



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:55 PM GMT

PDB ID : 1HW9
Title : COMPLEX OF THE CATALYTIC PORTION OF HUMAN HMG-COA REDUCTASE WITH SIMVASTATIN
Authors : Istvan, E.S.; Deisenhofer, J.
Deposited on : 2001-01-09
Resolution : 2.33 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

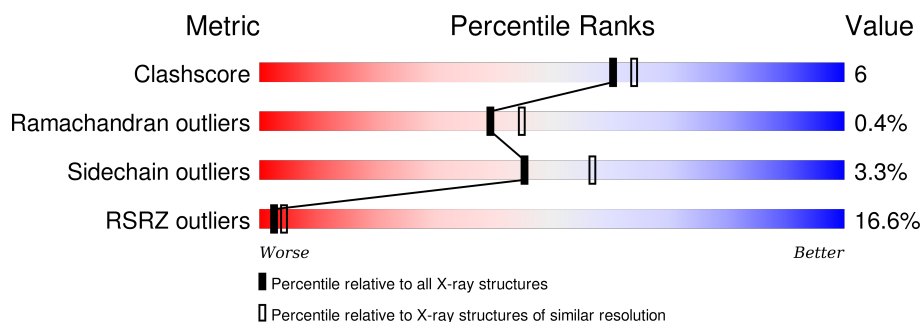
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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))
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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	467	<div> <div>15%</div> <div>75%</div> <div>12%</div> <div>•</div> <div>13%</div> </div>
1	B	467	<div> <div>15%</div> <div>73%</div> <div>11%</div> <div>•</div> <div>15%</div> </div>
1	C	467	<div> <div>13%</div> <div>73%</div> <div>9%</div> <div>•</div> <div>17%</div> </div>
1	D	467	<div> <div>12%</div> <div>72%</div> <div>10%</div> <div>•</div> <div>17%</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
2	ADP	A	102	-	-	-	X
2	ADP	B	104	-	-	-	X
2	ADP	C	103	-	-	-	X
2	ADP	D	105	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12185 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.

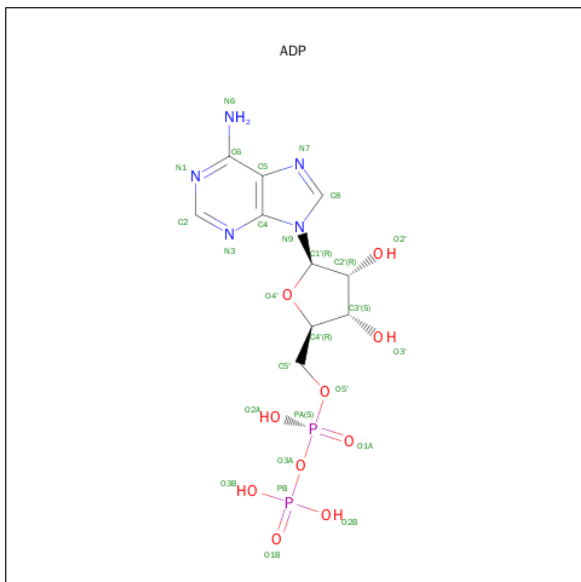
- Molecule 1 is a protein called HMG-COA REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3037	1892	533	582	30			
1	B	398	Total	C	N	O	S	0	0	0
			2952	1838	518	567	29			
1	C	389	Total	C	N	O	S	0	0	0
			2881	1792	504	556	29			
1	D	388	Total	C	N	O	S	0	0	0
			2880	1792	504	555	29			

There are 20 discrepancies between the modelled and reference sequences:

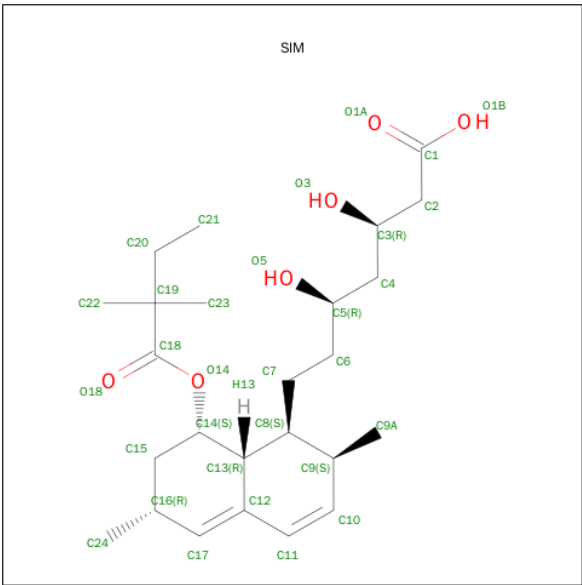
Chain	Residue	Modelled	Actual	Comment	Reference
A	422	GLY	-	INSERTION	UNP P04035
A	423	ALA	-	INSERTION	UNP P04035
A	424	MET	-	INSERTION	UNP P04035
A	425	ALA	-	INSERTION	UNP P04035
A	485	ILE	MET	ENGINEERED	UNP P04035
B	422	GLY	-	INSERTION	UNP P04035
B	423	ALA	-	INSERTION	UNP P04035
B	424	MET	-	INSERTION	UNP P04035
B	425	ALA	-	INSERTION	UNP P04035
B	485	ILE	MET	ENGINEERED	UNP P04035
C	422	GLY	-	INSERTION	UNP P04035
C	423	ALA	-	INSERTION	UNP P04035
C	424	MET	-	INSERTION	UNP P04035
C	425	ALA	-	INSERTION	UNP P04035
C	485	ILE	MET	ENGINEERED	UNP P04035
D	422	GLY	-	INSERTION	UNP P04035
D	423	ALA	-	INSERTION	UNP P04035
D	424	MET	-	INSERTION	UNP P04035
D	425	ALA	-	INSERTION	UNP P04035
D	485	ILE	MET	ENGINEERED	UNP P04035

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is SIMVASTATIN ACID (three-letter code: SIM) (formula: $C_{25}H_{40}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			31	25	6		
3	C	1	Total	C	O	0	0
			31	25	6		
3	B	1	Total	C	O	0	0
			31	25	6		
3	A	1	Total	C	O	0	0
			31	25	6		

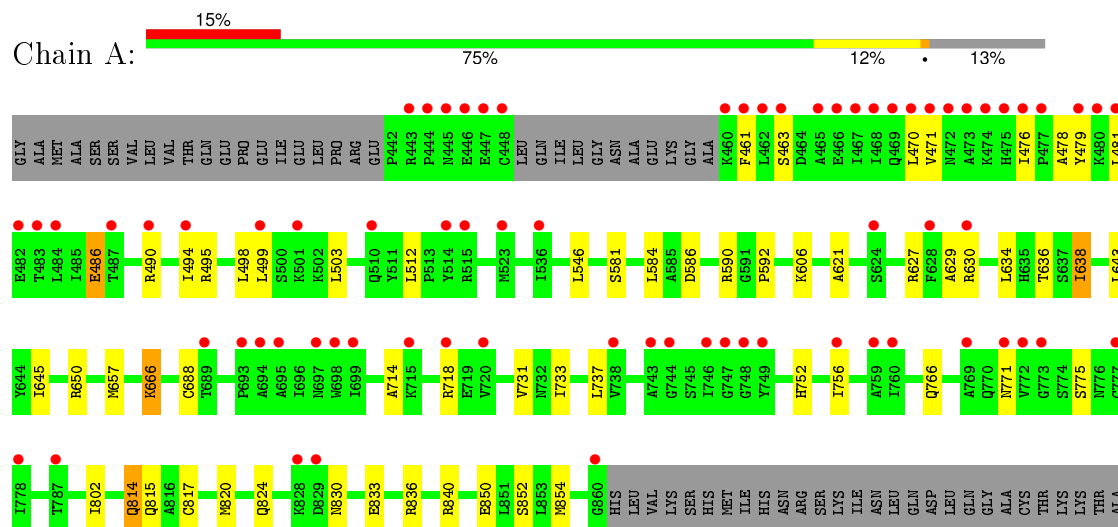
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	44	Total	O	0	0
			44	44		
4	B	49	Total	O	0	0
			49	49		
4	C	33	Total	O	0	0
			33	33		
4	D	50	Total	O	0	0
			50	50		

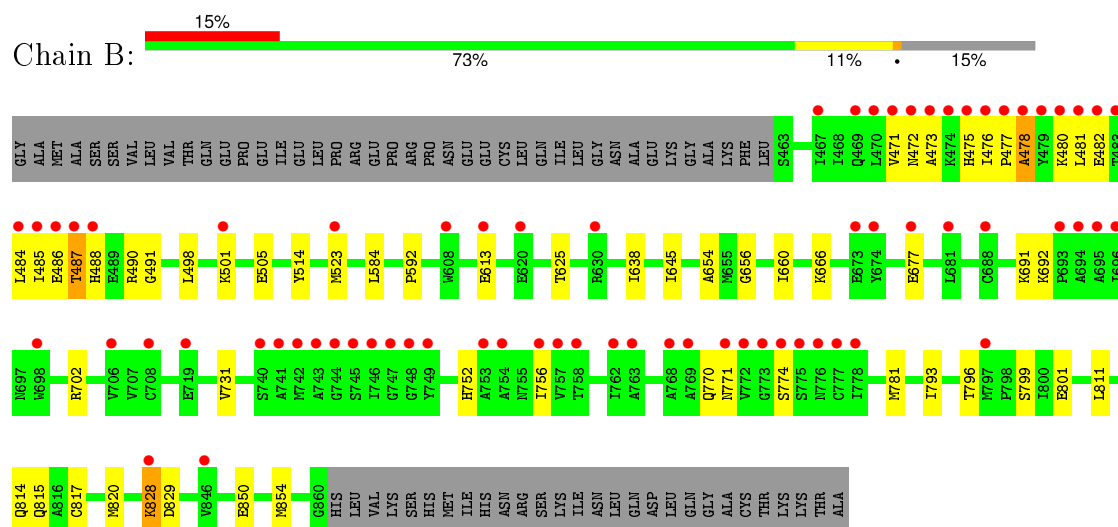
3 Residue-property plots

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: HMG-COA REDUCTASE

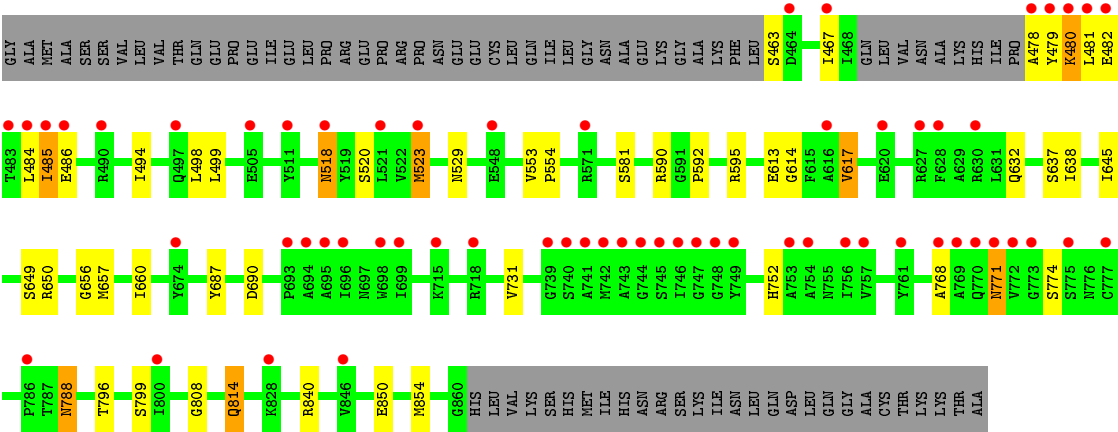


• Molecule 1: HMG-COA REDUCTASE

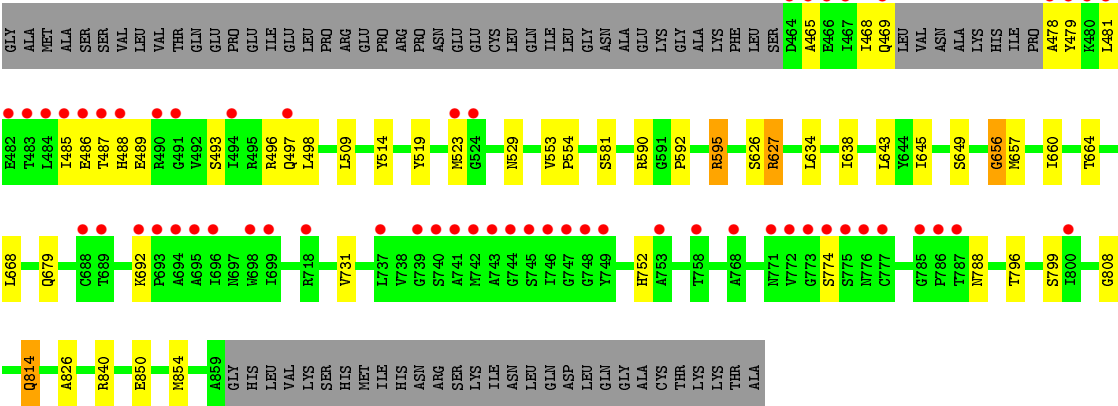


• Molecule 1: HMG-COA REDUCTASE





● Molecule 1: HMG-COA REDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.55Å 172.82Å 80.03Å 90.00° 117.56° 90.00°	Depositor
Resolution (Å)	43.43 – 2.33 52.40 – 2.33	Depositor EDS
% Data completeness (in resolution range)	96.4 (43.43-2.33) 91.8 (52.40-2.33)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.32Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.222 , 0.248 0.216 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.3	EDS
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 73786 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12185	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: SIM, ADP

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	0.44	0/3081	0.63	0/4164
1	B	0.43	0/2994	0.63	0/4049
1	C	0.41	0/2920	0.62	0/3946
1	D	0.46	0/2919	0.63	1/3945 (0.0%)
All	All	0.44	0/11914	0.63	1/16104 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	656	GLY	N-CA-C	5.09	125.82	113.10

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	3037	0	3072	37	0
1	B	2952	0	2989	39	0
1	C	2881	0	2911	31	0
1	D	2880	0	2911	34	0
2	A	27	0	12	0	0
2	B	54	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	27	0	12	0	0
2	D	27	0	12	2	0
3	A	31	0	39	0	0
3	B	31	0	39	0	0
3	C	62	0	78	1	0
4	A	44	0	0	0	0
4	B	49	0	0	0	0
4	C	33	0	0	0	0
4	D	50	0	0	0	0
All	All	12185	0	12099	136	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 6.

All (136) 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:B:625:THR:HG22	1:B:666:LYS:HD2	1.46	0.98
1:C:485:ILE:HG22	1:C:486:GLU:H	1.45	0.82
1:B:817:CYS:HA	1:B:820:MET:HE3	1.69	0.75
1:A:479:TYR:HA	1:A:495:ARG:HH21	1.54	0.72
1:D:808:GLY:O	1:D:814:GLN:HG3	1.93	0.69
1:D:488:HIS:HD2	1:D:523:MET:HG3	1.58	0.68
1:B:654:ALA:HB1	2:B:104:ADP:O1B	1.93	0.68
1:A:584:LEU:HD11	1:D:638:ILE:HD11	1.75	0.67
1:B:485:ILE:HG22	1:B:486:GLU:H	1.60	0.67
1:A:714:ALA:HB1	1:A:718:ARG:NH1	2.09	0.66
1:D:519:TYR:O	1:D:523:MET:HG2	1.96	0.66
1:A:471:VAL:HG11	1:A:498:LEU:HD21	1.78	0.66
1:B:485:ILE:HD12	1:B:491:GLY:HA2	1.78	0.65
1:A:629:ALA:O	1:A:630:ARG:HD2	1.96	0.64
1:D:656:GLY:O	1:D:660:ILE:HG12	1.97	0.64
1:B:485:ILE:HG22	1:B:486:GLU:N	2.13	0.64
1:B:656:GLY:O	1:B:660:ILE:HG12	1.99	0.63
1:B:781:MET:HE2	1:B:793:ILE:HD12	1.82	0.62
1:D:638:ILE:HG22	1:D:643:LEU:HD13	1.81	0.62
1:C:808:GLY:O	1:C:814:GLN:HG3	2.00	0.61
1:B:850:GLU:O	1:B:854:MET:HG2	2.01	0.60
1:A:766:GLN:OE1	1:A:802:ILE:HG13	2.02	0.59
1:A:731:VAL:HG12	1:A:854:MET:CE	2.32	0.59
1:A:714:ALA:HB1	1:A:718:ARG:HH12	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:485:ILE:HD11	1:C:494:ILE:HD12	1.85	0.58
1:C:850:GLU:O	1:C:854:MET:HG2	2.03	0.58
1:D:486:GLU:HG2	1:D:487:THR:H	1.67	0.58
1:A:606:LYS:HG3	1:A:636:THR:HG21	1.85	0.58
1:D:486:GLU:HG2	1:D:487:THR:N	2.20	0.57
1:B:584:LEU:HD22	1:C:638:ILE:HD12	1.86	0.57
1:D:581:SER:OG	1:D:840:ARG:HD2	2.05	0.57
1:C:480:LYS:O	1:C:484:LEU:HG	2.04	0.57
1:A:586:ASP:HB3	1:A:650:ARG:HE	1.70	0.56
1:C:581:SER:OG	1:C:840:ARG:HD2	2.05	0.56
1:D:850:GLU:O	1:D:854:MET:HG2	2.04	0.56
1:B:482:GLU:HG2	1:B:523:MET:HG2	1.88	0.56
1:B:487:THR:HG23	1:B:490:ARG:HB3	1.88	0.55
1:A:756:ILE:HD12	1:A:756:ILE:N	2.21	0.55
1:A:636:THR:HG23	1:A:643:LEU:HD11	1.89	0.55
1:C:482:GLU:HG2	1:C:523:MET:HG2	1.87	0.55
1:D:649:SER:HB3	1:D:660:ILE:HD12	1.89	0.55
1:D:485:ILE:HG22	1:D:486:GLU:N	2.23	0.55
1:A:581:SER:OG	1:A:840:ARG:HD2	2.07	0.54
1:A:731:VAL:HG12	1:A:854:MET:HE1	1.90	0.54
1:B:477:PRO:HG2	1:B:480:LYS:HZ3	1.73	0.54
1:A:817:CYS:HA	1:A:820:MET:HE3	1.89	0.53
1:D:493:SER:O	1:D:497:GLN:HG3	2.08	0.53
1:A:606:LYS:HG3	1:A:636:THR:CG2	2.39	0.53
1:C:656:GLY:O	1:C:660:ILE:HG12	2.09	0.52
1:B:475:HIS:O	1:B:476:ILE:HG13	2.10	0.52
1:B:828:LYS:CD	1:B:829:ASP:H	2.23	0.51
1:A:621:ALA:HB1	1:A:666:LYS:HE3	1.93	0.50
1:B:691:LYS:HE2	1:B:770:GLN:HG3	1.93	0.50
1:B:811:LEU:O	1:B:815:GLN:HG3	2.12	0.50
1:B:471:VAL:C	1:B:473:ALA:H	2.15	0.50
1:A:636:THR:CG2	1:A:643:LEU:HD11	2.41	0.50
1:A:627:ARG:H	1:A:627:ARG:HD3	1.76	0.49
1:B:477:PRO:HG2	1:B:480:LYS:NZ	2.27	0.49
1:B:731:VAL:HG12	1:B:854:MET:CE	2.43	0.49
1:C:768:ALA:O	1:C:771:ASN:HB3	2.13	0.49
1:D:731:VAL:HG12	1:D:854:MET:HE3	1.95	0.48
1:C:731:VAL:HG12	1:C:854:MET:CE	2.43	0.48
1:C:479:TYR:HB3	1:C:529:ASN:OD1	2.13	0.48
1:A:592:PRO:HD2	1:A:645:ILE:O	2.13	0.48
1:C:485:ILE:HG22	1:C:486:GLU:N	2.23	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:468:ILE:HG23	1:D:498:LEU:HD21	1.96	0.48
1:D:826:ALA:HB1	2:D:105:ADP:HN61	1.79	0.47
1:B:731:VAL:HG12	1:B:854:MET:HE3	1.96	0.47
1:C:731:VAL:HG12	1:C:854:MET:HE3	1.96	0.47
1:A:850:GLU:O	1:A:854:MET:HG2	2.15	0.47
1:B:477:PRO:O	1:B:478:ALA:CB	2.62	0.47
1:C:632:GLN:HE21	1:C:650:ARG:HG2	1.80	0.47
1:D:496:ARG:NH2	1:D:509:LEU:O	2.48	0.47
1:A:638:ILE:O	1:D:796:THR:HG21	2.15	0.47
1:B:592:PRO:HD2	1:B:645:ILE:O	2.14	0.47
1:A:771:ASN:ND2	1:A:775:SER:OG	2.48	0.47
1:C:463:SER:O	1:C:467:ILE:HG12	2.15	0.46
1:B:796:THR:HG21	1:C:638:ILE:O	2.15	0.46
1:D:731:VAL:HG12	1:D:854:MET:CE	2.45	0.46
1:D:487:THR:HG22	1:D:489:GLU:H	1.80	0.46
1:B:702:ARG:HD3	1:B:801:GLU:OE2	2.15	0.46
1:B:828:LYS:HD3	1:B:829:ASP:H	1.81	0.46
1:B:482:GLU:HG3	1:B:488:HIS:HD2	1.81	0.46
1:D:479:TYR:HB3	1:D:529:ASN:OD1	2.16	0.45
1:B:476:ILE:HD13	1:B:484:LEU:CD2	2.46	0.45
1:D:488:HIS:CD2	1:D:523:MET:HG3	2.46	0.45
1:B:498:LEU:O	1:B:501:LYS:HG2	2.17	0.45
1:B:828:LYS:HD3	1:B:829:ASP:N	2.31	0.45
1:D:626:SER:HA	1:D:627:ARG:HH11	1.82	0.45
1:C:518:ASN:ND2	1:C:520:SER:OG	2.50	0.44
1:D:592:PRO:HD2	1:D:645:ILE:O	2.18	0.44
1:C:592:PRO:HD2	1:C:645:ILE:O	2.16	0.44
1:A:590:ARG:HD3	1:A:590:ARG:HA	1.84	0.44
1:C:480:LYS:NZ	1:C:480:LYS:HB3	2.33	0.44
1:A:815:GLN:HG2	1:A:824:GLN:CG	2.48	0.44
1:B:638:ILE:O	1:C:796:THR:HG21	2.18	0.44
1:B:477:PRO:HD2	1:B:480:LYS:HD2	2.00	0.43
1:C:614:GLY:O	1:C:617:VAL:HG13	2.18	0.43
1:A:471:VAL:HG13	1:A:476:ILE:O	2.17	0.43
1:C:478:ALA:O	1:C:481:LEU:HG	2.18	0.43
1:A:731:VAL:HG12	1:A:854:MET:HE3	2.00	0.43
1:A:650:ARG:HH11	1:A:650:ARG:HG3	1.84	0.43
1:D:485:ILE:HG22	1:D:486:GLU:H	1.83	0.43
1:D:478:ALA:O	1:D:481:LEU:HG	2.18	0.43
1:A:490:ARG:O	1:A:494:ILE:HG12	2.19	0.43
1:C:553:VAL:HA	1:C:554:PRO:HD2	1.93	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:690:ASP:OD2	3:C:1:SIM:H41	2.18	0.42
1:A:546:LEU:HD11	1:A:581:SER:HB3	2.02	0.42
1:A:733:ILE:O	1:A:737:LEU:HB2	2.19	0.42
1:D:627:ARG:NH1	1:D:627:ARG:H	2.18	0.42
1:B:485:ILE:CG2	1:B:486:GLU:N	2.82	0.42
1:A:830:ASN:O	1:A:833:GLU:HB2	2.19	0.42
1:D:774:SER:HA	1:D:799:SER:O	2.20	0.42
1:D:590:ARG:HA	1:D:590:ARG:HD3	1.85	0.42
1:A:836:ARG:O	1:A:840:ARG:HG3	2.20	0.42
1:C:788:ASN:HA	1:C:788:ASN:HD22	1.65	0.42
1:A:657:MET:CE	1:A:657:MET:HA	2.50	0.42
1:C:649:SER:HB3	1:C:660:ILE:HD12	2.00	0.42
1:A:629:ALA:C	1:A:630:ARG:HD2	2.40	0.41
1:B:692:LYS:HB2	1:B:692:LYS:HE2	1.89	0.41
1:B:475:HIS:C	1:B:476:ILE:HG13	2.41	0.41
1:D:664:THR:O	1:D:668:LEU:HG	2.21	0.41
1:D:692:LYS:HB2	1:D:692:LYS:HE2	1.91	0.41
1:D:826:ALA:HB1	2:D:105:ADP:N6	2.35	0.41
1:C:590:ARG:HA	1:C:590:ARG:HD3	1.84	0.41
1:A:814:GLN:H	1:A:814:GLN:NE2	2.19	0.41
1:D:553:VAL:HA	1:D:554:PRO:HD2	1.95	0.40
1:A:478:ALA:O	1:A:481:LEU:HG	2.21	0.40
1:C:613:GLU:O	1:C:617:VAL:HG12	2.21	0.40
1:C:637:SER:HB2	1:C:687:TYR:OH	2.21	0.40
1:C:774:SER:HA	1:C:799:SER:O	2.21	0.40
1:B:478:ALA:O	1:B:481:LEU:HG	2.22	0.40
1:B:487:THR:HG23	1:B:490:ARG:CB	2.50	0.40
1:B:774:SER:HA	1:B:799:SER:O	2.22	0.40
1:D:595:ARG:HD2	1:D:679:GLN:OE1	2.21	0.40
1:B:756:ILE:HD12	1:B:756:ILE:N	2.36	0.40

There are no symmetry-related clashes.

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	404/467 (86%)	381 (94%)	22 (5%)	1 (0%)	52	61
1	B	396/467 (85%)	373 (94%)	20 (5%)	3 (1%)	24	25
1	C	385/467 (82%)	364 (94%)	20 (5%)	1 (0%)	46	54
1	D	384/467 (82%)	365 (95%)	17 (4%)	2 (0%)	34	37
All	All	1569/1868 (84%)	1483 (94%)	79 (5%)	7 (0%)	39	45

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	486	GLU
1	D	465	ALA
1	B	478	ALA
1	B	514	TYR
1	C	485	ILE
1	D	514	TYR
1	B	472	ASN

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	326/375 (87%)	312 (96%)	14 (4%)	35	45
1	B	316/375 (84%)	308 (98%)	8 (2%)	55	68
1	C	308/375 (82%)	296 (96%)	12 (4%)	39	51
1	D	308/375 (82%)	300 (97%)	8 (3%)	54	66
All	All	1258/1500 (84%)	1216 (97%)	42 (3%)	45	57

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	461	PHE

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Mol	Chain	Res	Type
1	A	463	SER
1	A	470	LEU
1	A	486	GLU
1	A	499	LEU
1	A	503	LEU
1	A	512	LEU
1	A	634	LEU
1	A	638	ILE
1	A	666	LYS
1	A	688	CYS
1	A	752	HIS
1	A	814	GLN
1	A	852	SER
1	B	487	THR
1	B	505	GLU
1	B	613	GLU
1	B	677	GLU
1	B	752	HIS
1	B	771	ASN
1	B	814	GLN
1	B	828	LYS
1	C	480	LYS
1	C	498	LEU
1	C	499	LEU
1	C	518	ASN
1	C	523	MET
1	C	595	ARG
1	C	617	VAL
1	C	657	MET
1	C	752	HIS
1	C	771	ASN
1	C	788	ASN
1	C	814	GLN
1	D	469	GLN
1	D	595	ARG
1	D	627	ARG
1	D	634	LEU
1	D	657	MET
1	D	752	HIS
1	D	788	ASN
1	D	814	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	635	HIS
1	A	771	ASN
1	A	788	ASN
1	A	814	GLN
1	B	488	HIS
1	B	635	HIS
1	B	771	ASN
1	B	776	ASN
1	C	518	ASN
1	C	552	GLN
1	C	635	HIS
1	C	771	ASN
1	C	788	ASN
1	C	819	GLN
1	D	488	HIS
1	D	552	GLN
1	D	771	ASN
1	D	788	ASN
1	D	819	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

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	ADP	A	102	-	22,29,29	1.26	2 (9%)	27,45,45	0.69	0
3	SIM	A	4	-	27,32,32	1.88	8 (29%)	26,46,46	1.27	4 (15%)
2	ADP	B	101	-	22,29,29	1.41	4 (18%)	27,45,45	0.77	0
2	ADP	B	104	-	22,29,29	1.60	5 (22%)	27,45,45	0.81	1 (3%)
3	SIM	B	3	-	27,32,32	1.83	7 (25%)	26,46,46	1.17	3 (11%)
3	SIM	C	1	-	27,32,32	1.87	7 (25%)	26,46,46	1.19	3 (11%)
2	ADP	C	103	-	22,29,29	1.27	2 (9%)	27,45,45	0.94	1 (3%)
3	SIM	C	2	-	27,32,32	1.77	7 (25%)	26,46,46	1.15	4 (15%)
2	ADP	D	105	-	22,29,29	1.43	3 (13%)	27,45,45	0.79	1 (3%)

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	ADP	A	102	-	-	0/12/32/32	0/3/3/3
3	SIM	A	4	-	-	0/24/55/55	0/2/2/2
2	ADP	B	101	-	-	0/12/32/32	0/3/3/3
2	ADP	B	104	-	-	0/12/32/32	0/3/3/3
3	SIM	B	3	-	-	0/24/55/55	0/2/2/2
3	SIM	C	1	-	-	0/24/55/55	0/2/2/2
2	ADP	C	103	-	-	0/12/32/32	0/3/3/3
3	SIM	C	2	-	-	0/24/55/55	0/2/2/2
2	ADP	D	105	-	-	0/12/32/32	0/3/3/3

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	103	ADP	C8-N7	-3.19	1.28	1.34
2	D	105	ADP	C8-N7	-3.15	1.28	1.34
2	A	102	ADP	C8-N7	-3.00	1.28	1.34
2	B	104	ADP	C8-N7	-2.98	1.28	1.34
2	B	101	ADP	C8-N7	-2.96	1.28	1.34
3	C	1	SIM	C11-C12	-2.26	1.36	1.43
3	C	2	SIM	C11-C12	-2.14	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	4	SIM	C11-C12	-2.07	1.37	1.43
2	B	104	ADP	O2'-C2'	2.03	1.47	1.43
3	B	3	SIM	O14-C18	2.04	1.38	1.34
2	B	101	ADP	C2'-C3'	2.07	1.59	1.53
3	B	3	SIM	C15-C14	2.11	1.56	1.52
3	A	4	SIM	C15-C14	2.18	1.56	1.52
2	C	103	ADP	C2'-C3'	2.18	1.59	1.53
3	C	2	SIM	C15-C14	2.18	1.56	1.52
2	A	102	ADP	O4'-C4'	2.27	1.50	1.45
3	C	2	SIM	C13-C8	2.28	1.58	1.54
3	A	4	SIM	O14-C18	2.41	1.38	1.34
2	B	104	ADP	C2'-C3'	2.45	1.60	1.53
3	A	4	SIM	C9-C10	2.45	1.54	1.50
3	C	2	SIM	C9-C10	2.56	1.55	1.50
3	A	4	SIM	C13-C8	2.59	1.58	1.54
2	D	105	ADP	O4'-C1'	2.61	1.44	1.41
3	C	1	SIM	C9-C10	2.63	1.55	1.50
3	B	3	SIM	C13-C8	2.74	1.58	1.54
3	B	3	SIM	C9-C10	2.76	1.55	1.50
3	C	1	SIM	C13-C8	2.77	1.58	1.54
2	D	105	ADP	O4'-C4'	2.81	1.51	1.45
2	B	101	ADP	O4'-C1'	2.81	1.44	1.41
2	B	104	ADP	O4'-C4'	2.87	1.51	1.45
3	C	1	SIM	O14-C18	2.93	1.39	1.34
2	B	101	ADP	O4'-C4'	3.00	1.51	1.45
3	C	2	SIM	C19-C18	3.45	1.58	1.52
3	B	3	SIM	C19-C18	3.56	1.58	1.52
3	B	3	SIM	C16-C17	3.57	1.54	1.50
3	C	2	SIM	C13-C12	3.57	1.57	1.52
3	A	4	SIM	C13-C12	3.64	1.57	1.52
3	C	1	SIM	C19-C18	3.69	1.58	1.52
2	B	104	ADP	O4'-C1'	3.72	1.45	1.41
3	C	1	SIM	C13-C12	3.75	1.57	1.52
3	A	4	SIM	C19-C18	3.84	1.58	1.52
3	B	3	SIM	C13-C12	3.96	1.57	1.52
3	C	1	SIM	C16-C17	4.06	1.55	1.50
3	C	2	SIM	C16-C17	4.37	1.55	1.50
3	A	4	SIM	C16-C17	4.40	1.55	1.50

All (17) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4	SIM	C24-C16-C17	-3.45	108.00	111.28
3	B	3	SIM	C24-C16-C17	-3.19	108.25	111.28
3	C	1	SIM	C24-C16-C17	-3.00	108.43	111.28
3	C	2	SIM	C24-C16-C17	-2.75	108.67	111.28
3	C	2	SIM	C9A-C9-C10	-2.70	106.39	110.90
3	A	4	SIM	C9A-C9-C10	-2.63	106.52	110.90
3	C	1	SIM	C9A-C9-C10	-2.59	106.57	110.90
3	B	3	SIM	C9A-C9-C10	-2.31	107.04	110.90
3	A	4	SIM	C23-C19-C22	-2.20	104.90	109.35
2	B	104	ADP	N3-C2-N1	-2.10	127.29	128.89
3	C	2	SIM	C23-C19-C22	-2.08	105.14	109.35
3	C	1	SIM	C23-C19-C22	-2.04	105.22	109.35
2	D	105	ADP	O4'-C1'-N9	2.10	112.50	108.10
3	B	3	SIM	O14-C14-C15	2.15	112.37	107.94
3	A	4	SIM	C14-O14-C18	2.21	121.03	117.37
3	C	2	SIM	C14-O14-C18	2.54	121.58	117.37
2	C	103	ADP	C4'-O4'-C1'	2.82	112.82	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	104	ADP	1	0
3	C	1	SIM	1	0
2	D	105	ADP	2	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	408/467 (87%)	0.97	72 (17%) 2 3	36, 57, 100, 101	0
1	B	398/467 (85%)	0.99	70 (17%) 2 3	38, 57, 91, 101	0
1	C	389/467 (83%)	0.86	62 (15%) 3 5	39, 58, 86, 101	0
1	D	388/467 (83%)	0.82	58 (14%) 3 5	36, 54, 83, 101	0
All	All	1583/1868 (84%)	0.91	262 (16%) 2 4	36, 57, 96, 101	0

All (262) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	483	THR	9.2
1	A	475	HIS	8.7
1	A	473	ALA	8.3
1	D	484	LEU	8.0
1	A	484	LEU	7.6
1	D	479	TYR	7.5
1	A	476	ILE	7.2
1	D	467	ILE	7.1
1	B	476	ILE	7.1
1	C	484	LEU	6.4
1	D	485	ILE	6.3
1	B	471	VAL	6.2
1	A	471	VAL	6.2
1	A	448	CYS	6.1
1	C	483	THR	6.0
1	A	479	TYR	6.0
1	B	483	THR	6.0
1	D	478	ALA	5.7
1	B	485	ILE	5.7
1	A	472	ASN	5.5
1	C	627	ARG	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	446	GLU	5.5
1	B	478	ALA	5.4
1	C	479	TYR	5.3
1	B	486	GLU	5.3
1	A	462	LEU	5.1
1	D	466	GLU	5.1
1	B	479	TYR	5.0
1	C	480	LYS	5.0
1	D	490	ARG	5.0
1	A	470	LEU	4.9
1	B	477	PRO	4.9
1	D	494	ILE	4.8
1	B	475	HIS	4.8
1	C	694	ALA	4.8
1	C	486	GLU	4.8
1	B	484	LEU	4.7
1	D	745	SER	4.6
1	A	523	MET	4.5
1	D	694	ALA	4.5
1	D	523	MET	4.4
1	B	746	ILE	4.4
1	D	480	LYS	4.3
1	D	469	GLN	4.2
1	A	481	LEU	4.2
1	D	743	ALA	4.2
1	A	461	PHE	4.2
1	C	773	GLY	4.1
1	C	628	PHE	4.1
1	A	772	VAL	4.1
1	D	746	ILE	4.1
1	A	445	ASN	4.1
1	A	746	ILE	4.1
1	B	481	LEU	4.1
1	A	693	PRO	4.1
1	B	630	ARG	4.0
1	D	695	ALA	4.0
1	A	447	GLU	4.0
1	A	483	THR	4.0
1	B	772	VAL	3.9
1	D	524	GLY	3.9
1	B	469	GLN	3.8
1	B	677	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	699	ILE	3.8
1	C	769	ALA	3.8
1	A	480	LYS	3.8
1	A	748	GLY	3.8
1	D	464	ASP	3.8
1	B	693	PRO	3.7
1	C	746	ILE	3.7
1	D	786	PRO	3.7
1	D	486	GLU	3.7
1	B	694	ALA	3.7
1	D	740	SER	3.7
1	B	698	TRP	3.7
1	B	523	MET	3.6
1	C	743	ALA	3.6
1	B	743	ALA	3.6
1	B	608	TRP	3.6
1	D	487	THR	3.5
1	A	514	TYR	3.5
1	A	698	TRP	3.5
1	A	460	LYS	3.5
1	B	754	ALA	3.5
1	D	772	VAL	3.5
1	A	769	ALA	3.5
1	C	772	VAL	3.4
1	B	777	CYS	3.4
1	A	466	GLU	3.4
1	B	776	ASN	3.4
1	A	777	CYS	3.4
1	B	758	THR	3.4
1	B	613	GLU	3.4
1	C	828	LYS	3.4
1	D	693	PRO	3.3
1	B	487	THR	3.3
1	C	481	LEU	3.3
1	D	465	ALA	3.3
1	A	628	PHE	3.3
1	C	698	TRP	3.3
1	D	771	ASN	3.3
1	A	482	GLU	3.3
1	C	741	ALA	3.3
1	B	501	LYS	3.2
1	B	828	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	696	ILE	3.2
1	A	499	LEU	3.2
1	B	695	ALA	3.2
1	B	773	GLY	3.2
1	C	695	ALA	3.2
1	B	757	VAL	3.2
1	B	472	ASN	3.1
1	B	771	ASN	3.1
1	B	470	LEU	3.1
1	C	770	GLN	3.1
1	D	747	GLY	3.1
1	A	694	ALA	3.1
1	A	689	THR	3.1
1	B	748	GLY	3.1
1	C	693	PRO	3.1
1	C	715	LYS	3.1
1	C	740	SER	3.1
1	D	774	SER	3.1
1	B	480	LYS	3.0
1	D	748	GLY	3.0
1	C	745	SER	3.0
1	D	491	GLY	3.0
1	C	630	ARG	3.0
1	A	828	LYS	3.0
1	A	743	ALA	3.0
1	B	769	ALA	3.0
1	C	482	GLU	3.0
1	C	771	ASN	3.0
1	A	747	GLY	3.0
1	D	698	TRP	3.0
1	B	474	LYS	3.0
1	C	757	VAL	2.9
1	B	775	SER	2.9
1	A	756	ILE	2.9
1	B	473	ALA	2.9
1	B	749	TYR	2.9
1	B	756	ILE	2.9
1	C	518	ASN	2.9
1	C	753	ALA	2.8
1	A	771	ASN	2.8
1	D	482	GLU	2.8
1	A	494	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	699	ILE	2.8
1	B	753	ALA	2.8
1	C	754	ALA	2.8
1	B	778	ILE	2.8
1	A	477	PRO	2.8
1	C	761	TYR	2.8
1	C	744	GLY	2.8
1	D	768	ALA	2.8
1	B	488	HIS	2.8
1	B	673	GLU	2.8
1	A	467	ILE	2.8
1	D	741	ALA	2.8
1	C	548	GLU	2.7
1	D	749	TYR	2.7
1	B	744	GLY	2.7
1	C	523	MET	2.7
1	A	718	ARG	2.7
1	B	741	ALA	2.7
1	A	778	ILE	2.7
1	A	469	GLN	2.7
1	A	444	PRO	2.7
1	B	774	SER	2.7
1	C	775	SER	2.7
1	A	715	LYS	2.6
1	C	505	GLU	2.6
1	A	468	ILE	2.6
1	D	699	ILE	2.6
1	A	749	TYR	2.6
1	D	744	GLY	2.6
1	A	787	THR	2.6
1	D	481	LEU	2.6
1	A	630	ARG	2.6
1	D	777	CYS	2.6
1	A	720	VAL	2.6
1	B	740	SER	2.6
1	B	745	SER	2.6
1	C	478	ALA	2.6
1	C	749	TYR	2.5
1	A	760	ILE	2.5
1	B	688	CYS	2.5
1	A	474	LYS	2.5
1	D	689	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	748	GLY	2.5
1	A	860	GLY	2.4
1	B	768	ALA	2.4
1	D	742	MET	2.4
1	C	742	MET	2.4
1	C	718	ARG	2.4
1	C	620	GLU	2.4
1	B	762	ILE	2.4
1	B	747	GLY	2.4
1	D	488	HIS	2.4
1	B	706	VAL	2.4
1	C	485	ILE	2.4
1	C	616	ALA	2.4
1	A	744	GLY	2.3
1	C	800	ILE	2.3
1	A	501	LYS	2.3
1	B	719	GLU	2.3
1	D	776	ASN	2.3
1	D	739	GLY	2.3
1	A	624	SER	2.3
1	C	768	ALA	2.3
1	D	773	GLY	2.3
1	D	800	ILE	2.3
1	A	697	ASN	2.3
1	D	718	ARG	2.3
1	B	620	GLU	2.3
1	B	696	ILE	2.3
1	C	467	ILE	2.3
1	C	696	ILE	2.3
1	B	674	TYR	2.3
1	D	753	ALA	2.3
1	B	797	MET	2.3
1	A	443	ARG	2.3
1	A	695	ALA	2.3
1	C	674	TYR	2.3
1	D	692	LYS	2.3
1	B	467	ILE	2.2
1	A	829	ASP	2.2
1	C	747	GLY	2.2
1	B	763	ALA	2.2
1	C	521	LEU	2.2
1	A	463	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	787	THR	2.2
1	B	681	LEU	2.2
1	C	571	ARG	2.1
1	B	482	GLU	2.1
1	D	737	LEU	2.1
1	D	775	SER	2.1
1	C	739	GLY	2.1
1	B	846	VAL	2.1
1	C	511	TYR	2.1
1	A	490	ARG	2.1
1	D	497	GLN	2.1
1	D	688	CYS	2.1
1	A	487	THR	2.1
1	A	465	ALA	2.1
1	B	708	CYS	2.1
1	C	490	ARG	2.1
1	C	497	GLN	2.1
1	A	510	GLN	2.1
1	A	738	VAL	2.1
1	A	515	ARG	2.1
1	A	536	ILE	2.1
1	C	777	CYS	2.0
1	A	759	ALA	2.0
1	C	464	ASP	2.0
1	C	756	ILE	2.0
1	A	773	GLY	2.0
1	C	786	PRO	2.0
1	D	785	GLY	2.0
1	C	846	VAL	2.0
1	D	758	THR	2.0
1	B	742	MET	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 [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	ADP	B	104	27/27	0.55	0.38	7.22	99,100,100,100	0
2	ADP	D	105	27/27	0.69	0.30	3.02	99,100,100,100	0
2	ADP	C	103	27/27	0.81	0.39	2.22	99,100,100,100	0
2	ADP	A	102	27/27	0.83	0.36	2.03	100,100,100,100	0
2	ADP	B	101	27/27	0.76	0.32	1.20	99,100,100,100	0
3	SIM	C	1	31/31	0.94	0.20	0.52	52,60,62,63	0
3	SIM	A	4	31/31	0.91	0.19	0.40	59,64,67,67	0
3	SIM	C	2	31/31	0.93	0.18	0.19	51,60,63,64	0
3	SIM	B	3	31/31	0.93	0.17	-0.11	50,59,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.