



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:23 PM UTC

PDB ID : 1XCR / pdb_00001xcr
Title : Crystal Structure of Longer Splice Variant of PTD012 from Homo sapiens reveals a novel Zinc-containing fold
Authors : Manjasetty, B.A.; Fieber-Erdmann, M.; Roske, Y.; Goetz, F.; Buessow, K.; Heinemann, U.
Deposited on : 2004-09-03
Resolution : 1.70 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

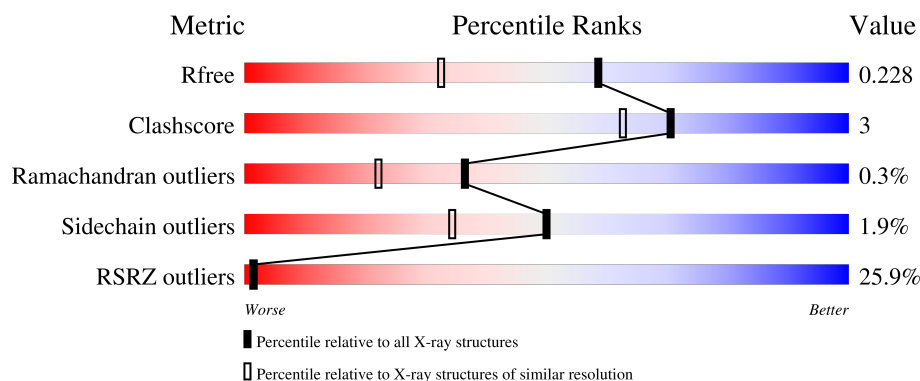
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	316	50% 91% 8% ..
1	B	316	% 92% 6% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACY	A	2001	-	-	X	-
3	ACY	B	2002	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5180 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 hypothetical protein PTD012.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	2	0
			2426	1568	401	442	15			
1	B	313	Total	C	N	O	S	0	4	0
			2434	1571	404	443	16			

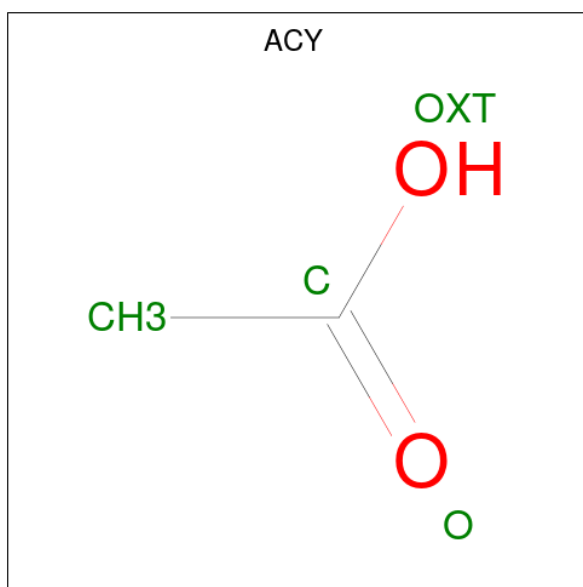
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	cloning artifact	UNP Q9H0W9
A	1	SER	-	cloning artifact	UNP Q9H0W9
B	0	GLY	-	cloning artifact	UNP Q9H0W9
B	1	SER	-	cloning artifact	UNP Q9H0W9

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

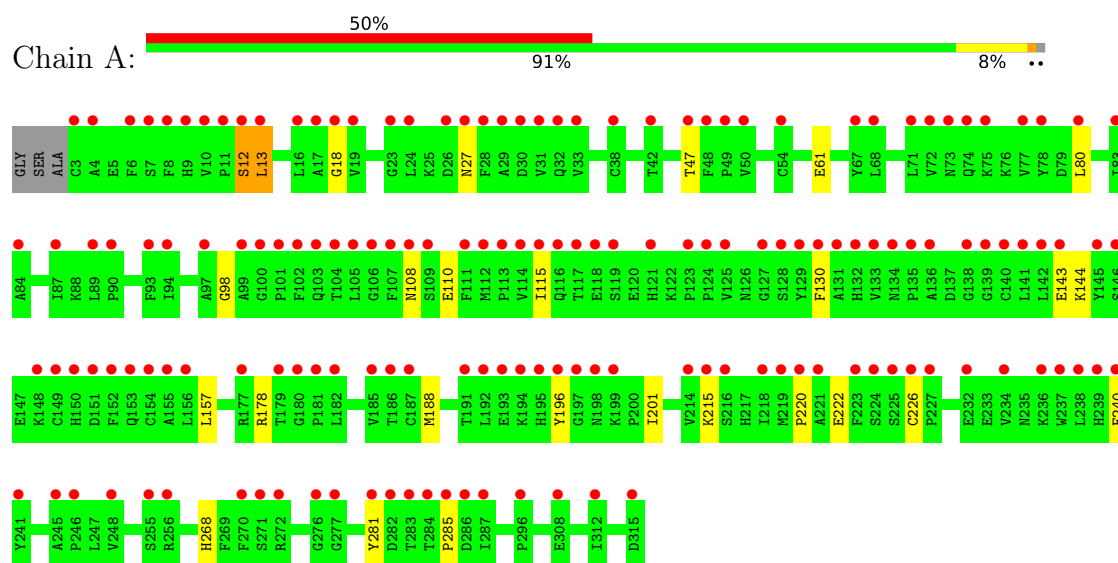
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	126	Total	O	0	0
			126	126		
4	B	184	Total	O	0	0
			184	184		

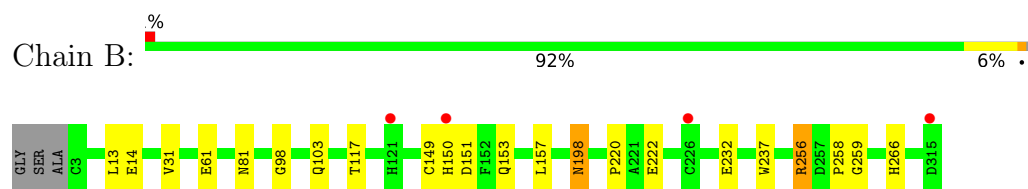
3 Residue-property plots [i](#)

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: hypothetical protein PTD012



• Molecule 1: hypothetical protein PTD012



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.57Å 52.89Å 124.48Å 90.00° 88.89° 90.00°	Depositor
Resolution (Å)	20.00 – 1.70 20.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	95.6 (20.00-1.70) 95.5 (20.00-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.47 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.190 , 0.222 0.198 , 0.228	Depositor DCC
R_{free} test set	3103 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5180	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% 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: ZN, ACY

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	0.73	3/2508 (0.1%)	0.76	2/3401 (0.1%)
1	B	0.64	0/2527	0.77	0/3427
All	All	0.69	3/5035 (0.1%)	0.76	2/6828 (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
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	18	GLY	C-O	10.70	1.37	1.23
1	A	188	MET	C-O	9.01	1.34	1.24
1	A	27	ASN	C-O	7.53	1.33	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	SER	N-CA-C	-6.00	101.77	110.24
1	A	13	LEU	N-CA-C	5.00	121.46	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	SER	Peptide

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	2426	0	2341	17	0
1	B	2434	0	2343	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	4	0	3	3	0
3	B	4	0	3	4	0
4	A	126	0	0	2	0
4	B	184	0	0	1	0
All	All	5180	0	4690	33	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 (33) 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:149[A]:CYS:SG	1:B:151:ASP:OD1	2.24	0.95
1:B:157:LEU:HD11	3:B:2002:ACY:H2	1.54	0.88
1:B:103:GLN:HE21	1:B:153:GLN:HE21	1.31	0.79
1:A:196:TYR:CD2	1:A:201:ILE:HD11	2.24	0.73
1:A:157:LEU:HD11	3:A:2001:ACY:H2	1.76	0.65
1:B:81:ASN:HD22	1:B:117:THR:HB	1.62	0.63
1:B:266:HIS:CE1	3:B:2002:ACY:H1	2.34	0.62
1:A:108[B]:ASN:ND2	4:A:2023:HOH:O	2.33	0.58
1:B:98:GLY:C	3:B:2002:ACY:H3	2.27	0.58
1:A:98:GLY:C	3:A:2001:ACY:H3	2.31	0.56
1:A:196:TYR:CG	1:A:201:ILE:HD11	2.41	0.56
1:B:14:GLU:H	1:B:14:GLU:CD	2.14	0.55
1:A:47:THR:HG22	1:A:47:THR:O	2.08	0.53
1:A:226:CYS:HB3	4:A:2011:HOH:O	2.10	0.52
1:A:196:TYR:CD2	1:A:201:ILE:CD1	2.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149[A]:CYS:SG	1:B:151:ASP:CG	2.93	0.51
1:B:103:GLN:HE21	1:B:153:GLN:NE2	2.04	0.51
1:B:157:LEU:CD1	3:B:2002:ACY:H2	2.35	0.49
1:B:198:ASN:HD22	1:B:198:ASN:C	2.24	0.46
1:B:256:ARG:NH2	1:B:258:PRO:HA	2.32	0.45
1:A:268:HIS:CE1	3:A:2001:ACY:H1	2.53	0.43
1:B:149[A]:CYS:SG	4:B:2179:HOH:O	2.61	0.43
1:A:215:LYS:HD3	1:A:281:TYR:CZ	2.54	0.43
1:A:80:LEU:HD13	1:A:115:ILE:HD12	2.01	0.42
1:A:178:ARG:N	1:A:285:PRO:O	2.53	0.41
1:B:14:GLU:CD	1:B:14:GLU:N	2.78	0.41
1:B:149[A]:CYS:SG	1:B:150:HIS:N	2.94	0.41
1:A:215:LYS:HE3	1:A:240:PHE:CD2	2.55	0.41
1:B:220:PRO:HG2	1:B:237:TRP:CE2	2.56	0.41
1:A:130:PHE:CZ	1:A:143:GLU:HB2	2.56	0.41
1:A:215:LYS:HE3	1:A:240:PHE:CE2	2.56	0.41
1:A:108[A]:ASN:HB2	1:A:220:PRO:O	2.21	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	313/316 (99%)	303 (97%)	9 (3%)	1 (0%)	36	22
1	B	315/316 (100%)	306 (97%)	8 (2%)	1 (0%)	36	22
All	All	628/632 (99%)	609 (97%)	17 (3%)	2 (0%)	36	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	LEU

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Mol	Chain	Res	Type
1	B	259	GLY

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	259/269 (96%)	256 (99%)	3 (1%)	63	51
1	B	261/269 (97%)	254 (97%)	7 (3%)	39	23
All	All	520/538 (97%)	510 (98%)	10 (2%)	50	34

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	GLU
1	A	144	LYS
1	A	222	GLU
1	B	13	LEU
1	B	31	VAL
1	B	61	GLU
1	B	198	ASN
1	B	222	GLU
1	B	232	GLU
1	B	256	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	198	ASN
1	A	210	GLN
1	A	273	HIS
1	B	74	GLN
1	B	81	ASN
1	B	121	HIS

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Mol	Chain	Res	Type
1	B	153	GLN
1	B	198	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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
3	ACY	B	2002	2	3,3,3	1.01	0	3,3,3	1.22	0
3	ACY	A	2001	2	3,3,3	0.92	0	3,3,3	1.11	0

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.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2002	ACY	4	0
3	A	2001	ACY	3	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	313/316 (99%)	2.18	158 (50%) 0 0	18, 26, 31, 41	2 (0%)
1	B	313/316 (99%)	0.44	4 (1%) 75 79	14, 24, 29, 40	4 (1%)
All	All	626/632 (99%)	1.31	162 (25%) 1 1	14, 25, 30, 41	6 (0%)

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	198	ASN	6.0
1	A	125	VAL	5.9
1	A	138	GLY	5.6
1	A	135	PRO	5.2
1	A	197	GLY	4.8
1	A	133	VAL	4.8
1	A	10	VAL	4.8
1	A	13	LEU	4.7
1	A	28	PHE	4.7
1	A	136	ALA	4.7
1	A	181	PRO	4.6
1	A	187	CYS	4.5
1	A	9	HIS	4.5
1	A	286	ASP	4.4
1	A	196	TYR	4.2
1	A	199	LYS	4.1
1	A	141	LEU	4.1
1	A	255	SER	4.0
1	A	124	PRO	3.9
1	A	142	LEU	3.9
1	A	149	CYS	3.9
1	A	105	LEU	3.9
1	A	17	ALA	3.9
1	A	241	TYR	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	114	VAL	3.7
1	A	155	ALA	3.7
1	A	179	THR	3.7
1	A	223	PHE	3.7
1	A	12	SER	3.7
1	A	111	PHE	3.6
1	A	220	PRO	3.6
1	A	193	GLU	3.6
1	A	238	LEU	3.6
1	A	315	ASP	3.6
1	A	237	TRP	3.5
1	A	283	THR	3.5
1	A	139	GLY	3.5
1	A	33	VAL	3.5
1	A	48	PHE	3.5
1	A	130	PHE	3.4
1	A	152	PHE	3.4
1	A	115	ILE	3.4
1	A	80	LEU	3.4
1	A	107	PHE	3.4
1	A	77	VAL	3.4
1	A	99	ALA	3.3
1	A	19	VAL	3.3
1	A	50	VAL	3.3
1	A	72	VAL	3.3
1	A	23	GLY	3.2
1	A	30	ASP	3.2
1	A	182	LEU	3.2
1	A	256	ARG	3.2
1	A	83	ILE	3.2
1	A	287	ILE	3.2
1	A	180	GLY	3.2
1	A	16	LEU	3.1
1	A	145	TYR	3.1
1	A	18	GLY	3.1
1	A	218	ILE	3.1
1	A	186	THR	3.1
1	A	271	SER	3.1
1	A	101	PRO	3.0
1	A	239	HIS	3.0
1	A	106	GLY	3.0
1	A	104	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	121	HIS	3.0
1	A	154	CYS	3.0
1	A	226	CYS	3.0
1	A	236	LYS	3.0
1	A	102	PHE	3.0
1	A	240	PHE	3.0
1	A	284	THR	2.9
1	A	151	ASP	2.9
1	A	195	HIS	2.9
1	A	24	LEU	2.9
1	A	71	LEU	2.9
1	A	148	LYS	2.9
1	A	215	LYS	2.9
1	A	8	PHE	2.9
1	A	132	HIS	2.9
1	A	150	HIS	2.9
1	A	134	ASN	2.8
1	A	194	LYS	2.8
1	A	127	GLY	2.8
1	A	128	SER	2.8
1	A	177	ARG	2.8
1	A	281	TYR	2.8
1	A	100	GLY	2.8
1	A	272	ARG	2.7
1	A	140	CYS	2.7
1	A	117	THR	2.7
1	A	27	ASN	2.7
1	A	191	THR	2.7
1	A	221	ALA	2.7
1	A	146	SER	2.7
1	A	68	LEU	2.7
1	A	123	PRO	2.6
1	A	270	PHE	2.6
1	A	192	LEU	2.6
1	A	94	ILE	2.6
1	A	49	PRO	2.6
1	A	42	THR	2.6
1	A	29	ALA	2.6
1	A	90	PRO	2.6
1	B	315	ASP	2.6
1	A	109	SER	2.6
1	A	312	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	84	ALA	2.6
1	A	26	ASP	2.5
1	B	150	HIS	2.5
1	A	225	SER	2.5
1	A	11	PRO	2.5
1	A	219[A]	MET	2.5
1	A	73	ASN	2.5
1	A	32	GLN	2.5
1	A	47	THR	2.5
1	A	119	SER	2.5
1	A	153	GLN	2.4
1	A	93	PHE	2.4
1	A	216	SER	2.4
1	A	4	ALA	2.4
1	A	31	VAL	2.4
1	A	54	CYS	2.4
1	A	246	PRO	2.4
1	A	78	TYR	2.4
1	A	75	LYS	2.3
1	A	6	PHE	2.3
1	A	143	GLU	2.3
1	A	308	GLU	2.3
1	A	227	PRO	2.3
1	A	38	CYS	2.3
1	A	129	TYR	2.3
1	A	276	GLY	2.3
1	A	108[A]	ASN	2.2
1	A	234	VAL	2.2
1	A	7	SER	2.2
1	A	89	LEU	2.2
1	A	156	LEU	2.2
1	A	113	PRO	2.2
1	B	226	CYS	2.2
1	A	74	GLN	2.2
1	A	248	VAL	2.1
1	A	232	GLU	2.1
1	B	121	HIS	2.1
1	A	112	MET	2.1
1	A	296	PRO	2.1
1	A	87	ILE	2.1
1	A	97	ALA	2.1
1	A	131	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	277	GLY	2.1
1	A	3	CYS	2.1
1	A	118	GLU	2.1
1	A	224	SER	2.1
1	A	285	PRO	2.1
1	A	67	TYR	2.1
1	A	245	ALA	2.0
1	A	103	GLN	2.0
1	A	116	GLN	2.0
1	A	282	ASP	2.0
1	A	185	VAL	2.0
1	A	214	VAL	2.0

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
3	ACY	B	2002	4/4	0.90	0.17	17,18,19,20	3
3	ACY	A	2001	4/4	0.91	0.17	25,26,26,27	3
2	ZN	A	1001	1/1	0.98	0.12	25,25,25,25	0
2	ZN	B	1002	1/1	1.00	0.15	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.