



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:27 AM UTC

PDB ID : 3DLJ / pdb_00003dlj
Title : Crystal structure of human carnosine dipeptidase 1
Authors : Dong, A.; Dobrovetsky, E.; Seitova, A.; He, H.; Tempel, W.; Kozieradzki, I.; Arrowsmith, C.H.; Weigelt, J.; Bountra, C.; Edwards, A.M.; Bochkarev, A.; Cossar, D.; Structural Genomics Consortium (SGC)
Deposited on : 2008-06-27
Resolution : 2.26 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

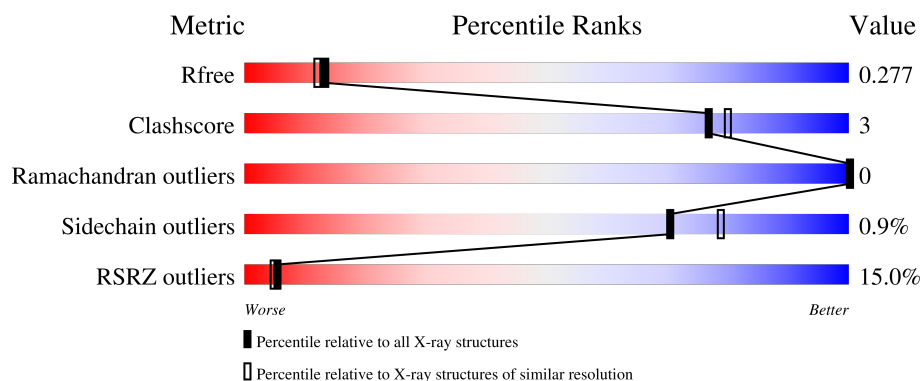
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	485	5% 93% . .
1	B	485	24% 84% 12% .

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	UNX	A	2004	-	-	-	X
3	UNX	A	2005	-	-	-	X
3	UNX	A	2006	-	-	-	X
3	UNX	A	2007	-	-	-	X
3	UNX	A	2008	-	-	-	X
3	UNX	A	2009	-	-	-	X
3	UNX	A	2010	-	-	-	X
3	UNX	A	2011	-	-	-	X
3	UNX	A	2012	-	-	-	X
3	UNX	B	2003	-	-	-	X
3	UNX	B	2004	-	-	-	X
3	UNX	B	2005	-	-	-	X
3	UNX	B	2006	-	-	-	X
3	UNX	B	2007	-	-	-	X
3	UNX	B	2008	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7420 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 Beta-Ala-His dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	471	Total	C	N	O	S	0	0	0
			3600	2322	591	672	15			
1	B	467	Total	C	N	O	S	0	0	0
			3583	2300	598	670	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q96KN2
A	-2	ALA	-	expression tag	UNP Q96KN2
A	-1	MET	-	expression tag	UNP Q96KN2
A	0	ASP	-	expression tag	UNP Q96KN2
B	-3	GLY	-	expression tag	UNP Q96KN2
B	-2	ALA	-	expression tag	UNP Q96KN2
B	-1	MET	-	expression tag	UNP Q96KN2
B	0	ASP	-	expression tag	UNP Q96KN2

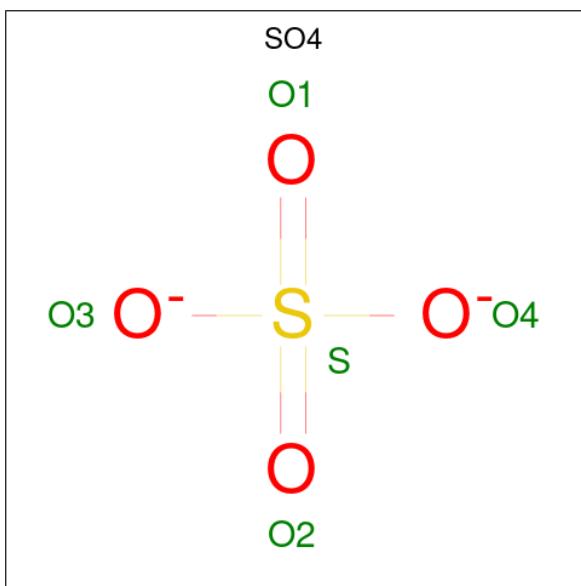
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	X	0	0
			9	9		
3	B	6	Total	X	0	0
			6	6		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

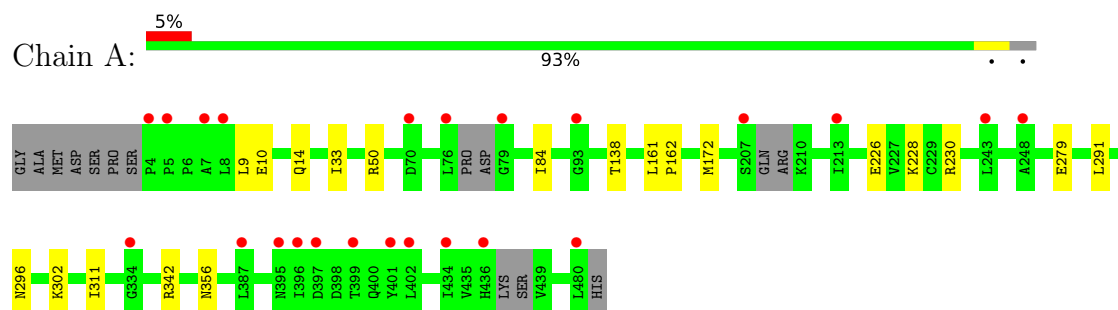
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	109	Total	O	0	0
			109	109		
5	B	104	Total	O	0	0
			104	104		

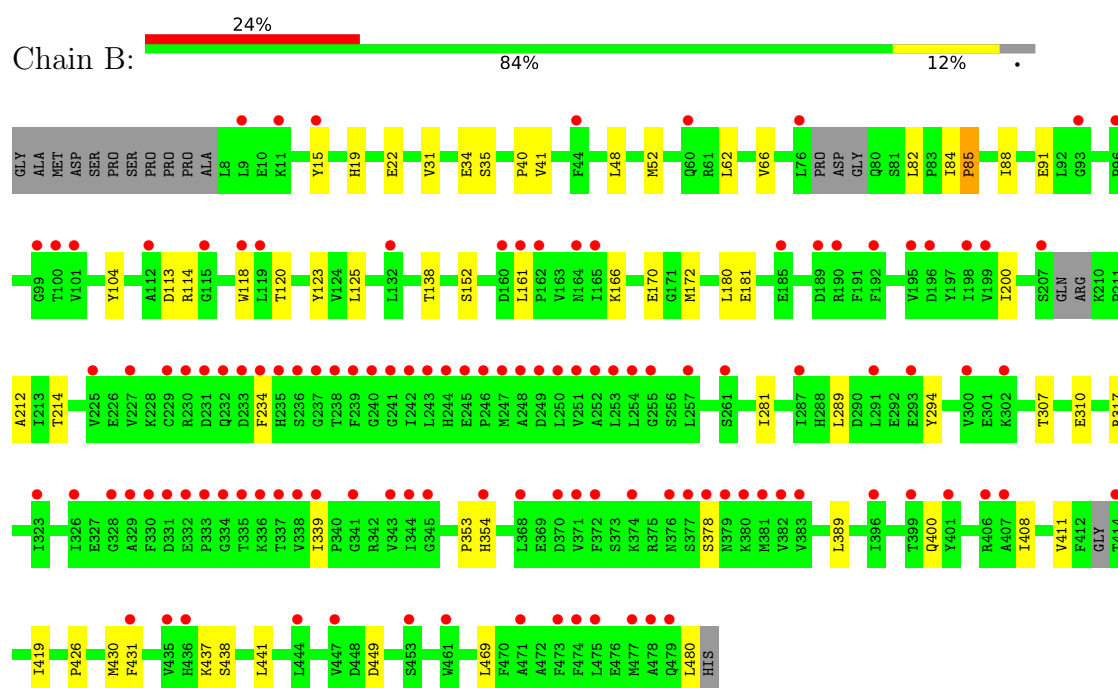
3 Residue-property plots

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: Beta-Ala-His dipeptidase



• Molecule 1: Beta-Ala-His dipeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.11Å 75.61Å 103.72Å 90.00° 109.79° 90.00°	Depositor
Resolution (Å)	29.91 – 2.26 29.91 – 2.26	Depositor EDS
% Data completeness (in resolution range)	97.3 (29.91-2.26) 97.2 (29.91-2.26)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.26Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.200 , 0.254 0.235 , 0.277	Depositor DCC
R_{free} test set	1051 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7420	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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, UNX, SO4

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	0.77	0/3683	0.95	3/5010 (0.1%)
1	B	0.81	2/3663 (0.1%)	0.93	4/4984 (0.1%)
All	All	0.79	2/7346 (0.0%)	0.94	7/9994 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	480	LEU	C-O	14.71	1.52	1.23
1	B	85	PRO	CA-C	5.64	1.54	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	9	LEU	N-CA-C	-7.88	102.65	111.71
1	B	161	LEU	CA-C-N	5.59	125.69	119.32
1	B	161	LEU	C-N-CA	5.59	125.69	119.32
1	B	66	VAL	N-CA-C	5.49	115.76	107.75
1	A	296	ASN	N-CA-C	5.44	117.29	111.36
1	B	480	LEU	CA-C-O	-5.28	111.83	120.80
1	A	230	ARG	N-CA-C	-5.14	101.61	108.86

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	3600	0	3474	11	0
1	B	3583	0	3440	32	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	9	0	0	0	0
3	B	6	0	0	0	0
4	A	5	0	0	0	0
5	A	109	0	0	1	0
5	B	104	0	0	0	0
All	All	7420	0	6914	41	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 (41) 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:302:LYS:HG2	1:B:378:SER:HB3	1.72	0.71
1:B:48:LEU:HG	1:B:85:PRO:HG3	1.76	0.68
1:B:200:ILE:HB	1:B:441:LEU:HD22	1.74	0.68
1:B:35:SER:HB2	1:B:48:LEU:HD13	1.78	0.65
1:A:10:GLU:O	1:A:14:GLN:HG3	2.00	0.62
1:B:307:THR:HG23	1:B:310:GLU:H	1.71	0.56
1:B:411:VAL:HG21	1:B:469:LEU:HA	1.91	0.52
1:B:52:MET:HE3	1:B:88:ILE:HD12	1.91	0.52
1:B:289:LEU:HD11	1:B:294:TYR:HB2	1.91	0.52
1:A:33:ILE:HG12	1:A:50:ARG:NH1	2.26	0.51
1:B:180:LEU:HG	1:B:430:MET:HE1	1.94	0.50
1:B:84:ILE:HG23	1:B:172:MET:HG3	1.93	0.50
1:A:226:GLU:OE2	1:A:342:ARG:CZ	2.61	0.47
1:B:91:GLU:HB3	1:B:166:LYS:HG2	1.95	0.47
1:B:408:ILE:HG13	1:B:469:LEU:HD11	1.97	0.47
1:B:104:TYR:HB3	1:B:200:ILE:HG12	1.97	0.46
1:B:138:THR:HG21	1:B:449:ASP:HB3	1.97	0.46
1:A:291:LEU:HD11	1:A:311:ILE:HG13	1.98	0.46
1:B:181:GLU:HA	1:B:430:MET:HE3	1.98	0.46
1:A:84:ILE:HG23	1:A:172:MET:HG3	1.97	0.45
1:B:234:PHE:HB2	1:B:339:ILE:HB	1.99	0.45
1:B:31:VAL:HG21	1:B:125:LEU:HD13	1.98	0.44
1:B:104:TYR:OH	1:B:170:GLU:OE2	2.24	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:353:PRO:HA	1:B:354:HIS:HA	1.74	0.44
1:A:161:LEU:HA	1:A:162:PRO:HD3	1.88	0.44
1:A:302:LYS:CG	1:B:378:SER:HB3	2.45	0.43
1:B:40:PRO:C	1:B:82:LEU:HD11	2.43	0.43
1:B:212:ALA:HB1	1:B:419:ILE:HG12	2.01	0.42
1:A:356:ASN:ND2	5:A:2097:HOH:O	2.52	0.42
1:B:400:GLN:HG3	1:B:438:SER:OG	2.19	0.42
1:B:62:LEU:HD21	1:B:152:SER:HB3	2.01	0.42
1:B:118:TRP:HB3	1:B:120:THR:O	2.19	0.42
1:B:431:PHE:CE2	1:B:437:LYS:HB2	2.55	0.42
1:B:389:LEU:HD22	1:B:426:PRO:HB3	2.02	0.42
1:A:228:LYS:HD2	1:A:342:ARG:HD2	2.02	0.41
1:B:19:HIS:O	1:B:22:GLU:HG2	2.20	0.41
1:B:15:TYR:CE1	1:B:19:HIS:CE1	3.08	0.41
1:B:48:LEU:O	1:B:52:MET:HG2	2.20	0.41
1:B:34:GLU:HG2	1:B:123:TYR:CG	2.56	0.41
1:B:214:THR:HB	1:B:441:LEU:HB2	2.02	0.40
1:A:228:LYS:HB2	1:A:342:ARG:HG3	2.02	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	463/485 (96%)	452 (98%)	11 (2%)	0	100	100
1	B	459/485 (95%)	448 (98%)	11 (2%)	0	100	100
All	All	922/970 (95%)	900 (98%)	22 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	371/418 (89%)	369 (100%)	2 (0%)	81	87
1	B	370/418 (88%)	365 (99%)	5 (1%)	59	70
All	All	741/836 (89%)	734 (99%)	7 (1%)	70	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	THR
1	A	279	GLU
1	B	41	VAL
1	B	113	ASP
1	B	114	ARG
1	B	281	ILE
1	B	317	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	GLN
1	A	354	HIS
1	B	19	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 are monoatomic and 15 are unknown - leaving 1 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	$\# Z > 2$
4	SO4	A	2003	-	4,4,4	0.27	0	6,6,6	0.79	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.

No monomer is involved in short contacts.

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	471/485 (97%)	0.63	23 (4%) 35 34	28, 36, 50, 58	0
1	B	467/485 (96%)	1.41	118 (25%) 1 1	26, 36, 45, 56	0
All	All	938/970 (96%)	1.02	141 (15%) 5 5	26, 36, 48, 58	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	LEU	5.4
1	B	252	ALA	4.5
1	B	246	PRO	4.5
1	B	227	VAL	4.4
1	B	242	ILE	4.3
1	B	334	GLY	4.3
1	B	248	ALA	4.3
1	B	474	PHE	4.3
1	B	328	GLY	4.3
1	B	100	THR	4.2
1	A	396	ILE	4.1
1	B	339	ILE	3.9
1	B	477	MET	3.9
1	A	8	LEU	3.9
1	B	250	LEU	3.9
1	A	79	GLY	3.8
1	B	189	ASP	3.7
1	B	240	GLY	3.7
1	B	115	GLY	3.7
1	A	399	THR	3.6
1	B	338	VAL	3.6
1	B	237	GLY	3.6
1	B	407	ALA	3.6
1	B	471	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	337	THR	3.5
1	B	236	SER	3.5
1	B	232	GLN	3.4
1	A	480	LEU	3.3
1	B	378	SER	3.3
1	A	434	ILE	3.3
1	B	238	THR	3.3
1	B	93	GLY	3.2
1	B	235	HIS	3.2
1	B	161	LEU	3.2
1	B	198	ILE	3.1
1	B	230	ARG	3.1
1	B	329	ALA	3.1
1	B	478	ALA	3.1
1	B	333	PRO	3.1
1	B	99	GLY	3.1
1	B	323	ILE	3.0
1	B	11	LYS	3.0
1	A	93	GLY	3.0
1	B	372	PHE	2.9
1	B	225	VAL	2.9
1	B	399	THR	2.9
1	B	241	GLY	2.9
1	B	76	LEU	2.9
1	B	332	GLU	2.8
1	B	234	PHE	2.8
1	B	368	LEU	2.8
1	B	326	ILE	2.7
1	B	377	SER	2.7
1	B	291	LEU	2.7
1	B	160	ASP	2.7
1	A	7	ALA	2.7
1	B	343	VAL	2.7
1	B	335	THR	2.7
1	B	15	TYR	2.7
1	B	164	ASN	2.7
1	B	376	ASN	2.7
1	B	255	GLY	2.6
1	B	254	LEU	2.6
1	B	461	TRP	2.6
1	A	334	GLY	2.6
1	B	239	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	380	LYS	2.6
1	B	247	MET	2.5
1	B	251	VAL	2.5
1	B	382	VAL	2.5
1	B	119	LEU	2.5
1	B	118	TRP	2.5
1	A	207	SER	2.5
1	B	207	SER	2.5
1	B	300	VAL	2.5
1	A	402	LEU	2.5
1	A	4	PRO	2.5
1	B	345	GLY	2.5
1	B	101	VAL	2.4
1	A	243	LEU	2.4
1	B	9	LEU	2.4
1	B	244	HIS	2.4
1	B	233	ASP	2.4
1	B	406	ARG	2.4
1	B	185	GLU	2.4
1	B	199	VAL	2.4
1	B	371	VAL	2.4
1	B	473	PHE	2.4
1	B	229	CYS	2.4
1	B	431	PHE	2.4
1	B	257	LEU	2.4
1	B	341	GLY	2.3
1	B	330	PHE	2.3
1	A	76	LEU	2.3
1	B	302	LYS	2.3
1	B	447	VAL	2.3
1	B	475	LEU	2.3
1	B	96	PRO	2.3
1	B	293	GLU	2.3
1	B	253	LEU	2.3
1	A	401	TYR	2.3
1	B	112	ALA	2.3
1	B	190	ARG	2.3
1	B	344	ILE	2.3
1	B	192	PHE	2.2
1	B	231	ASP	2.2
1	B	331	ASP	2.2
1	B	370	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	261	SER	2.2
1	B	374	LYS	2.2
1	A	248	ALA	2.2
1	B	336	LYS	2.2
1	A	213	ILE	2.2
1	B	354	HIS	2.2
1	B	165	ILE	2.2
1	A	70	ASP	2.2
1	B	435	VAL	2.2
1	A	5	PRO	2.2
1	A	395	ASN	2.1
1	A	397	ASP	2.1
1	B	60	GLN	2.1
1	B	453	SER	2.1
1	B	401	TYR	2.1
1	B	444	LEU	2.1
1	B	245	GLU	2.1
1	B	196	ASP	2.1
1	B	287	ILE	2.1
1	B	379	ASN	2.1
1	B	383	VAL	2.1
1	B	44	PHE	2.1
1	A	387	LEU	2.1
1	B	396	ILE	2.1
1	B	414	THR	2.0
1	B	381	MET	2.0
1	A	436	HIS	2.0
1	B	479	GLN	2.0
1	B	132	LEU	2.0
1	B	249	ASP	2.0
1	B	195	VAL	2.0
1	B	436	HIS	2.0
1	B	162	PRO	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	UNX	A	2010	1/1	-0.74	1.20	2,2,2,2	1
3	UNX	A	2005	1/1	-0.37	1.30	2,2,2,2	1
3	UNX	B	2008	1/1	-0.22	1.35	2,2,2,2	1
3	UNX	A	2008	1/1	-0.21	1.50	2,2,2,2	1
3	UNX	A	2011	1/1	-0.19	1.71	2,2,2,2	1
3	UNX	A	2007	1/1	-0.09	1.36	2,2,2,2	1
3	UNX	A	2009	1/1	0.00	1.83	2,2,2,2	1
3	UNX	A	2006	1/1	0.03	1.67	2,2,2,2	1
3	UNX	B	2005	1/1	0.22	1.92	2,2,2,2	1
3	UNX	B	2004	1/1	0.32	1.51	2,2,2,2	1
3	UNX	B	2003	1/1	0.38	1.57	2,2,2,2	1
3	UNX	B	2006	1/1	0.44	1.58	2,2,2,2	1
3	UNX	A	2004	1/1	0.52	1.60	2,2,2,2	1
3	UNX	B	2007	1/1	0.60	1.90	2,2,2,2	1
3	UNX	A	2012	1/1	0.65	1.64	2,2,2,2	1
4	SO4	A	2003	5/5	0.95	0.14	34,36,38,40	0
2	ZN	A	2001	1/1	0.96	0.08	34,34,34,34	0
2	ZN	B	2001	1/1	0.97	0.07	26,26,26,26	0
2	ZN	B	2002	1/1	0.97	0.07	29,29,29,29	0
2	ZN	A	2002	1/1	0.99	0.09	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.