



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 01:26 PM UTC

PDB ID : 3EUL / pdb_00003eul
Title : Structure of the signal receiver domain of the putative response regulator NarL from Mycobacterium tuberculosis
Authors : Schneider, G.; Schnell, R.; Agren, D.
Deposited on : 2008-10-10
Resolution : 1.90 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

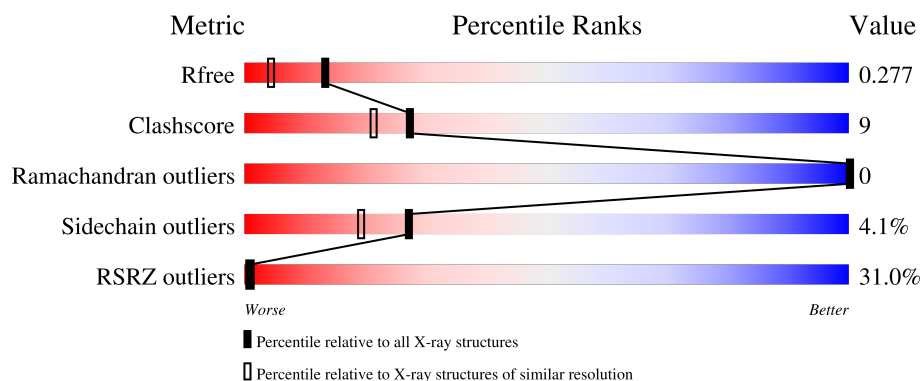
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	152	
1	B	152	
1	C	152	
1	D	152	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3443 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 POSSIBLE NITRATE/NITRITE RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN NARL (DNA-binding response regulator, LuxR family).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	123	Total	C	N	O	S	0	0	0
			916	576	163	174	3			
1	B	124	Total	C	N	O	S	0	0	0
			923	581	164	175	3			
1	C	120	Total	C	N	O	S	0	0	0
			892	563	157	169	3			
1	D	72	Total	C	N	O	S	0	0	0
			537	338	92	106	1			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	expression tag	UNP O53856
A	-5	HIS	-	expression tag	UNP O53856
A	-4	HIS	-	expression tag	UNP O53856
A	-3	HIS	-	expression tag	UNP O53856
A	-2	HIS	-	expression tag	UNP O53856
A	-1	HIS	-	expression tag	UNP O53856
A	0	HIS	-	expression tag	UNP O53856
B	-6	MET	-	expression tag	UNP O53856
B	-5	HIS	-	expression tag	UNP O53856
B	-4	HIS	-	expression tag	UNP O53856
B	-3	HIS	-	expression tag	UNP O53856
B	-2	HIS	-	expression tag	UNP O53856
B	-1	HIS	-	expression tag	UNP O53856
B	0	HIS	-	expression tag	UNP O53856
C	-6	MET	-	expression tag	UNP O53856
C	-5	HIS	-	expression tag	UNP O53856
C	-4	HIS	-	expression tag	UNP O53856
C	-3	HIS	-	expression tag	UNP O53856
C	-2	HIS	-	expression tag	UNP O53856

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	HIS	-	expression tag	UNP O53856
C	0	HIS	-	expression tag	UNP O53856
D	-6	MET	-	expression tag	UNP O53856
D	-5	HIS	-	expression tag	UNP O53856
D	-4	HIS	-	expression tag	UNP O53856
D	-3	HIS	-	expression tag	UNP O53856
D	-2	HIS	-	expression tag	UNP O53856
D	-1	HIS	-	expression tag	UNP O53856
D	0	HIS	-	expression tag	UNP O53856

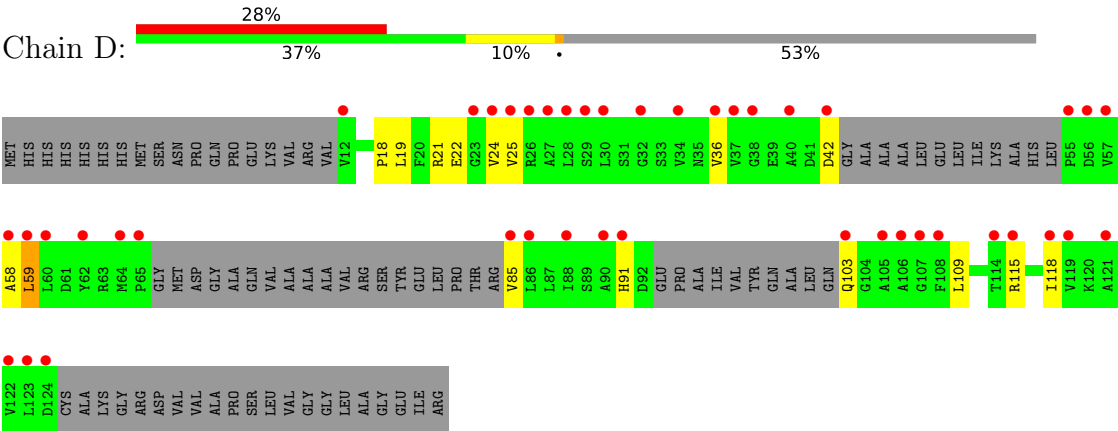
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	65	Total O 65 65	0	0
3	B	65	Total O 65 65	0	0
3	C	18	Total O 18 18	0	0
3	D	26	Total O 26 26	0	0

● Molecule 1: POSSIBLE NITRATE/NITRITE RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN NARL (DNA-binding response regulator, LuxR family)



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	85.53Å 90.04Å 126.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 1.90 45.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.00-1.90) 99.3 (45.00-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.217 , 0.270 0.250 , 0.277	Depositor DCC
R_{free} test set	1933 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.056 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3443	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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	0.91	0/928	0.98	3/1259 (0.2%)
1	B	0.88	0/936	0.97	0/1270
1	C	0.71	1/904 (0.1%)	0.89	1/1228 (0.1%)
1	D	0.60	0/541	0.83	0/730
All	All	0.80	1/3309 (0.0%)	0.93	4/4487 (0.1%)

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	1	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	74	ALA	C-O	8.40	1.34	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	74	ALA	O-C-N	5.84	128.86	122.20
1	A	7	GLU	N-CA-C	5.35	125.99	111.00
1	A	17	HIS	CA-C-N	5.09	124.53	119.24
1	A	17	HIS	C-N-CA	5.09	124.53	119.24

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	7	GLU	CA

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	916	0	936	19	0
1	B	923	0	944	14	0
1	C	892	0	914	17	0
1	D	537	0	537	18	0
2	B	1	0	0	0	0
3	A	65	0	0	0	1
3	B	65	0	0	2	0
3	C	18	0	0	0	0
3	D	26	0	0	0	0
All	All	3443	0	3331	60	1

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 9.

All (60) 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:118:ILE:CD1	1:D:19:LEU:HD11	1.52	1.38
1:A:118:ILE:HD13	1:D:19:LEU:CD1	1.57	1.32
1:A:118:ILE:CD1	1:D:19:LEU:CD1	2.25	0.97
1:A:118:ILE:HD13	1:D:19:LEU:HD11	0.91	0.91
1:B:59:LEU:HD21	1:B:118:ILE:HD11	1.60	0.82
1:A:118:ILE:HD12	1:D:19:LEU:HD11	1.66	0.76
1:C:59:LEU:HD21	1:C:118:ILE:HD11	1.68	0.75
1:D:59:LEU:HD21	1:D:118:ILE:HD11	1.73	0.70
1:A:118:ILE:CD1	1:D:19:LEU:HD12	2.23	0.64
1:D:109:LEU:CD1	1:D:118:ILE:HD13	2.28	0.63
1:C:76:VAL:HA	1:C:81:LEU:HD12	1.82	0.61
1:D:18:PRO:O	1:D:22:GLU:HG3	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ASP:HB3	1:A:110:LEU:HD11	1.83	0.60
1:D:25:VAL:HG13	1:D:36:VAL:HG21	1.84	0.59
1:D:58:ALA:HB3	1:D:85:VAL:HG22	1.84	0.59
1:D:59:LEU:CD2	1:D:118:ILE:HD11	2.33	0.58
1:A:98:TYR:O	1:A:102:GLN:HG2	2.03	0.58
1:B:128:GLY:O	1:B:129:ARG:CG	2.54	0.55
1:C:62:TYR:CZ	1:C:96:ILE:HG23	2.43	0.53
1:A:99:GLN:HE22	1:A:103:GLN:CG	2.22	0.53
1:C:67:MET:HE2	1:C:72:VAL:HA	1.90	0.53
1:A:67:MET:HE2	1:A:72:VAL:HA	1.90	0.53
1:C:51:LYS:O	1:C:54:LEU:HD13	2.10	0.52
1:C:69:GLY:HA3	1:C:87:LEU:HD21	1.94	0.50
1:A:19:LEU:HD13	1:D:24:VAL:HG22	1.93	0.50
1:C:76:VAL:HG13	1:C:81:LEU:HB2	1.94	0.50
1:A:47:LEU:HD22	1:A:67:MET:HE1	1.93	0.50
1:B:20:PHE:CE1	1:B:111:LYS:HG2	2.47	0.49
1:B:115:ARG:O	1:B:118:ILE:HG22	2.13	0.49
1:C:62:TYR:CE2	1:C:96:ILE:HG23	2.48	0.49
1:D:109:LEU:HD13	1:D:118:ILE:HD13	1.94	0.48
1:D:109:LEU:CD1	1:D:118:ILE:CD1	2.92	0.48
1:A:99:GLN:HE22	1:A:103:GLN:HG3	1.78	0.48
1:B:59:LEU:CD2	1:B:118:ILE:HD11	2.37	0.48
1:B:84:ARG:NE	1:B:125:CYS:O	2.44	0.47
1:C:115:ARG:O	1:C:118:ILE:HG22	2.13	0.47
1:A:76:VAL:HG13	1:A:81:LEU:HB2	1.97	0.46
1:B:66:GLY:HA3	3:B:212:HOH:O	2.14	0.46
1:C:109:LEU:HD11	1:C:121:ALA:CB	2.47	0.44
1:A:99:GLN:NE2	1:A:103:GLN:HG3	2.32	0.44
1:C:84:ARG:NE	1:C:125:CYS:O	2.48	0.44
1:B:59:LEU:HD21	1:B:118:ILE:CD1	2.42	0.43
1:B:81:LEU:O	3:B:162:HOH:O	2.21	0.43
1:B:76:VAL:HG13	1:B:81:LEU:HB2	2.00	0.43
1:A:43:GLY:HA3	1:A:67:MET:O	2.19	0.42
1:C:62:TYR:HA	1:C:87:LEU:HD22	2.00	0.42
1:C:87:LEU:HD12	1:C:105:ALA:HB2	2.02	0.42
1:A:118:ILE:HD13	1:D:19:LEU:HD12	1.74	0.42
1:C:51:LYS:O	1:C:54:LEU:CD1	2.68	0.42
1:B:64:MET:HE3	1:B:64:MET:HB2	1.91	0.42
1:C:93:GLU:HB2	1:C:96:ILE:HD12	2.02	0.41
1:A:64:MET:HB2	1:A:64:MET:HE3	1.77	0.41
1:D:21:ARG:O	1:D:25:VAL:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:ARG:O	1:D:118:ILE:HG22	2.20	0.41
1:B:51:LYS:HG2	1:B:81:LEU:HD11	2.03	0.40
1:C:64:MET:HE2	1:C:69:GLY:HA2	2.04	0.40
1:A:74:ALA:HB2	1:A:103:GLN:HE21	1.86	0.40
1:B:128:GLY:O	1:B:129:ARG:CB	2.70	0.40
1:B:40:ALA:HB2	1:B:49:LEU:HD12	2.02	0.40
1:C:18:PRO:O	1:C:22:GLU:HG2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:189:HOH:O	3:A:195:HOH:O[3_555]	2.08	0.12

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	121/152 (80%)	119 (98%)	2 (2%)	0	100	100
1	B	122/152 (80%)	121 (99%)	1 (1%)	0	100	100
1	C	118/152 (78%)	115 (98%)	3 (2%)	0	100	100
1	D	64/152 (42%)	60 (94%)	4 (6%)	0	100	100
All	All	425/608 (70%)	415 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	95/119 (80%)	92 (97%)	3 (3%)	34	27
1	B	96/119 (81%)	93 (97%)	3 (3%)	35	29
1	C	93/119 (78%)	89 (96%)	4 (4%)	26	18
1	D	59/119 (50%)	55 (93%)	4 (7%)	14	7
All	All	343/476 (72%)	329 (96%)	14 (4%)	27	19

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	54	LEU
1	A	110	LEU
1	B	41	ASP
1	B	54	LEU
1	B	110	LEU
1	C	42	ASP
1	C	48	GLU
1	C	54	LEU
1	C	110	LEU
1	D	42	ASP
1	D	59	LEU
1	D	91	HIS
1	D	103	GLN

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	99	GLN
1	B	17	HIS
1	B	53	HIS
1	B	99	GLN
1	C	53	HIS
1	C	71	GLN
1	C	102	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](#)

Of 1 ligands modelled in this entry, 1 is 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 [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	123/152 (80%)	0.42	7 (5%) 29 31	16, 22, 32, 51	0
1	B	124/152 (81%)	0.45	2 (1%) 70 74	15, 22, 30, 47	0
1	C	120/152 (78%)	2.58	84 (70%) 0 0	28, 43, 53, 55	0
1	D	72/152 (47%)	2.32	43 (59%) 0 0	35, 44, 52, 55	0
All	All	439/608 (72%)	1.33	136 (30%) 1 1	15, 29, 51, 55	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	66	GLY	5.3
1	C	82	PRO	5.1
1	C	96	ILE	5.0
1	C	70	ALA	4.9
1	C	74	ALA	4.5
1	A	91	HIS	4.4
1	D	12	VAL	4.3
1	C	62	TYR	4.2
1	C	79	TYR	4.2
1	C	91	HIS	4.1
1	C	69	GLY	4.1
1	D	58	ALA	4.1
1	C	83	THR	4.0
1	C	81	LEU	4.0
1	C	92	ASP	4.0
1	D	106	ALA	4.0
1	C	78	SER	4.0
1	C	47	LEU	3.9
1	C	75	ALA	3.9
1	C	76	VAL	3.9
1	D	38	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	102	GLN	3.7
1	C	72	VAL	3.7
1	C	98	TYR	3.7
1	C	87	LEU	3.7
1	C	100	ALA	3.6
1	B	6	PRO	3.6
1	D	55	PRO	3.6
1	C	9	VAL	3.6
1	C	36	VAL	3.6
1	C	104	GLY	3.5
1	C	108	PHE	3.5
1	D	123	LEU	3.5
1	D	57	VAL	3.5
1	D	91	HIS	3.5
1	D	108	PHE	3.5
1	C	73	ALA	3.4
1	D	36	VAL	3.4
1	D	90	ALA	3.4
1	C	101	LEU	3.4
1	D	30	LEU	3.4
1	D	62	TYR	3.3
1	D	122	VAL	3.3
1	C	34	VAL	3.3
1	C	97	VAL	3.3
1	B	7	GLU	3.3
1	C	56	ASP	3.2
1	D	86	LEU	3.2
1	D	107	GLY	3.2
1	C	106	ALA	3.2
1	C	28	LEU	3.1
1	D	32	GLY	3.1
1	C	11	VAL	3.1
1	C	105	ALA	3.1
1	C	122	VAL	3.1
1	C	54	LEU	3.0
1	C	77	ARG	3.0
1	C	37	VAL	3.0
1	C	67	MET	3.0
1	C	88	ILE	3.0
1	C	50	ILE	2.9
1	C	85	VAL	2.9
1	A	128	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	16	ASP	2.9
1	D	29	SER	2.9
1	D	85	VAL	2.9
1	A	129	ARG	2.9
1	D	24	VAL	2.8
1	D	27	ALA	2.8
1	C	86	LEU	2.8
1	C	55	PRO	2.8
1	C	57	VAL	2.8
1	C	64	MET	2.8
1	D	23	GLY	2.8
1	D	28	LEU	2.8
1	D	88	ILE	2.8
1	C	80	GLU	2.8
1	C	90	ALA	2.8
1	C	99	GLN	2.8
1	C	41	ASP	2.8
1	C	68	ASP	2.8
1	D	34	VAL	2.7
1	D	42	ASP	2.7
1	C	123	LEU	2.7
1	D	60	LEU	2.7
1	D	37	VAL	2.7
1	D	119	VAL	2.7
1	D	121	ALA	2.7
1	C	14	GLY	2.7
1	C	43	GLY	2.7
1	C	125	CYS	2.7
1	C	59	LEU	2.7
1	C	35	ASN	2.7
1	C	52	ALA	2.6
1	A	79	TYR	2.6
1	C	12	VAL	2.6
1	C	44	ALA	2.6
1	C	49	LEU	2.6
1	C	46	ALA	2.6
1	D	65	PRO	2.6
1	D	118	ILE	2.5
1	C	126	ALA	2.5
1	D	40	ALA	2.5
1	C	103	GLN	2.5
1	C	71	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	103	GLN	2.5
1	C	51	LYS	2.5
1	D	115	ARG	2.5
1	C	45	ALA	2.4
1	A	7	GLU	2.4
1	C	17	HIS	2.4
1	D	59	LEU	2.4
1	D	64	MET	2.4
1	C	53	HIS	2.4
1	C	121	ALA	2.3
1	D	25	VAL	2.3
1	D	26	ARG	2.3
1	D	56	ASP	2.3
1	D	124	ASP	2.3
1	C	93	GLU	2.3
1	C	63	ARG	2.2
1	A	118	ILE	2.2
1	C	25	VAL	2.2
1	C	95	ALA	2.2
1	C	127	LYS	2.2
1	C	48	GLU	2.2
1	C	42	ASP	2.2
1	C	112	ASP	2.2
1	C	38	GLY	2.1
1	C	13	VAL	2.1
1	C	39	GLU	2.1
1	A	90	ALA	2.1
1	C	110	LEU	2.1
1	C	58	ALA	2.1
1	D	105	ALA	2.0
1	D	114	THR	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

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	B	146	1/1	0.99	0.14	16,16,16,16	0

6.5 Other polymers

There are no such residues in this entry.