



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2018 – 03:16 PM EST

PDB ID : 2JIH
Title : Crystal Structure of Human ADAMTS-1 catalytic Domain and Cysteine- Rich Domain (complex-form)
Authors : Gerhardt, S.; Hassall, G.; Hawtin, P.; McCall, E.; Flavell, L.; Minshull, C.; Hargreaves, D.; Ting, A.; Paupit, R.A.; Parker, A.E.; Abbott, W.M.
Deposited on : 2007-06-28
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030736

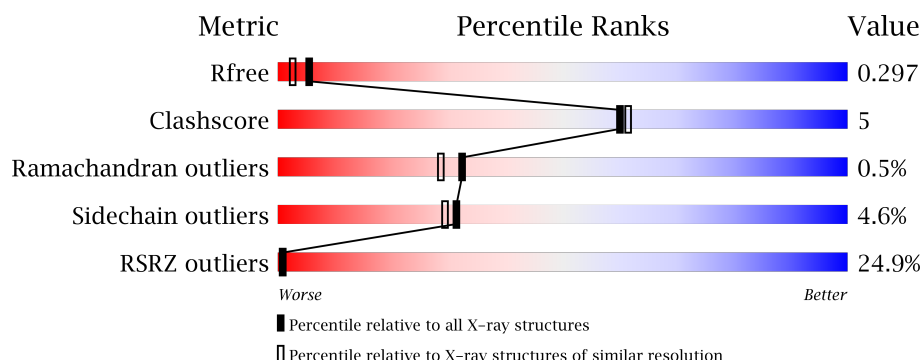
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	300	<div> <div>12%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>• 5%</div> </div> </div>
1	B	300	<div> <div>35%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>• 5%</div> </div> </div>

2 Entry composition [i](#)

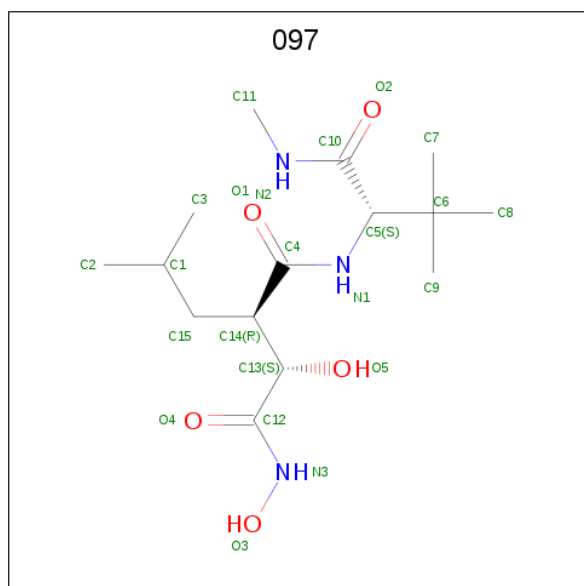
There are 8 unique types of molecules in this entry. The entry contains 4667 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ADAMTS-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2181	1354	379	423	25			
1	B	286	Total	C	N	O	S	0	0	0
			2199	1363	385	426	25			

- Molecule 2 is (2S,3R)-N 4 -[(1S)-2,2-dimethyl-1-(methylcarbamoyl)propyl]-N 1 ,2-dihydroxy-3-(2-methylpropyl)butanediamide (three-letter code: 097) (formula: C₁₅H₂₉N₃O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	15	3	5		
2	B	1	Total	C	N	O	0	0
			23	15	3	5		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Zn 1	0	0
3	A	1	Total 1	Zn 1	0	0

- Molecule 4 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total 2	Cd 2	0	0
4	A	4	Total 4	Cd 4	0	0

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	5	Total 5	Ni 5	0	0
5	A	7	Total 7	Ni 7	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	4	Total 4	Mg 4	0	0
6	A	2	Total 2	Mg 2	0	0

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	122	Total 122	O 122	0	0

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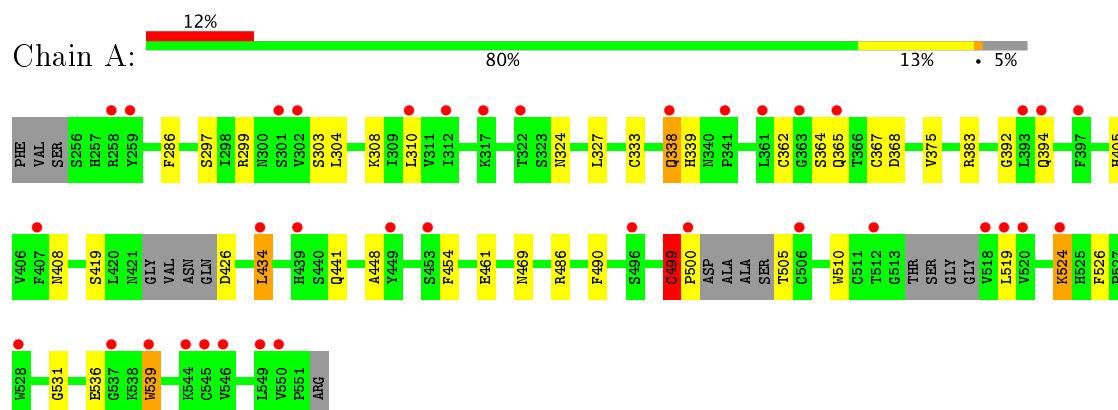
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	88	Total	O	0	0
			88	88		

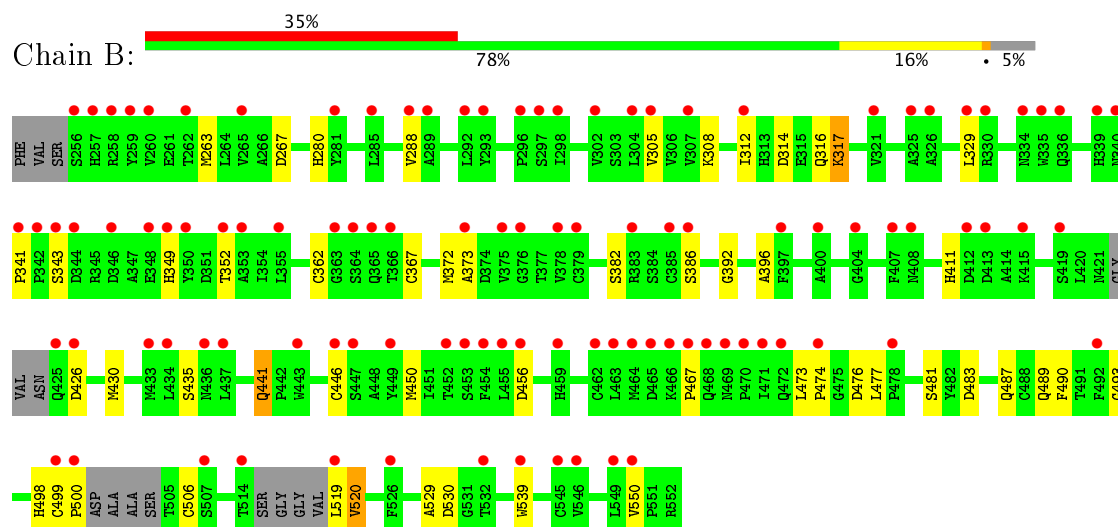
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: ADAMTS-1



• Molecule 1: ADAMTS-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.58Å 64.40Å 113.52Å 90.00° 90.91° 90.00°	Depositor
Resolution (Å)	56.90 – 2.10 56.75 – 2.09	Depositor EDS
% Data completeness (in resolution range)	82.6 (56.90-2.10) 79.4 (56.75-2.09)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, R_{free}	0.224 , 0.282 0.281 , 0.297	Depositor DCC
R_{free} test set	1788 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.107 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4667	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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: NI, ZN, NA, MG, 097, CD

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	0.64	0/2233	0.70	1/3032 (0.0%)
1	B	0.62	0/2251	0.70	1/3055 (0.0%)
All	All	0.63	0/4484	0.70	2/6087 (0.0%)

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	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	483	ASP	CB-CG-OD2	7.15	124.74	118.30
1	A	524	LYS	CD-CE-NZ	5.31	123.91	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	499	CYS	Peptide

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	2181	0	2046	26	0
1	B	2199	0	2060	21	1
2	A	23	0	29	5	0
2	B	23	0	28	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	0	0	0
4	B	2	0	0	0	0
5	A	7	0	0	0	0
5	B	5	0	0	0	0
6	A	2	0	0	0	0
6	B	4	0	0	0	0
7	A	3	0	0	0	0
7	B	2	0	0	0	0
8	A	122	0	0	1	0
8	B	88	0	0	0	0
All	All	4667	0	4163	46	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 5.

All (46) 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:434:LEU:CD1	2:A:1001:097:H112	2.07	0.85
1:A:394:GLN:NE2	1:A:526:PHE:CD1	2.59	0.71
1:B:267:ASP:HA	1:B:312:ILE:HD12	1.80	0.64
1:A:434:LEU:HD12	2:A:1001:097:H112	1.79	0.64
1:B:362:CYS:HA	1:B:367:CYS:HA	1.81	0.62
1:A:392:GLY:HA2	1:A:490:PHE:HB3	1.82	0.61
1:A:297:SER:HB3	1:A:441:GLN:HE21	1.67	0.59
1:B:487:GLN:HE22	1:B:529:ALA:H	1.52	0.57
1:A:500:PRO:HD3	1:A:510:TRP:HB2	1.88	0.55
1:B:373:ALA:HB2	1:B:386:SER:HB3	1.92	0.52
1:B:341:PRO:O	1:B:349:HIS:ND1	2.29	0.51
1:A:368:ASP:HB3	2:A:1001:097:H92	1.94	0.50
1:B:441:GLN:HG3	1:B:441:GLN:O	2.14	0.48
1:B:519:LEU:O	1:B:520:VAL:HG23	2.13	0.48
1:A:434:LEU:HD12	2:A:1001:097:C11	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:411:HIS:HA	1:B:430:MET:O	2.14	0.47
1:B:329:LEU:HD22	1:B:372:MET:HG2	1.97	0.46
1:A:461:GLU:HB3	8:A:2079:HOH:O	2.15	0.46
1:A:286:PHE:CZ	1:A:304:LEU:HB3	2.50	0.46
1:A:524:LYS:CE	1:A:526:PHE:HE1	2.29	0.46
1:A:394:GLN:NE2	1:A:526:PHE:CE1	2.81	0.46
1:B:392:GLY:HA2	1:B:490:PHE:HB3	1.98	0.46
1:A:324:ASN:ND2	1:A:327:LEU:HB2	2.31	0.45
1:A:408:ASN:HB2	1:A:454:PHE:CD2	2.52	0.45
1:A:524:LYS:HE3	1:A:526:PHE:HE1	1.80	0.45
1:A:308:LYS:NZ	1:A:310:LEU:HD21	2.32	0.45
1:A:338:GLN:NE2	1:A:339:HIS:NE2	2.65	0.45
1:B:263:MET:SD	1:B:308:LYS:HD3	2.57	0.45
1:B:498:HIS:CE1	1:B:500:PRO:HA	2.51	0.45
1:A:362:CYS:HA	1:A:367:CYS:HA	1.98	0.45
1:A:486:ARG:HD3	1:B:280:HIS:HB2	2.00	0.44
1:B:477:LEU:HD13	1:B:530:ASP:HB3	2.00	0.43
1:A:499:CYS:HB3	1:A:500:PRO:CD	2.48	0.43
1:B:305:VAL:HG21	1:B:467:PRO:HG3	2.01	0.43
1:A:524:LYS:HE3	1:A:526:PHE:CE1	2.54	0.43
1:A:333:CYS:SG	1:A:383:ARG:HA	2.59	0.43
1:B:314:ASP:HB3	1:B:317:LYS:HG2	2.01	0.43
1:A:434:LEU:HD12	2:A:1001:097:O2	2.18	0.42
1:B:473:LEU:HA	1:B:474:PRO:HD3	1.92	0.41
1:A:299:ARG:HG2	1:A:448:ALA:HB1	2.02	0.41
1:B:499:CYS:O	1:B:500:PRO:C	2.58	0.41
1:A:375:VAL:HA	1:A:405:HIS:O	2.20	0.41
1:B:489:GLN:HA	1:B:493:GLY:O	2.21	0.40
1:B:288:VAL:HB	1:B:396:ALA:HB1	2.04	0.40
1:A:531:GLY:HA2	1:A:539:TRP:CE3	2.57	0.40
1:B:446:CYS:O	1:B:450:MET:HG2	2.21	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)
1:B:456:ASP:OD2	1:B:550:VAL:CG2[2_656]	2.09	0.11

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	276/300 (92%)	268 (97%)	6 (2%)	2 (1%)	25	20
1	B	278/300 (93%)	267 (96%)	10 (4%)	1 (0%)	38	35
All	All	554/600 (92%)	535 (97%)	16 (3%)	3 (0%)	32	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	499	CYS
1	A	519	LEU
1	B	506	CYS

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	247/259 (95%)	236 (96%)	11 (4%)	32	30
1	B	248/259 (96%)	236 (95%)	12 (5%)	30	27
All	All	495/518 (96%)	472 (95%)	23 (5%)	31	29

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	SER
1	A	338	GLN
1	A	364	SER

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Mol	Chain	Res	Type
1	A	365	GLN
1	A	419	SER
1	A	426	ASP
1	A	434	LEU
1	A	469	ASN
1	A	505	THR
1	A	536	GLU
1	A	539	TRP
1	B	316	GLN
1	B	317	LYS
1	B	343	SER
1	B	352	THR
1	B	382	SER
1	B	426	ASP
1	B	435	SER
1	B	441	GLN
1	B	476	ASP
1	B	481	SER
1	B	520	VAL
1	B	539	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	324	ASN
1	A	338	GLN
1	A	359	GLN
1	A	441	GLN
1	A	457	ASN
1	A	469	ASN
1	B	268	GLN
1	B	408	ASN
1	B	487	GLN

5.3.3 RNA ⓘ

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 33 ligands modelled in this entry, 31 are monoatomic - leaving 2 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
2	097	A	1001	3	22,22,22	1.02	1 (4%)	25,31,31	1.46	4 (16%)
2	097	B	1001	3	22,22,22	0.93	1 (4%)	25,31,31	1.02	1 (4%)

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
2	097	A	1001	3	-	0/34/34/34	0/0/0/0
2	097	B	1001	3	-	0/34/34/34	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	097	C10-N2	2.04	1.35	1.32
2	A	1001	097	C10-N2	2.49	1.36	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1001	097	O1-C4-C14	-2.60	118.52	121.64
2	A	1001	097	C6-C5-C10	-2.29	110.55	112.81
2	B	1001	097	C13-C12-N3	2.61	119.83	116.28
2	A	1001	097	C14-C4-N1	3.41	120.22	116.05
2	A	1001	097	C11-N2-C10	3.78	128.82	122.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	097	5	0

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	284/300 (94%)	1.14	37 (13%) 4 5	28, 38, 50, 58	0
1	B	286/300 (95%)	1.78	105 (36%) 0 0	30, 38, 51, 58	0
All	All	570/600 (95%)	1.47	142 (24%) 1 1	28, 38, 50, 58	0

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	519	LEU	7.2
1	A	518	VAL	6.7
1	B	449	TYR	6.1
1	B	514	THR	4.9
1	B	292	LEU	4.6
1	B	404	GLY	4.5
1	B	397	PHE	4.2
1	B	455	LEU	4.2
1	B	453	SER	4.2
1	B	348	GLU	4.2
1	B	550	VAL	4.1
1	B	297	SER	4.0
1	B	325	ALA	4.0
1	B	334	ASN	3.9
1	B	304	LEU	3.9
1	B	346	ASP	3.9
1	B	379	CYS	3.8
1	A	537	GLY	3.8
1	A	397	PHE	3.8
1	B	350	TYR	3.7
1	B	471	ILE	3.7
1	B	363	GLY	3.7
1	B	344	ASP	3.6
1	B	258	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	425	GLN	3.6
1	B	259	TYR	3.5
1	B	293	TYR	3.5
1	B	260	VAL	3.4
1	B	355	LEU	3.3
1	B	408	ASN	3.3
1	B	415	LYS	3.3
1	B	340	ASN	3.2
1	B	330	ARG	3.2
1	B	285	LEU	3.2
1	B	443	TRP	3.2
1	A	545	CYS	3.1
1	A	338	GLN	3.1
1	B	500	PRO	3.1
1	B	373	ALA	3.1
1	B	456	ASP	3.1
1	B	256	SER	3.0
1	B	296	PRO	3.0
1	B	407	PHE	2.9
1	B	339	HIS	2.9
1	B	436	ASN	2.9
1	B	526	PHE	2.9
1	B	378	VAL	2.9
1	B	341	PRO	2.8
1	B	343	SER	2.8
1	B	365	GLN	2.8
1	B	400	ALA	2.8
1	B	385	CYS	2.8
1	B	452	THR	2.8
1	B	466	LYS	2.8
1	A	506	CYS	2.8
1	B	419	SER	2.8
1	A	439	HIS	2.7
1	B	321	VAL	2.7
1	B	375	VAL	2.7
1	B	492	PHE	2.7
1	B	462	CYS	2.7
1	B	281	TYR	2.7
1	B	305	VAL	2.7
1	B	349	HIS	2.6
1	B	469	ASN	2.6
1	A	546	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	258	ARG	2.6
1	B	353	ALA	2.5
1	A	259	TYR	2.5
1	A	539	TRP	2.5
1	B	434	LEU	2.5
1	B	289	ALA	2.5
1	B	413	ASP	2.5
1	A	549	LEU	2.5
1	B	437	LEU	2.5
1	B	446	CYS	2.5
1	B	336	GLN	2.5
1	B	352	THR	2.5
1	B	307	VAL	2.5
1	B	447	SER	2.5
1	A	520	VAL	2.4
1	A	528	TRP	2.4
1	B	539	TRP	2.4
1	A	434	LEU	2.4
1	B	265	VAL	2.4
1	B	459	HIS	2.4
1	B	464	MET	2.4
1	B	545	CYS	2.4
1	B	549	LEU	2.4
1	B	412	ASP	2.4
1	A	363	GLY	2.3
1	B	519	LEU	2.3
1	B	426	ASP	2.3
1	B	288	VAL	2.3
1	A	301	SER	2.3
1	B	329	LEU	2.3
1	A	302	VAL	2.3
1	A	512	THR	2.3
1	B	302	VAL	2.3
1	A	394	GLN	2.3
1	B	454	PHE	2.2
1	B	364	SER	2.2
1	B	386	SER	2.2
1	A	544	LYS	2.2
1	A	312	ILE	2.2
1	B	433	MET	2.2
1	A	550	VAL	2.2
1	A	317	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	393	LEU	2.2
1	B	472	GLN	2.2
1	B	326	ALA	2.2
1	B	383	ARG	2.2
1	B	467	PRO	2.2
1	A	407	PHE	2.2
1	B	546	VAL	2.2
1	A	365	GLN	2.1
1	B	474	PRO	2.2
1	B	298	ILE	2.1
1	B	312	ILE	2.1
1	B	463	LEU	2.1
1	B	376	GLY	2.1
1	B	468	GLN	2.1
1	A	453	SER	2.1
1	A	310	LEU	2.1
1	B	507	SER	2.1
1	A	449	TYR	2.1
1	A	341	PRO	2.1
1	B	532	THR	2.1
1	A	500	PRO	2.1
1	B	470	PRO	2.1
1	B	478	PRO	2.1
1	A	524	LYS	2.1
1	B	335	TRP	2.1
1	A	361	LEU	2.0
1	A	322	THR	2.0
1	A	496	SER	2.0
1	B	465	ASP	2.0
1	B	366	THR	2.0
1	B	342	PRO	2.0
1	B	257	HIS	2.0
1	B	262	THR	2.0
1	B	499	CYS	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 [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
2	097	B	1001	23/23	0.86	0.26	1.61	36,43,46,50	0
7	NA	B	1564	1/1	0.73	0.26	1.58	51,51,51,51	0
2	097	A	1001	23/23	0.91	0.21	1.06	39,44,46,48	0
4	CD	A	1554	1/1	0.95	0.15	-0.17	38,38,38,38	0
4	CD	A	1558	1/1	0.96	0.13	-1.02	44,44,44,44	0
7	NA	A	1565	1/1	0.99	0.11	-1.82	37,37,37,37	0
7	NA	A	1567	1/1	0.89	0.12	-1.86	36,36,36,36	0
5	NI	B	1558	1/1	0.91	0.13	-3.22	26,26,26,26	0
4	CD	B	1557	1/1	0.93	0.12	-3.65	43,43,43,43	0
6	MG	B	1562	1/1	0.75	0.21	-	40,40,40,40	0
5	NI	A	1562	1/1	0.88	0.10	-	68,68,68,68	0
4	CD	A	1557	1/1	0.97	0.18	-	42,42,42,42	0
3	ZN	B	1554	1/1	0.85	0.17	-	29,29,29,29	0
6	MG	B	1560	1/1	0.66	0.21	-	55,55,55,55	0
5	NI	B	1563	1/1	0.93	0.19	-	41,41,41,41	0
6	MG	A	1560	1/1	0.87	0.21	-	35,35,35,35	0
5	NI	A	1563	1/1	0.90	0.15	-	43,43,43,43	0
7	NA	A	1566	1/1	0.88	0.22	-	34,34,34,34	0
5	NI	B	1561	1/1	0.72	0.15	-	44,44,44,44	0
7	NA	B	1565	1/1	0.85	0.17	-	37,37,37,37	0
5	NI	A	1561	1/1	0.75	0.17	-	50,50,50,50	0
4	CD	B	1555	1/1	0.85	0.18	-	47,47,47,47	0
5	NI	A	1559	1/1	0.92	0.10	-	70,70,70,70	0
6	MG	B	1567	1/1	0.93	0.33	-	20,20,20,20	0
4	CD	A	1555	1/1	0.97	0.13	-	45,45,45,45	0
5	NI	A	1568	1/1	0.91	0.15	-	42,42,42,42	0
5	NI	A	1556	1/1	0.92	0.12	-	44,44,44,44	0
5	NI	B	1559	1/1	0.97	0.21	-	38,38,38,38	0
6	MG	B	1566	1/1	0.85	0.24	-	30,30,30,30	0
3	ZN	A	1553	1/1	0.99	0.22	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	MG	A	1569	1/1	0.89	0.20	-	26,26,26,26	0
5	NI	B	1556	1/1	0.94	0.15	-	53,53,53,53	0
5	NI	A	1564	1/1	0.89	0.14	-	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.