



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:26 AM UTC

PDB ID : 5NWT / pdb_00005nwt
Title : Crystal Structure of Escherichia coli RNA polymerase - Sigma54 Holoenzyme complex
Authors : Zhang, X.; Buck, M.; Darbari, V.C.; Yang, Y.; Zhang, N.; Lu, D.; Glyde, R.; Wang, Y.; Winkelman, J.; Gourse, R.L.; Murakami, K.S.
Deposited on : 2017-05-08
Resolution : 3.76 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

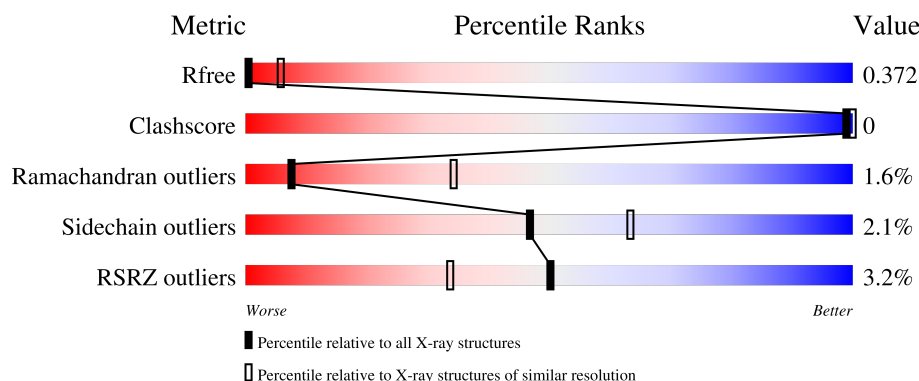
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.76 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	1029 (3.90-3.62)
Clashscore	190562	1061 (3.90-3.62)
Ramachandran outliers	187476	1014 (3.90-3.62)
Sidechain outliers	187428	1009 (3.90-3.62)
RSRZ outliers	180081	1028 (3.90-3.62)

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	329	 2% 91% 7%
1	B	329	 0% 65% 35%
2	C	1342	 3% 96% 1%
3	D	1407	 4% 94% 2%
4	E	91	 0% 85% 14%

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Mol	Chain	Length	Quality of chain
5	M	477	4% 86% • • 10%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 22461 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			1888	1159	348	375	6			
1	B	215	Total	C	N	O	S	0	0	0
			1272	781	233	254	4			

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1318	Total	C	N	O	S	0	0	0
			8247	5047	1515	1661	24			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1358	Total	C	N	O	S	0	0	0
			8092	4936	1535	1598	23			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	78	Total	C	N	O	S	0	0	0
			589	358	108	122	1			

- Molecule 5 is a protein called RNA polymerase sigma-54 factor, RNA polymerase sigma-54 factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	M	431	Total	C	N	O	Se	51	0	0
			2370	1442	444	476	8			

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	2	Total 2	Zn 2	0	0

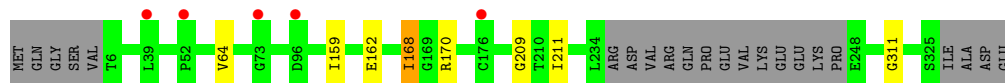
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total 1	Mg 1	0	0

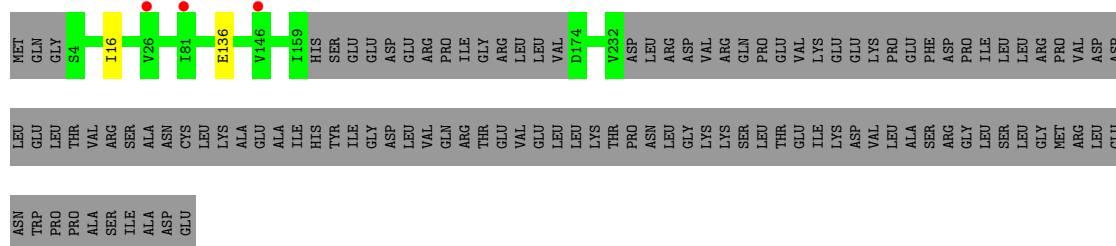
3 Residue-property plots

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.

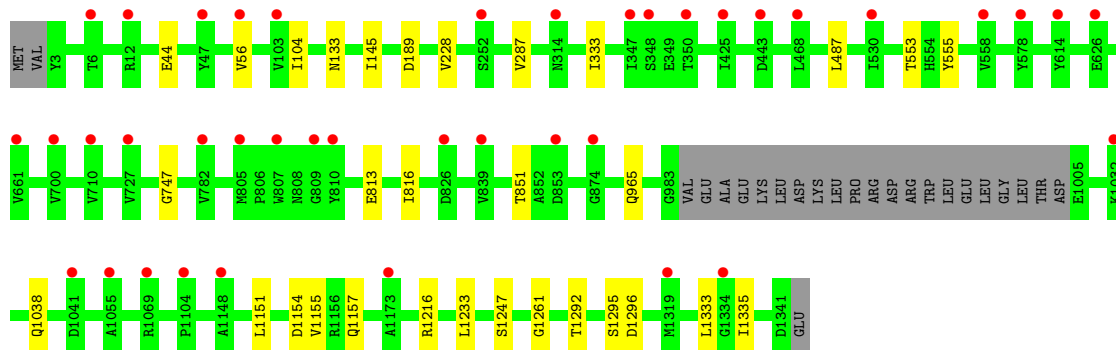
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha



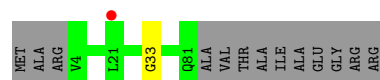
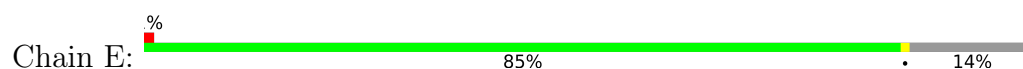
- Molecule 2: DNA-directed RNA polymerase subunit beta



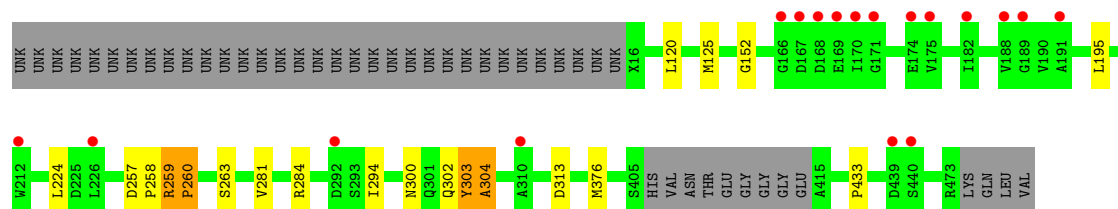
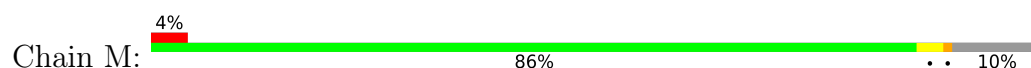
- Molecule 3: DNA-directed RNA polymerase subunit beta'



- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma-54 factor, RNA polymerase sigma-54 factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	208.48Å 151.53Å 195.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	195.28 – 3.76 195.28 – 3.76	Depositor EDS
% Data completeness (in resolution range)	98.2 (195.28-3.76) 98.2 (195.28-3.76)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.75Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.313 , 0.370 0.316 , 0.372	Depositor DCC
R_{free} test set	3078 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	142.0	Xtriage
Anisotropy	0.740	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 201.7	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	0.91	EDS
Total number of atoms	22461	wwPDB-VP
Average B, all atoms (Å ²)	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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: MG, ZN

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	0.56	0/1913	0.83	0/2643
1	B	0.54	0/1284	0.83	0/1779
2	C	0.54	0/8363	0.83	2/11499 (0.0%)
3	D	0.54	0/8201	0.88	0/11314
4	E	0.58	0/591	0.82	0/801
5	M	0.57	1/1986 (0.1%)	0.95	4/2746 (0.1%)
All	All	0.54	1/22338 (0.0%)	0.86	6/30782 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	313	ASP	C-N	6.71	1.42	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	257	ASP	CA-C-N	6.91	128.47	119.84
5	M	257	ASP	C-N-CA	6.91	128.47	119.84
5	M	259	ARG	CA-C-N	6.60	128.09	119.84
5	M	259	ARG	C-N-CA	6.60	128.09	119.84
2	C	287	VAL	CA-C-N	5.26	126.39	120.66
2	C	287	VAL	C-N-CA	5.26	126.39	120.66

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	1888	0	1450	1	0
1	B	1272	0	946	0	0
2	C	8247	0	6196	2	0
3	D	8092	0	5804	5	0
4	E	589	0	559	0	0
5	M	2370	0	1363	6	0
6	D	2	0	0	1	0
7	D	1	0	0	0	0
All	All	22461	0	16318	14	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 0.

All (14) 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)
5:M:152:GLY:O	5:M:260:PRO:HG3	1.65	0.96
3:D:72:CYS:SG	6:D:1501:ZN:ZN	1.81	0.70
5:M:152:GLY:HA3	5:M:260:PRO:HG2	1.81	0.61
5:M:152:GLY:HA3	5:M:260:PRO:CG	2.34	0.57
3:D:322:ARG:CB	3:D:323:PRO:CD	2.84	0.56
5:M:303:TYR:O	5:M:304:ALA:HB3	2.09	0.53
5:M:259:ARG:HA	5:M:260:PRO:HD2	1.68	0.45
2:C:145:ILE:HD12	2:C:145:ILE:N	2.33	0.44
1:A:159:ILE:O	1:A:159:ILE:HG23	2.17	0.43
3:D:322:ARG:CB	3:D:323:PRO:HD2	2.49	0.42
3:D:821:MET:HE3	3:D:879:ALA:HB1	2.02	0.41
5:M:152:GLY:C	5:M:260:PRO:HG3	2.41	0.41
2:C:1333:LEU:CD1	2:C:1335:ILE:HD12	2.51	0.41
3:D:848:VAL:HG11	3:D:880:VAL:HG13	2.03	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	303/329 (92%)	260 (86%)	36 (12%)	7 (2%)	5	29
1	B	211/329 (64%)	186 (88%)	23 (11%)	2 (1%)	14	43
2	C	1310/1342 (98%)	1156 (88%)	140 (11%)	14 (1%)	11	40
3	D	1354/1407 (96%)	1182 (87%)	152 (11%)	20 (2%)	8	35
4	E	76/91 (84%)	69 (91%)	6 (8%)	1 (1%)	9	37
5	M	349/477 (73%)	276 (79%)	59 (17%)	14 (4%)	2	20
All	All	3603/3975 (91%)	3129 (87%)	416 (12%)	58 (2%)	7	34

All (58) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	119	SER
1	B	16	ILE
2	C	333	ILE
3	D	120	LEU
3	D	322	ARG
3	D	323	PRO
3	D	325	LYS
3	D	1000	GLY
3	D	1085	GLY
3	D	1107	VAL
3	D	1192	LYS
4	E	33	GLY
5	M	258	PRO
5	M	263	SER
5	M	281	VAL
5	M	294	ILE
5	M	302	GLN
5	M	303	TYR
2	C	747	GLY
2	C	813	GLU

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Mol	Chain	Res	Type
2	C	1157	GLN
2	C	1292	THR
3	D	805	GLN
3	D	1344	LEU
5	M	120	LEU
5	M	224	LEU
5	M	300	ASN
1	A	162	GLU
1	A	168	ILE
1	A	211	ILE
2	C	1154	ASP
2	C	1295	SER
3	D	140	TYR
3	D	1246	VAL
3	D	1345	ARG
5	M	304	ALA
1	A	170	ARG
1	A	311	GLY
1	B	136	GLU
2	C	555	TYR
2	C	851	THR
2	C	1151	LEU
2	C	1155	VAL
2	C	1247	SER
3	D	585	LYS
3	D	908	ILE
3	D	1134	ILE
5	M	195	LEU
5	M	284	ARG
5	M	433	PRO
3	D	316	ILE
2	C	228	VAL
1	A	64	VAL
1	A	209	GLY
2	C	1261	GLY
3	D	1014	GLY
3	D	552	ILE
5	M	260	PRO

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	127/286 (44%)	126 (99%)	1 (1%)	73	75
1	B	77/286 (27%)	77 (100%)	0	100	100
2	C	546/1157 (47%)	533 (98%)	13 (2%)	43	61
3	D	439/1168 (38%)	427 (97%)	12 (3%)	39	58
4	E	59/75 (79%)	59 (100%)	0	100	100
5	M	82/314 (26%)	80 (98%)	2 (2%)	43	61
All	All	1330/3286 (40%)	1302 (98%)	28 (2%)	47	63

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168	ILE
2	C	44	GLU
2	C	56	VAL
2	C	104	ILE
2	C	133	ASN
2	C	189	ASP
2	C	487	LEU
2	C	553	THR
2	C	816	ILE
2	C	965	GLN
2	C	1038	GLN
2	C	1216	ARG
2	C	1233	LEU
2	C	1296	ASP
3	D	11	GLN
3	D	190	LYS
3	D	245	LEU
3	D	374	LEU
3	D	424	ASN
3	D	473	THR
3	D	474	LEU
3	D	475	GLU

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Mol	Chain	Res	Type
3	D	538	ARG
3	D	832	LYS
3	D	857	LEU
3	D	1247	LYS
5	M	125	MSE
5	M	376	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	283	GLN
1	B	37	HIS
2	C	193	ASN
2	C	219	GLN
2	C	450	ASN
2	C	573	ASN
2	C	752	ASN
2	C	1108	ASN
2	C	1336	ASN
3	D	11	GLN
3	D	266	ASN
3	D	276	ASN
3	D	861	ASN

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 [i](#)

Of 3 ligands modelled in this entry, 3 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.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	2
5	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	66:UNK	C	85:UNK	N	16.93
1	C	336:LEU	C	337:PHE	N	3.66
1	C	225:PHE	C	226:GLU	N	3.29

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	307/329 (93%)	-0.02	5 (1%)	70 47	91, 180, 277, 375	0
1	B	215/329 (65%)	-0.08	3 (1%)	73 50	141, 222, 314, 352	0
2	C	1318/1342 (98%)	0.09	40 (3%)	52 35	78, 189, 358, 534	0
3	D	1358/1407 (96%)	0.06	50 (3%)	45 30	79, 189, 316, 397	0
4	E	78/91 (85%)	-0.17	1 (1%)	75 52	127, 187, 317, 381	0
5	M	341/477 (71%)	0.28	18 (5%)	32 24	6, 141, 223, 314	6 (1%)
All	All	3617/3975 (90%)	0.07	117 (3%)	50 34	6, 185, 323, 534	6 (0%)

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	M	170	ILE	19.0
5	M	167	ASP	15.8
5	M	169	GLU	12.5
5	M	171	GLY	10.9
5	M	168	ASP	10.0
5	M	166	GLY	6.6
3	D	577	ALA	5.5
3	D	91	GLU	4.9
2	C	809	GLY	4.8
3	D	1099	TYR	4.7
2	C	1041	ASP	4.5
3	D	896	ALA	4.4
5	M	440	SER	4.1
5	M	292	ASP	4.1
3	D	927	GLY	3.9
2	C	1148	ALA	3.8
2	C	558	VAL	3.7
3	D	899	TYR	3.7
3	D	637	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
3	D	639	VAL	3.6
2	C	350	THR	3.5
2	C	810	TYR	3.4
2	C	252	SER	3.4
5	M	175	VAL	3.4
2	C	103	VAL	3.3
1	A	39	LEU	3.3
3	D	317	THR	3.3
2	C	710	VAL	3.1
2	C	853	ASP	3.1
3	D	1078	LEU	3.1
2	C	1104	PRO	3.1
5	M	188	VAL	3.0
3	D	463	GLY	2.9
3	D	357	VAL	2.9
2	C	6	THR	2.9
3	D	82	GLY	2.9
3	D	344	GLY	2.9
3	D	792	ASN	2.8
3	D	1217	PRO	2.8
3	D	95	THR	2.8
2	C	1069	ARG	2.8
3	D	794	GLY	2.7
5	M	226	LEU	2.7
1	A	52	PRO	2.7
3	D	766	GLY	2.7
3	D	793	SER	2.6
2	C	347	ILE	2.6
3	D	1100	PHE	2.6
5	M	212	TRP	2.6
3	D	83	VAL	2.6
2	C	578	TYR	2.5
3	D	415	VAL	2.5
4	E	21	LEU	2.5
2	C	425	ILE	2.5
1	B	26	VAL	2.5
3	D	825	VAL	2.5
3	D	249	LEU	2.4
3	D	343	LEU	2.4
3	D	502	PRO	2.4
2	C	614	TYR	2.4
5	M	182	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	1055	ALA	2.4
3	D	912	GLY	2.4
3	D	982	LEU	2.4
3	D	51	PRO	2.4
2	C	727	VAL	2.4
3	D	909	ILE	2.4
5	M	439	ASP	2.4
1	A	96	ASP	2.3
1	B	146	VAL	2.3
3	D	904	ALA	2.3
5	M	310	ALA	2.3
2	C	56	VAL	2.3
2	C	807	TRP	2.3
2	C	805	MET	2.3
3	D	902	ASP	2.3
3	D	880	VAL	2.3
2	C	12	ARG	2.3
2	C	314	ASN	2.3
3	D	419	HIS	2.3
3	D	245	LEU	2.3
2	C	874	GLY	2.3
5	M	189	GLY	2.3
3	D	621	ALA	2.2
2	C	47	TYR	2.2
2	C	1319	MET	2.2
5	M	191	ALA	2.2
2	C	626	GLU	2.2
2	C	782	VAL	2.2
2	C	1173	ALA	2.2
2	C	661	VAL	2.2
1	A	73	GLY	2.2
1	A	176	CYS	2.2
2	C	348	SER	2.2
3	D	894	VAL	2.2
3	D	532	GLU	2.2
2	C	443	ASP	2.2
3	D	316	ILE	2.2
3	D	1319	PHE	2.2
3	D	19	ALA	2.1
1	B	81	ILE	2.1
2	C	530	ILE	2.1
2	C	839	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
3	D	839	VAL	2.1
3	D	589	TYR	2.1
3	D	790	THR	2.1
3	D	1142	ALA	2.1
2	C	468	LEU	2.1
2	C	826	ASP	2.1
2	C	1334	GLY	2.1
3	D	341	ASN	2.1
3	D	1198	VAL	2.1
2	C	1032	LYS	2.0
5	M	174	GLU	2.0
2	C	700	VAL	2.0
3	D	897	HIS	2.0
3	D	142	GLU	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
7	MG	D	1502	1/1	0.87	0.09	163,163,163,163	0
6	ZN	D	1503	1/1	0.95	0.11	156,156,156,156	0
6	ZN	D	1501	1/1	0.96	0.06	120,120,120,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.