



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 07:51 PM GMT

PDB ID : 3KG6
Title : Dehydratase domain from CurF module of Curacin polyketide synthase
Authors : Akey, D.L.; Smith, J.L.
Deposited on : 2009-10-28
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

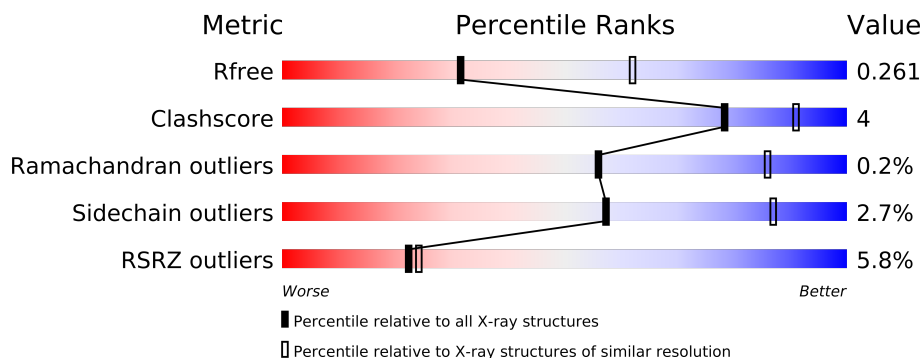
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	285	
1	B	285	
1	C	285	
1	D	285	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8859 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CurF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2177	1397	359	419	2			
1	B	279	Total	C	N	O	S	0	0	0
			2216	1419	366	429	2			
1	C	277	Total	C	N	O	S	0	0	0
			2204	1413	364	425	2			
1	D	278	Total	C	N	O	S	0	0	0
			2205	1413	365	425	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1684	SER	-	EXPRESSION TAG	UNP Q6DNE7
A	1685	ASN	-	EXPRESSION TAG	UNP Q6DNE7
A	1686	ALA	-	EXPRESSION TAG	UNP Q6DNE7
B	1684	SER	-	EXPRESSION TAG	UNP Q6DNE7
B	1685	ASN	-	EXPRESSION TAG	UNP Q6DNE7
B	1686	ALA	-	EXPRESSION TAG	UNP Q6DNE7
C	1684	SER	-	EXPRESSION TAG	UNP Q6DNE7
C	1685	ASN	-	EXPRESSION TAG	UNP Q6DNE7
C	1686	ALA	-	EXPRESSION TAG	UNP Q6DNE7
D	1684	SER	-	EXPRESSION TAG	UNP Q6DNE7
D	1685	ASN	-	EXPRESSION TAG	UNP Q6DNE7
D	1686	ALA	-	EXPRESSION TAG	UNP Q6DNE7

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	D	2	Total	Ca	0	0
			2	2		

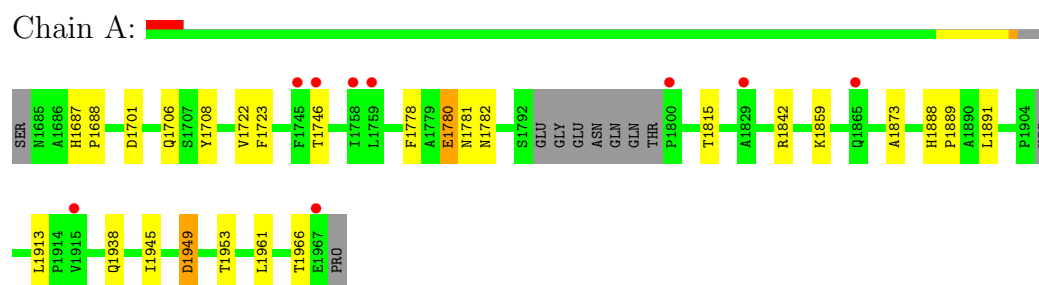
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total 33	O 33	0	0
3	B	6	Total 6	O 6	0	0
3	C	5	Total 5	O 5	0	0
3	D	8	Total 8	O 8	0	0

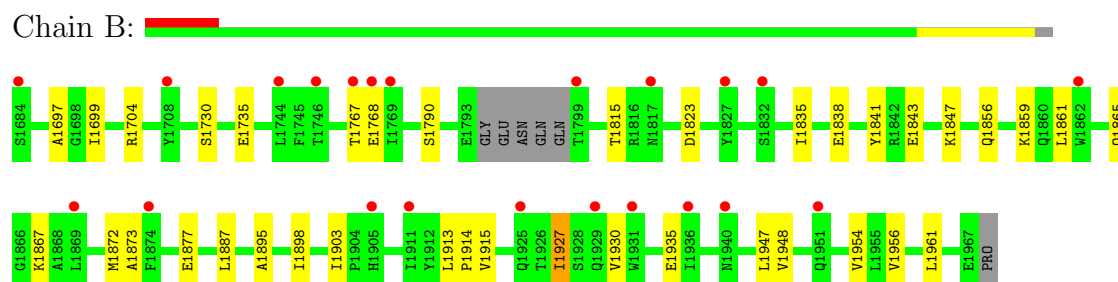
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

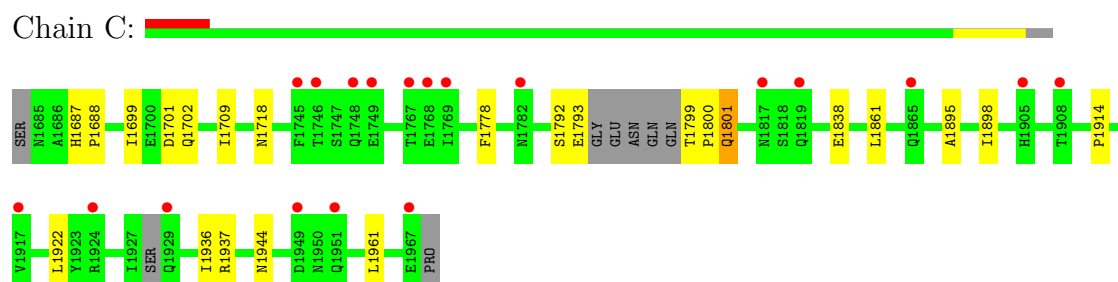
• Molecule 1: CurF



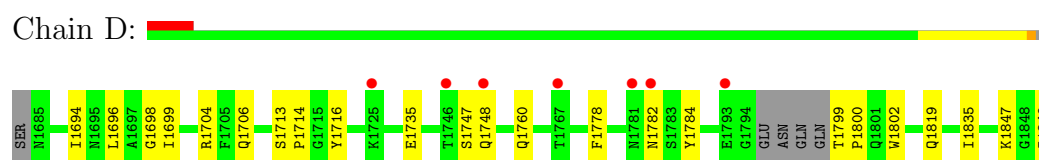
• Molecule 1: CurF



• Molecule 1: CurF



• Molecule 1: CurF





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.38Å 198.38Å 146.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.89 – 2.70 38.58 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.2 (41.89-2.70) 99.2 (38.58-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.29 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.213 , 0.265 0.209 , 0.261	Depositor DCC
R_{free} test set	1980 reflections (5.95%)	DCC
Wilson B-factor (Å ²)	60.7	Xtriage
Anisotropy	0.527	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 74.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 35270 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8859	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.34	0/2223	0.50	0/3013
1	B	0.32	0/2264	0.48	0/3072
1	C	0.32	0/2251	0.46	0/3053
1	D	0.33	0/2253	0.48	0/3057
All	All	0.33	0/8991	0.48	0/12195

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2177	0	2148	14	0
1	B	2216	0	2180	21	0
1	C	2204	0	2169	11	0
1	D	2205	0	2172	26	0
2	A	3	0	0	0	0
2	D	2	0	0	0	0
3	A	33	0	0	0	0
3	B	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	5	0	0	0	0
3	D	8	0	0	0	0
All	All	8859	0	8669	63	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (63) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:1704:ARG:HH12	1:D:1698:GLY:H	1.28	0.79
1:B:1697:ALA:O	1:D:1704:ARG:NH1	2.14	0.79
1:D:1849:ILE:HD11	1:D:1911:ILE:HG13	1.71	0.73
1:C:1799:THR:N	1:C:1800:PRO:CD	2.59	0.65
1:C:1792:SER:O	1:C:1793:GLU:HB2	2.00	0.61
1:B:1927:ILE:HD13	1:B:1927:ILE:H	1.66	0.61
1:C:1799:THR:N	1:C:1800:PRO:HD3	2.16	0.60
1:B:1947:LEU:HB2	1:B:1956:VAL:HB	1.84	0.60
1:A:1746:THR:H	1:D:1747:SER:HB3	1.67	0.59
1:B:1867:LYS:HG2	1:B:1935:GLU:HG2	1.90	0.54
1:D:1926:THR:HG21	1:D:1955:LEU:HD13	1.90	0.54
1:A:1949:ASP:HB2	1:A:1953:THR:HB	1.89	0.54
1:B:1697:ALA:HB2	1:D:1802:TRP:CD2	2.43	0.53
1:D:1696:LEU:HD11	1:D:1704:ARG:HD2	1.91	0.53
1:C:1701:ASP:HB3	1:C:1778:PHE:HB2	1.89	0.53
1:A:1945:ILE:HD11	1:A:1961:LEU:HD22	1.91	0.53
1:B:1838:GLU:CD	1:B:1838:GLU:H	2.11	0.52
1:A:1701:ASP:HB3	1:A:1778:PHE:HB3	1.92	0.52
1:B:1767:THR:HG23	1:B:1768:GLU:HG3	1.92	0.52
1:B:1699:ILE:HB	1:D:1704:ARG:HH22	1.76	0.51
1:B:1704:ARG:HH22	1:D:1699:ILE:N	2.09	0.50
1:A:1722:VAL:HG12	1:A:1723:PHE:HD1	1.77	0.49
1:A:1859:LYS:HG3	1:A:1873:ALA:HB2	1.95	0.49
1:A:1782:ASN:HB3	1:D:1782:ASN:HB2	1.95	0.49
1:A:1782:ASN:HD22	1:D:1782:ASN:HB3	1.77	0.49
1:B:1859:LYS:HB2	1:B:1873:ALA:HB2	1.95	0.48
1:C:1801:GLN:HG2	1:D:1819:GLN:HG3	1.96	0.48
1:D:1849:ILE:CD1	1:D:1911:ILE:HG13	2.42	0.47
1:D:1947:LEU:HB2	1:D:1956:VAL:HB	1.96	0.47
1:D:1835:ILE:HB	1:D:1861:LEU:HB3	1.96	0.46
1:C:1914:PRO:HB3	1:C:1961:LEU:HD11	1.98	0.46
1:B:1914:PRO:HB3	1:B:1961:LEU:HD11	1.98	0.46
1:B:1948:VAL:HG12	1:B:1954:VAL:HA	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1913:LEU:HD12	1:A:1966:THR:HG21	1.98	0.46
1:B:1699:ILE:HG23	1:B:1699:ILE:O	2.15	0.45
1:D:1847:LYS:HD2	1:D:1908:THR:O	2.17	0.45
1:B:1872:MET:HG3	1:B:1930:VAL:HG23	1.98	0.45
1:D:1778:PHE:HD1	1:D:1784:TYR:CZ	2.35	0.45
1:B:1835:ILE:HB	1:B:1861:LEU:HG	1.99	0.45
1:A:1888:HIS:HB3	1:A:1891:LEU:HG	2.00	0.44
1:D:1945:ILE:HD11	1:D:1961:LEU:HD22	1.99	0.44
1:D:1933:ILE:O	1:D:1945:ILE:HA	2.18	0.44
1:D:1694:ILE:HD11	1:D:1706:GLN:HB2	1.99	0.43
1:C:1895:ALA:O	1:C:1898:ILE:HG12	2.18	0.43
1:C:1937:ARG:HD3	1:C:1944:ASN:OD1	2.19	0.43
1:B:1895:ALA:O	1:B:1898:ILE:HG12	2.17	0.43
1:B:1865:GLN:H	1:B:1865:GLN:CD	2.22	0.43
1:D:1849:ILE:HD11	1:D:1911:ILE:CG1	2.45	0.43
1:A:1706:GLN:NE2	1:A:1708:TYR:OH	2.52	0.43
1:C:1699:ILE:CG2	1:C:1702:GLN:HB3	2.48	0.42
1:A:1780:GLU:HG2	1:A:1781:ASN:N	2.34	0.42
1:D:1847:LYS:HE3	1:D:1911:ILE:HB	2.01	0.42
1:B:1843:GLU:O	1:B:1847:LYS:HG3	2.20	0.42
1:C:1687:HIS:HA	1:C:1688:PRO:HD3	1.95	0.42
1:B:1841:TYR:CZ	1:B:1856:GLN:HA	2.56	0.41
1:D:1912:TYR:HB3	1:D:1963:VAL:HB	2.02	0.41
1:B:1887:LEU:HD13	1:B:1927:ILE:HD11	2.01	0.41
1:C:1936:ILE:HG12	1:C:1937:ARG:N	2.35	0.41
1:D:1714:PRO:HB2	1:D:1716:TYR:CE1	2.56	0.41
1:A:1888:HIS:HA	1:A:1889:PRO:HD3	1.93	0.40
1:A:1687:HIS:HA	1:A:1688:PRO:HD3	1.92	0.40
1:D:1713:SER:HA	1:D:1714:PRO:HA	1.91	0.40
1:D:1799:THR:N	1:D:1800:PRO:CD	2.85	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	268/285 (94%)	258 (96%)	9 (3%)	1 (0%)	43	76
1	B	275/285 (96%)	267 (97%)	7 (2%)	1 (0%)	43	76
1	C	271/285 (95%)	263 (97%)	8 (3%)	0	100	100
1	D	274/285 (96%)	265 (97%)	9 (3%)	0	100	100
All	All	1088/1140 (95%)	1053 (97%)	33 (3%)	2 (0%)	56	86

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1780	GLU
1	B	1823	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	235/245 (96%)	231 (98%)	4 (2%)	73	94
1	B	240/245 (98%)	231 (96%)	9 (4%)	44	76
1	C	238/245 (97%)	232 (98%)	6 (2%)	60	89
1	D	238/245 (97%)	231 (97%)	7 (3%)	55	85
All	All	951/980 (97%)	925 (97%)	26 (3%)	57	87

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1815	THR
1	A	1842	ARG
1	A	1938	GLN
1	A	1949	ASP
1	B	1730	SER
1	B	1735	GLU
1	B	1790	SER
1	B	1815	THR
1	B	1877	GLU
1	B	1903	ILE

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Mol	Chain	Res	Type
1	B	1913	LEU
1	B	1915	VAL
1	B	1927	ILE
1	C	1709	ILE
1	C	1718	ASN
1	C	1801	GLN
1	C	1838	GLU
1	C	1861	LEU
1	C	1922	LEU
1	D	1735	GLU
1	D	1748	GLN
1	D	1760	GLN
1	D	1861	LEU
1	D	1876	GLU
1	D	1911	ILE
1	D	1953	THR

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

Mol	Chain	Res	Type
1	A	1782	ASN
1	D	1781	ASN
1	D	1951	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 5 are 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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	274/285 (96%)	0.25	10 (3%)	41 46	59, 69, 90, 100	0
1	B	279/285 (97%)	0.45	22 (7%)	13 13	57, 68, 79, 83	0
1	C	277/285 (97%)	0.56	19 (6%)	17 18	61, 71, 82, 92	0
1	D	278/285 (97%)	0.40	13 (4%)	30 34	59, 69, 83, 98	0
All	All	1108/1140 (97%)	0.41	64 (5%)	22 24	57, 70, 83, 100	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1746	THR	6.1
1	B	1832	SER	5.3
1	C	1929	GLN	5.2
1	C	1817	ASN	4.9
1	A	1746	THR	4.9
1	C	1865	GLN	4.7
1	B	1767	THR	4.5
1	C	1748	GLN	4.3
1	C	1746	THR	4.2
1	C	1905	HIS	4.0
1	A	1865	GLN	3.9
1	C	1767	THR	3.5
1	C	1949	ASP	3.5
1	B	1905	HIS	3.4
1	C	1768	GLU	3.3
1	B	1827	TYR	3.3
1	D	1746	THR	3.2
1	B	1769	ILE	3.1
1	D	1782	ASN	3.1
1	C	1769	ILE	3.1
1	B	1940	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	1799	THR	3.1
1	B	1951	GLN	3.0
1	A	1759	LEU	2.9
1	A	1800	PRO	2.9
1	C	1908	THR	2.8
1	D	1767	THR	2.8
1	B	1869	LEU	2.8
1	D	1915	VAL	2.7
1	D	1966	THR	2.7
1	B	1768	GLU	2.5
1	B	1862	TRP	2.5
1	C	1819	GLN	2.5
1	B	1931	TRP	2.4
1	C	1924	ARG	2.4
1	C	1951	GLN	2.5
1	D	1865	GLN	2.4
1	A	1829	ALA	2.4
1	A	1758	ILE	2.4
1	D	1916	GLY	2.4
1	B	1684	SER	2.3
1	B	1925	GLN	2.3
1	B	1911	ILE	2.3
1	B	1929	GLN	2.3
1	D	1793	GLU	2.3
1	C	1745	PHE	2.2
1	A	1967	GLU	2.2
1	A	1915	VAL	2.2
1	B	1817	ASN	2.2
1	D	1748	GLN	2.2
1	C	1749	GLU	2.2
1	D	1925	GLN	2.2
1	B	1708	TYR	2.2
1	A	1909	ASP	2.1
1	D	1781	ASN	2.1
1	B	1874	PHE	2.1
1	B	1936	ILE	2.1
1	D	1924	ARG	2.1
1	C	1782	ASN	2.1
1	D	1725	LYS	2.0
1	C	1967	GLU	2.0
1	A	1745	PHE	2.0
1	B	1744	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	1917	VAL	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

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CA	D	1	1/1	0.26	0.19	59,59,59,59	1
2	CA	A	1	1/1	0.24	-0.58	47,47,47,47	1
2	CA	D	1969	1/1	0.08	-2.25	117,117,117,117	0
2	CA	A	1969	1/1	0.07	-2.33	112,112,112,112	0
2	CA	A	1970	1/1	0.04	-6.28	63,63,63,63	0

6.5 Other polymers

There are no such residues in this entry.