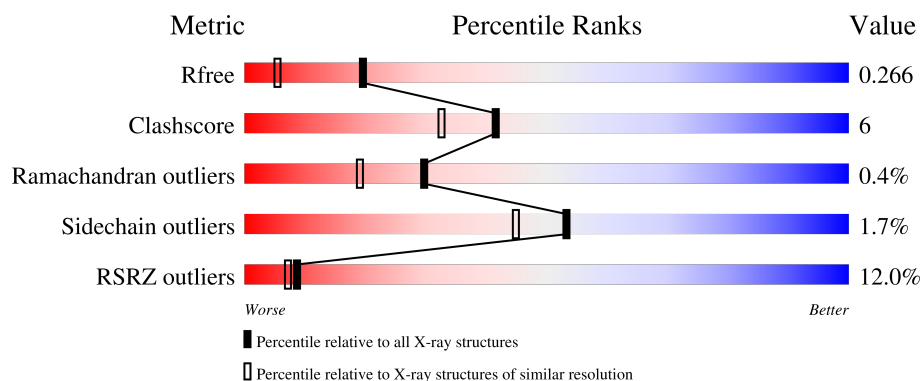
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	296	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>11%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	296	<div> <div>10%</div> <div> <div></div> <div>76%</div> <div>9%</div> <div>•</div> <div>14%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4157 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 disulfide isomerase-like 2-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	1	0
			1952	1254	319	373	6			
1	B	254	Total	C	N	O	S	0	0	0
			1942	1248	319	369	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	146	GLY	-	expression tag	UNP Q67UF5
A	147	PRO	-	expression tag	UNP Q67UF5
A	148	LEU	-	expression tag	UNP Q67UF5
A	195	ALA	CYS	engineered mutation	UNP Q67UF5
A	198	ALA	CYS	engineered mutation	UNP Q67UF5
A	388	ARG	LYS	conflict	UNP Q67UF5
B	146	GLY	-	expression tag	UNP Q67UF5
B	147	PRO	-	expression tag	UNP Q67UF5
B	148	LEU	-	expression tag	UNP Q67UF5
B	195	ALA	CYS	engineered mutation	UNP Q67UF5
B	198	ALA	CYS	engineered mutation	UNP Q67UF5
B	388	ARG	LYS	conflict	UNP Q67UF5

- Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

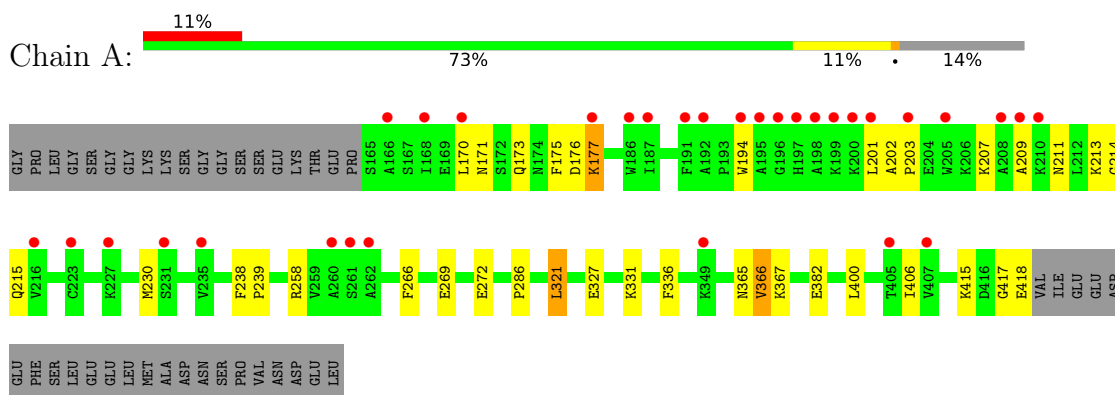
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	132	Total	O	0	0
			132	132		
3	B	103	Total	O	0	0
			103	103		

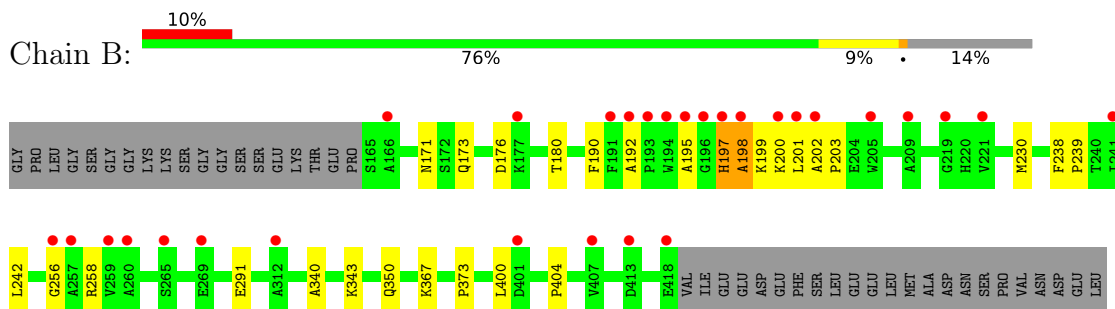
3 Residue-property plots

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: Protein disulfide isomerase-like 2-3



• Molecule 1: Protein disulfide isomerase-like 2-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	35.17Å 171.46Å 52.73Å 90.00° 106.27° 90.00°	Depositor
Resolution (Å)	28.33 – 1.80 28.33 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.7 (28.33-1.80) 96.7 (28.33-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0431	Depositor
R, R_{free}	0.221 , 0.266 0.221 , 0.266	Depositor DCC
R_{free} test set	2710 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4157	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BTB

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	0.52	0/2001	1.14	4/2705 (0.1%)
1	B	0.51	0/1988	1.11	3/2688 (0.1%)
All	All	0.51	0/3989	1.12	7/5393 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	400	LEU	N-CA-CB	-6.67	100.16	109.97
1	B	291	GLU	N-CA-CB	-6.12	100.87	110.30
1	A	336	PHE	CA-CB-CG	-5.74	108.06	113.80
1	B	400	LEU	N-CA-CB	-5.41	102.07	110.29
1	A	365	ASN	CB-CA-C	5.34	120.40	111.22
1	B	180	THR	CA-CB-OG1	-5.24	101.74	109.60
1	A	382	GLU	CB-CG-CD	5.01	121.11	112.60

There are no chirality outliers.

There are no planarity outliers.

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	1952	0	1938	25	0
1	B	1942	0	1928	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	14	0	19	2	0
2	B	14	0	19	0	0
3	A	132	0	0	4	0
3	B	103	0	0	2	0
All	All	4157	0	3904	50	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 (50) 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:350:GLN:HE22	1:B:404:PRO:HA	1.22	0.99
1:A:171:ASN:OD1	1:A:173:GLN:HB2	1.66	0.93
1:B:350:GLN:NE2	1:B:404:PRO:HA	1.94	0.81
1:A:201:LEU:HD13	1:A:258:ARG:HB3	1.66	0.78
1:A:194:TRP:HZ2	1:B:230:MET:HE2	1.49	0.77
1:A:201:LEU:HD23	1:A:239:PRO:HG2	1.68	0.75
1:A:194:TRP:CZ2	1:B:230:MET:HE2	2.21	0.74
1:B:197:HIS:C	1:B:199:LYS:H	2.00	0.69
1:B:197:HIS:HA	1:B:200:LYS:HB2	1.77	0.67
1:B:350:GLN:HE22	1:B:404:PRO:CA	2.04	0.66
1:A:366:VAL:HG13	3:A:682:HOH:O	1.95	0.65
1:A:201:LEU:CD2	1:A:239:PRO:HG2	2.29	0.62
1:B:201:LEU:HD22	1:B:239:PRO:HG3	1.81	0.62
1:B:201:LEU:HD13	1:B:258:ARG:HB3	1.84	0.57
1:A:230:MET:HE3	1:A:238:PHE:CZ	2.39	0.56
1:A:170:LEU:HD23	1:A:175:PHE:CE2	2.41	0.55
1:B:367:LYS:HD3	3:B:703:HOH:O	2.06	0.55
1:A:321:LEU:C	1:A:321:LEU:HD23	2.33	0.54
1:A:230:MET:HE3	1:A:238:PHE:HZ	1.73	0.54
1:A:230:MET:CE	1:A:238:PHE:HZ	2.20	0.53
1:A:272:GLU:OE2	1:A:331:LYS:NZ	2.39	0.52
1:B:198:ALA:HA	1:B:202:ALA:HB3	1.91	0.52
1:A:417:GLY:O	1:A:418:GLU:HB2	2.12	0.50
2:A:501:BTB:H31	2:A:501:BTB:H81	1.93	0.50
1:B:202:ALA:N	1:B:203:PRO:HD2	2.27	0.48
1:B:197:HIS:C	1:B:199:LYS:N	2.68	0.48
1:B:340:ALA:HB3	1:B:343:LYS:HG3	1.95	0.48
1:A:266:PHE:HA	1:A:269:GLU:OE1	2.13	0.48
1:A:209:ALA:O	1:A:213:LYS:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:PHE:HA	1:A:239:PRO:HA	1.68	0.46
1:A:415:LYS:O	3:A:601:HOH:O	2.20	0.46
1:B:197:HIS:O	1:B:199:LYS:N	2.48	0.46
1:B:192:ALA:O	1:B:197:HIS:NE2	2.48	0.46
1:A:215:GLN:NE2	3:A:612:HOH:O	2.50	0.45
2:A:501:BTB:H81	2:A:501:BTB:C3	2.47	0.45
1:B:201:LEU:C	1:B:203:PRO:HD2	2.42	0.45
1:A:286:PRO:HD3	1:A:406:ILE:O	2.18	0.44
1:B:230:MET:CE	1:B:238:PHE:HZ	2.31	0.44
1:B:202:ALA:N	1:B:203:PRO:CD	2.82	0.42
1:A:214:GLY:N	3:A:614:HOH:O	2.53	0.42
1:B:256:GLY:O	1:B:258:ARG:HD2	2.20	0.42
1:B:373:PRO:HD2	3:B:627:HOH:O	2.19	0.42
1:A:177:LYS:HB2	1:A:177:LYS:NZ	2.34	0.42
1:A:202:ALA:N	1:A:203:PRO:HD2	2.35	0.41
1:B:195:ALA:HB3	1:B:197:HIS:CD2	2.55	0.41
1:A:367:LYS:HE3	1:A:367:LYS:HB3	1.73	0.41
1:B:171:ASN:C	1:B:173:GLN:H	2.27	0.41
1:A:203:PRO:O	1:A:207:LYS:HG3	2.21	0.41
1:B:190:PHE:CE1	1:B:242:LEU:HD12	2.56	0.40
1:B:198:ALA:HA	1:B:202:ALA:CB	2.51	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	253/296 (86%)	242 (96%)	11 (4%)	0	100	100
1	B	252/296 (85%)	231 (92%)	19 (8%)	2 (1%)	16	6
All	All	505/592 (85%)	473 (94%)	30 (6%)	2 (0%)	30	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	198	ALA
1	B	197	HIS

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	203/237 (86%)	196 (97%)	7 (3%)	32	20
1	B	201/237 (85%)	200 (100%)	1 (0%)	81	80
All	All	404/474 (85%)	396 (98%)	8 (2%)	53	38

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	176	ASP
1	A	177	LYS
1	A	211	ASN
1	A	321	LEU
1	A	327[A]	GLU
1	A	327[B]	GLU
1	A	366	VAL
1	B	176	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	211	ASN
1	A	270	GLN
1	A	397	ASN
1	B	255	GLN
1	B	274	ASN
1	B	316	ASN
1	B	350	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BTB	A	501	-	13,13,13	1.07	1 (7%)	7,16,16	0.67	0
2	BTB	B	501	-	13,13,13	1.34	2 (15%)	7,16,16	0.77	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BTB	A	501	-	-	0/21/21/21	-
2	BTB	B	501	-	-	2/21/21/21	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	BTB	C5-N	3.03	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	BTB	C5-N	2.79	1.51	1.48
2	B	501	BTB	C2-N	2.69	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	BTB	N-C7-C8-O8
2	B	501	BTB	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	BTB	2	0

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	254/296 (85%)	0.68	32 (12%) 8 6	13, 39, 80, 114	1 (0%)
1	B	254/296 (85%)	0.78	29 (11%) 10 8	16, 43, 82, 122	0
All	All	508/592 (85%)	0.73	61 (12%) 9 7	13, 41, 81, 122	1 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	194	TRP	5.8
1	A	192	ALA	4.6
1	A	194	TRP	4.6
1	A	200	LYS	4.4
1	A	197	HIS	4.0
1	A	166	ALA	3.5
1	B	407	VAL	3.4
1	B	202	ALA	3.4
1	A	235	VAL	3.3
1	B	418	GLU	3.2
1	B	192	ALA	3.2
1	A	203	PRO	3.2
1	B	198	ALA	3.1
1	A	198	ALA	3.0
1	A	260	ALA	3.0
1	A	170	LEU	2.9
1	A	191	PHE	2.9
1	B	257	ALA	2.9
1	B	260	ALA	2.9
1	B	191	PHE	2.9
1	A	262	ALA	2.9
1	B	193	PRO	2.8
1	B	209	ALA	2.8
1	B	265	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	196	GLY	2.8
1	A	195	ALA	2.7
1	B	197	HIS	2.7
1	A	209	ALA	2.7
1	A	199	LYS	2.7
1	B	401	ASP	2.6
1	B	196	GLY	2.6
1	A	205	TRP	2.6
1	B	256	GLY	2.6
1	B	205	TRP	2.5
1	A	405	THR	2.5
1	B	221	VAL	2.5
1	B	195	ALA	2.4
1	A	216	VAL	2.4
1	A	349	LYS	2.4
1	A	201	LEU	2.3
1	A	208	ALA	2.3
1	A	231	SER	2.3
1	A	407	VAL	2.3
1	B	312	ALA	2.2
1	B	166	ALA	2.2
1	A	187	ILE	2.2
1	B	177	LYS	2.2
1	B	259	VAL	2.2
1	A	261	SER	2.2
1	B	413	ASP	2.1
1	B	241	ILE	2.1
1	B	200	LYS	2.1
1	A	177	LYS	2.1
1	A	223	CYS	2.1
1	A	210	LYS	2.0
1	A	227	LYS	2.0
1	B	219	GLY	2.0
1	A	186	TRP	2.0
1	B	201	LEU	2.0
1	B	269	GLU	2.0
1	A	168	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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(\AA^2)	Q<0.9
2	BTB	A	501	14/14	0.91	0.10	22,30,33,41	0
2	BTB	B	501	14/14	0.93	0.09	22,27,31,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.