



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:30 PM GMT

PDB ID : 3ZNR
Title : HDAC7 bound with inhibitor TMP269
Authors : Lobera, m.; madauss, k.; pohlhaus, d.; trump, r.; nolan, m.
Deposited on : 2013-02-15
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

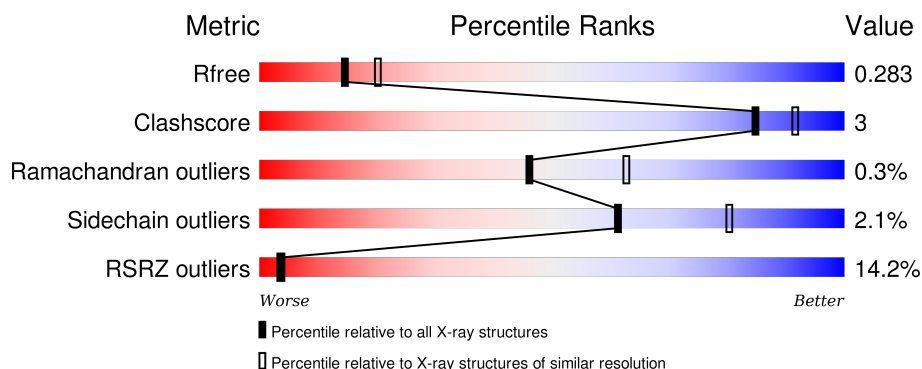
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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. 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	423	<div> <div>10%</div> <div> <div></div> <div>79%</div> <div>8%</div> <div>13%</div> </div> </div>
1	B	423	<div> <div>12%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>10%</div> </div> </div>
1	C	423	<div> <div>15%</div> <div> <div></div> <div>77%</div> <div>7%</div> <div>15%</div> </div> </div>

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	K	A	202	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8454 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 HISTONE DEACETYLASE 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	0	1	0
			2778	1744	499	516	19			
1	B	381	Total	C	N	O	S	0	0	0
			2872	1801	515	537	19			
1	C	359	Total	C	N	O	S	0	1	0
			2712	1696	493	505	18			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	GLY	-	EXPRESSION TAG	UNP Q8WUI4
B	481	GLY	-	EXPRESSION TAG	UNP Q8WUI4
C	481	GLY	-	EXPRESSION TAG	UNP Q8WUI4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

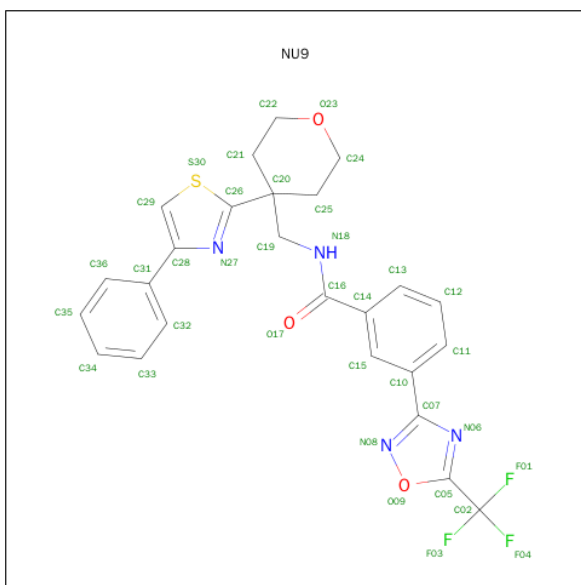
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	K	0	0
			2	2		
3	A	2	Total	K	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	2	Total K 2 2	0	0

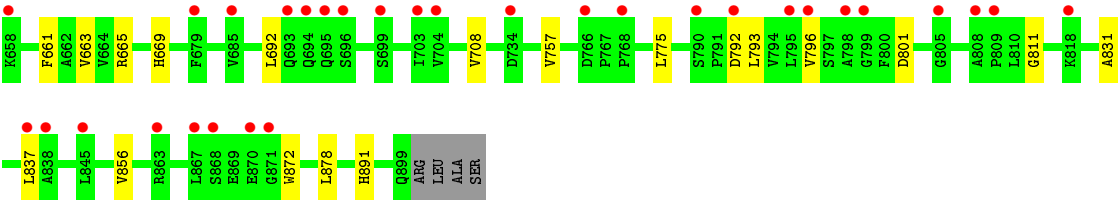
- Molecule 4 is N-{[4-(4-PHENYL-1,3-THIAZOL-2-YL)TETRAHYDRO-2H-PYRAN-4-YL]METHYL}-3-[5-(TRIFLUOROMETHYL)-1,2,4-OXADIAZOL-3-YL]BENZAMIDE (three-letter code: NU9) (formula: C₂₅H₂₁F₃N₄O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	S	
			36	25	3	4	3	1	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	16	Total O 16 16	0	0
5	B	21	Total O 21 21	0	0
5	C	7	Total O 7 7	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	81.39 Å 81.39 Å 149.26 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	70.49 – 2.40 27.50 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (70.49-2.40) 99.4 (27.50-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.241 0.262 , 0.283	Depositor DCC
R_{free} test set	2178 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 24.5	EDS
Estimated twinning fraction	0.007 for -h,-k,l 0.043 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 42955 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8454	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, K, NU9

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	0.27	0/2849	0.43	0/3869
1	B	0.28	0/2939	0.44	0/3988
1	C	0.28	0/2781	0.43	0/3778
All	All	0.28	0/8569	0.43	0/11635

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2778	0	2657	16	0
1	B	2872	0	2753	16	0
1	C	2712	0	2583	15	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	36	0	21	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	16	0	0	0	0
5	B	21	0	0	0	0
5	C	7	0	0	0	0
All	All	8454	0	8014	47	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 (47) 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:C:523:ILE:HG21	1:C:644:SER:HB3	1.66	0.77
1:C:623:VAL:HG22	1:C:627:THR:HB	1.74	0.69
1:B:623:VAL:HG22	1:B:627:THR:HB	1.77	0.66
1:A:623:VAL:HG22	1:A:627:THR:HB	1.77	0.65
1:B:523:ILE:HG21	1:B:644:SER:HB3	1.79	0.64
1:A:523:ILE:HG21	1:A:644:SER:HB3	1.80	0.64
1:C:661:PHE:CE2	1:C:663:VAL:HG22	2.33	0.63
1:C:692:LEU:HD21	1:C:793:LEU:HD13	1.82	0.61
1:C:555:LEU:HD23	1:C:560:LEU:HD12	1.84	0.59
1:A:744:VAL:HG12	1:A:890:VAL:HG21	1.86	0.58
1:A:520:THR:HG23	1:A:860:LEU:HD23	1.86	0.57
1:B:520:THR:HG22	1:B:659:ASN:OD1	2.06	0.56
1:B:808:ALA:HB3	1:B:809:PRO:HD3	1.87	0.55
1:A:519:THR:HG22	1:A:520:THR:H	1.71	0.55
1:A:824:THR:HG21	1:A:859:LEU:HD13	1.89	0.53
1:B:548:ILE:HD13	1:B:665:ARG:HG2	1.91	0.51
1:C:567:LEU:HD11	1:C:651:LYS:HE3	1.93	0.50
1:C:548:ILE:HD13	1:C:665:ARG:HG2	1.94	0.50
1:C:757:VAL:HG22	1:C:891:HIS:CE1	2.47	0.50
1:A:765:LEU:HD11	1:A:808:ALA:HB2	1.93	0.50
1:A:795:LEU:HD23	1:A:836:VAL:HB	1.95	0.49
1:C:529:LEU:HD23	1:C:548:ILE:HD11	1.95	0.48
1:A:650:PHE:CE1	1:A:692:LEU:HD12	2.49	0.47
1:B:649:ALA:HB1	1:B:692:LEU:HD21	1.97	0.47
1:C:796:VAL:HB	1:C:837:LEU:HD23	1.97	0.46
1:C:555:LEU:HD21	1:C:856:VAL:HG21	1.98	0.45
1:A:577:LEU:HD11	1:A:639:ARG:HG2	1.97	0.45
1:A:520:THR:HG22	1:A:659:ASN:OD1	2.15	0.45
1:C:541:HIS:CE1	1:C:628:ILE:HD11	2.52	0.45
1:A:548:ILE:HD13	1:A:665:ARG:HG2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:577:LEU:HD23	1:B:687:ILE:HD13	1.98	0.45
1:B:796:VAL:HB	1:B:837:LEU:HD22	1.99	0.44
1:A:725:LEU:HD21	1:A:785:ILE:HG22	2.00	0.44
1:B:659:ASN:HB2	1:B:859:LEU:HD22	2.01	0.43
1:C:708:VAL:HG12	1:C:801:ASP:CG	2.39	0.43
1:B:548:ILE:HB	1:B:663:VAL:HG12	2.01	0.42
1:C:792:ASP:O	1:C:831:ALA:HB1	2.20	0.42
1:C:775:LEU:HD11	1:C:872:TRP:CD2	2.55	0.41
1:B:628:ILE:HD12	1:B:628:ILE:C	2.41	0.41
1:A:688:ALA:O	1:A:692:LEU:HD13	2.21	0.41
1:B:708:VAL:HG12	1:B:801:ASP:CG	2.41	0.41
1:B:616:LEU:HD22	1:B:625:THR:HA	2.01	0.41
1:B:688:ALA:O	1:B:692:LEU:HD13	2.21	0.40
1:A:574:LEU:HD21	1:A:591:THR:HG22	2.03	0.40
1:B:761:TRP:CE3	1:B:769:MET:CE	3.04	0.40
1:B:593:PRO:HA	1:B:594:LEU:HA	1.80	0.40
1:A:818:LYS:HE2	1:A:864: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	365/423 (86%)	354 (97%)	10 (3%)	1 (0%)	46	63
1	B	377/423 (89%)	365 (97%)	11 (3%)	1 (0%)	46	63
1	C	356/423 (84%)	343 (96%)	12 (3%)	1 (0%)	46	63
All	All	1098/1269 (86%)	1062 (97%)	33 (3%)	3 (0%)	46	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	811	GLY
1	B	811	GLY
1	C	811	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	289/336 (86%)	283 (98%)	6 (2%)	61	80
1	B	298/336 (89%)	290 (97%)	8 (3%)	52	73
1	C	281/336 (84%)	277 (99%)	4 (1%)	74	88
All	All	868/1008 (86%)	850 (98%)	18 (2%)	61	80

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	519	THR
1	A	655	ARG
1	A	669	HIS
1	A	706	TRP
1	A	745	ASP
1	A	859	LEU
1	B	584	ARG
1	B	647	ASP
1	B	669	HIS
1	B	706	TRP
1	B	765	LEU
1	B	769	MET
1	B	839	LEU
1	B	889	ARG
1	C	554	ARG
1	C	567	LEU
1	C	669	HIS
1	C	878	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	636	ASN
1	A	673	HIS
1	A	879	ASN
1	A	899	GLN
1	B	610	GLN
1	B	636	ASN
1	B	825	GLN
1	B	879	ASN
1	B	899	GLN
1	C	636	ASN
1	C	695	GLN
1	C	756	ASN
1	C	879	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 12 are monoatomic - 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	NU9	A	1000	2	34,40,40	2.57	7 (20%)	39,58,58	1.81	6 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NU9	A	1000	2	-	0/21/40/40	1/4/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1000	NU9	C31-C28	-6.02	1.39	1.48
4	A	1000	NU9	C26-S30	-5.88	1.54	1.73
4	A	1000	NU9	C29-S30	-5.51	1.61	1.70
4	A	1000	NU9	C10-C07	-3.43	1.39	1.48
4	A	1000	NU9	C07-N06	3.43	1.40	1.35
4	A	1000	NU9	C16-N18	4.23	1.43	1.33
4	A	1000	NU9	C28-N27	8.36	1.63	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1000	NU9	C28-C29-S30	-2.87	108.27	111.79
4	A	1000	NU9	O23-C22-C21	2.28	113.77	111.57
4	A	1000	NU9	C31-C28-N27	2.80	124.45	120.62
4	A	1000	NU9	C02-C05-N06	3.43	125.76	122.41
4	A	1000	NU9	C05-N06-C07	5.85	108.30	101.45
4	A	1000	NU9	C10-C07-N08	5.96	126.63	119.11

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1000	NU9	C20-C21-C22-C24-C25-O23

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	368/423 (86%)	0.71	43 (11%) 6 6	16, 22, 27, 31	0
1	B	381/423 (90%)	0.84	52 (13%) 4 4	16, 22, 28, 35	0
1	C	359/423 (84%)	0.89	62 (17%) 2 2	19, 23, 26, 28	0
All	All	1108/1269 (87%)	0.81	157 (14%) 4 3	16, 23, 27, 35	0

All (157) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	594	LEU	7.3
1	B	704	VAL	5.3
1	B	593	PRO	5.0
1	C	539	SER	5.0
1	B	797	SER	4.6
1	C	616	LEU	4.5
1	B	685	VAL	4.4
1	A	796	VAL	4.3
1	C	796	VAL	4.3
1	B	596	ARG	4.2
1	B	796	VAL	4.2
1	A	838	ALA	4.1
1	C	564	CYS	4.1
1	A	809	PRO	3.9
1	C	562	SER	3.8
1	C	768	PRO	3.8
1	A	797	SER	3.7
1	C	623	VAL	3.7
1	C	625	THR	3.6
1	A	798	ALA	3.6
1	B	838	ALA	3.5
1	A	595	SER	3.4
1	A	706	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	668	GLY	3.4
1	A	685	VAL	3.4
1	B	560	LEU	3.4
1	B	798	ALA	3.4
1	C	809	PRO	3.4
1	C	617	PRO	3.3
1	B	539	SER	3.3
1	C	549	GLN	3.3
1	C	537	ASP	3.3
1	C	540	ARG	3.3
1	B	684	SER	3.3
1	B	714	THR	3.3
1	B	734	ASP	3.3
1	C	805	GLY	3.2
1	B	799	GLY	3.2
1	B	597	LEU	3.2
1	C	656	GLU	3.2
1	C	870	GLU	3.2
1	A	703	ILE	3.1
1	C	655	ARG	3.1
1	B	706	TRP	3.1
1	C	837	LEU	3.0
1	B	705	ASP	3.0
1	B	727	ILE	3.0
1	B	680	CYS	3.0
1	B	837	LEU	3.0
1	B	703	ILE	3.0
1	A	666	PRO	3.0
1	C	626	ASP	2.9
1	B	669	HIS	2.9
1	C	693	GLN	2.9
1	B	711	GLY	2.9
1	A	736	ASN	2.8
1	A	808	ALA	2.8
1	B	610	GLN	2.8
1	C	695	GLN	2.7
1	B	839	LEU	2.7
1	B	726	TYR	2.7
1	A	686	ALA	2.7
1	C	699	SER	2.7
1	B	664	VAL	2.7
1	C	704	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	647	ASP	2.7
1	A	664	VAL	2.7
1	C	808	ALA	2.7
1	C	592	ASN	2.7
1	B	780	ILE	2.6
1	C	587	LEU	2.6
1	A	768	PRO	2.6
1	B	782	VAL	2.6
1	B	517	PRO	2.6
1	B	870	GLU	2.6
1	C	536	GLY	2.6
1	A	518	PHE	2.6
1	B	728	SER	2.6
1	A	734	ASP	2.6
1	C	568	ARG	2.6
1	A	704	VAL	2.6
1	B	862	ASN	2.6
1	C	560	LEU	2.5
1	C	766	ASP	2.5
1	A	592	ASN	2.5
1	C	657	LEU	2.5
1	A	680	CYS	2.5
1	B	537	ASP	2.5
1	B	777	ALA	2.5
1	A	616	LEU	2.5
1	A	837	LEU	2.5
1	C	838	ALA	2.5
1	C	627	THR	2.5
1	A	684	SER	2.5
1	B	865	ASP	2.5
1	B	729	LEU	2.5
1	C	798	ALA	2.5
1	B	666	PRO	2.4
1	A	839	LEU	2.4
1	A	687	ILE	2.4
1	A	593	PRO	2.4
1	A	697	LYS	2.4
1	C	653	ALA	2.4
1	B	595	SER	2.4
1	A	539	SER	2.4
1	B	683	ASN	2.3
1	C	799	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	555	LEU	2.3
1	A	778	PHE	2.3
1	A	594	LEU	2.3
1	A	765	LEU	2.3
1	C	696	SER	2.3
1	B	687	ILE	2.3
1	C	658	LYS	2.3
1	A	882	ARG	2.3
1	A	840	GLU	2.3
1	C	868	SER	2.3
1	A	645	VAL	2.3
1	B	809	PRO	2.3
1	B	592	ASN	2.2
1	C	845	LEU	2.2
1	B	645	VAL	2.2
1	B	654	SER	2.2
1	C	734	ASP	2.2
1	C	542	PRO	2.2
1	C	790	SER	2.2
1	C	519	THR	2.2
1	B	841	GLY	2.2
1	C	685	VAL	2.2
1	A	683	ASN	2.2
1	B	688	ALA	2.1
1	C	703	ILE	2.1
1	C	863	ARG	2.1
1	C	679	PHE	2.1
1	A	843	HIS	2.1
1	A	863	ARG	2.1
1	A	705	ASP	2.1
1	C	591	THR	2.1
1	C	818	LYS	2.1
1	C	628	ILE	2.1
1	C	867	LEU	2.1
1	A	782	VAL	2.1
1	A	862	ASN	2.1
1	C	538	ASN	2.1
1	A	725	LEU	2.1
1	C	871	GLY	2.1
1	C	792	ASP	2.1
1	C	694	GLN	2.0
1	B	584	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	667	PRO	2.0
1	B	682	PHE	2.0
1	C	557	GLU	2.0
1	A	662	ALA	2.0
1	C	619	GLY	2.0
1	B	667	PRO	2.0
1	C	795	LEU	2.0
1	C	524	TYR	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	K	A	202	1/1	0.09	0.42	4.24	80,80,80,80	0
3	K	C	202	1/1	0.47	0.20	0.92	73,73,73,73	0
3	K	C	201	1/1	0.87	0.23	0.48	45,45,45,45	0
4	NU9	A	1000	36/36	0.81	0.25	0.42	67,68,69,69	0
3	K	B	202	1/1	0.89	0.19	-0.18	42,42,42,42	0
2	ZN	B	101	1/1	0.99	0.20	-0.99	32,32,32,32	0
2	ZN	C	102	1/1	0.93	0.10	-1.04	21,21,21,21	0
3	K	B	201	1/1	0.99	0.23	-1.09	38,38,38,38	0
3	K	A	201	1/1	0.95	0.16	-1.47	36,36,36,36	0
2	ZN	A	102	1/1	0.95	0.04	-2.13	24,24,24,24	0
2	ZN	B	102	1/1	0.99	0.02	-2.17	19,19,19,19	0
2	ZN	C	101	1/1	0.98	0.10	-3.70	27,27,27,27	0
2	ZN	A	101	1/1	0.97	0.11	-3.70	28,28,28,28	0

6.5 Other polymers

There are no such residues in this entry.