



Full wwPDB X-ray Structure Validation Report

Mar 12, 2014 – 05:29 PM GMT

PDB ID : 1HW8
Title : COMPLEX OF THE CATALYTIC PORTION OF HUMAN HMG-COA REDUCTASE WITH COMPACTIN (ALSO KNOWN AS MEVASTATIN)
Authors : Istvan, E.S.; Deisenhofer, J.
Deposited on : 2001-01-09
Resolution : 2.10 Å(reported)

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

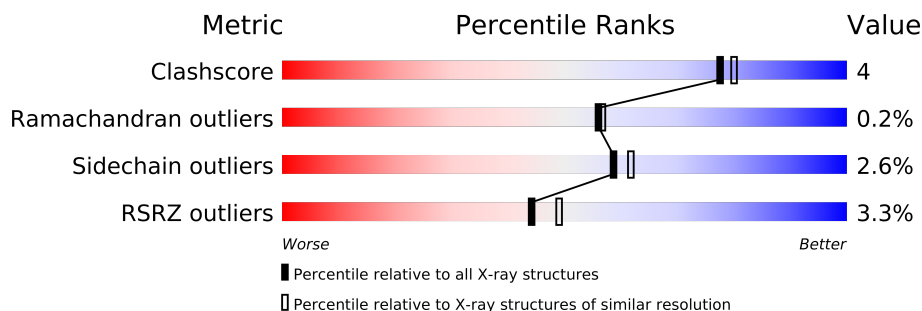
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : trunk22714
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk22714

1 Overall quality at a glance

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))
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	467	
1	B	467	
1	C	467	
1	D	467	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	ADP	D	102	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12022 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

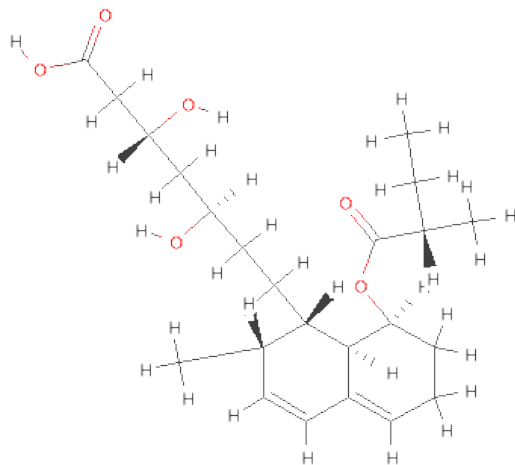
- Molecule 1 is a protein called HMG-COA REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	0	0
			3004	1867	527	580	30			
1	B	410	Total	C	N	O	S	0	0	0
			3055	1904	536	585	30			
1	C	373	Total	C	N	O	S	0	0	0
			2755	1711	487	528	29			
1	D	372	Total	C	N	O	S	0	0	0
			2751	1709	486	527	29			

There are 20 discrepancies between the modelled and reference sequences:

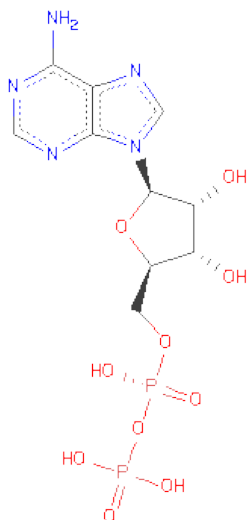
Chain	Residue	Modelled	Actual	Comment	Reference
A	422	GLY	-	INSERTION	UNP P04035
A	423	ALA	-	INSERTION	UNP P04035
A	424	MET	-	INSERTION	UNP P04035
A	425	ALA	-	INSERTION	UNP P04035
A	485	ILE	MET	ENGINEERED	UNP P04035
B	422	GLY	-	INSERTION	UNP P04035
B	423	ALA	-	INSERTION	UNP P04035
B	424	MET	-	INSERTION	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 (3R,5R)-3,5-DIHYDROXY-7-[(1S,2S,8S,8AR)-2-METHYL-8-{[(2S)-2-METHYLBUTANOYL]OXY}-1,2,6,7,8,8A-HEXAHYDRONAPHTHALEN-1-YL]HEPTANOIC ACID (three-letter code: 114) (formula: $C_{23}H_{36}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			29	23	6		
2	A	1	Total	C	O	0	0
			29	23	6		
2	D	1	Total	C	O	0	0
			29	23	6		
2	C	1	Total	C	O	0	0
			29	23	6		

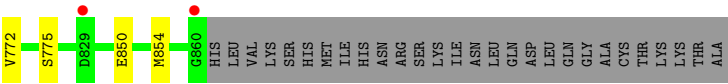
- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	66	Total	O	0	0
			66	66		
4	B	79	Total	O	0	0
			79	79		
4	C	67	Total	O	0	0
			67	67		
4	D	75	Total	O	0	0
			75	75		



● Molecule 1: HMG-COA REDUCTASE

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.83Å 173.00Å 75.18Å 90.00° 118.38° 90.00°	Depositor
Resolution (Å)	43.13 – 2.10 52.54 – 2.09	Depositor EDS
% Data completeness (in resolution range)	92.7 (43.13-2.10) 88.2 (52.54-2.09)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.08Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.191 , 0.223 0.193 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.5	EDS
Estimated twinning fraction	0.006 for -h-l,k,h 0.006 for l,k,-h-l 0.028 for h,-k,-h-l 0.028 for -h-l,-k,l 0.019 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 89748 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12022	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 114, 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	0.49	0/3046	0.68	0/4117
1	B	0.52	0/3098	0.68	0/4187
1	C	0.50	0/2794	0.67	1/3776 (0.0%)
1	D	0.53	0/2790	0.70	1/3771 (0.0%)
All	All	0.51	0/11728	0.68	2/15851 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	596	LEU	CA-CB-CG	-6.27	100.89	115.30
1	D	596	LEU	CA-CB-CG	-6.14	101.18	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3004	0	3026	38	0
1	B	3055	0	3094	18	0
1	C	2755	0	2784	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2751	0	2781	13	0
2	A	29	0	35	2	0
2	B	29	0	35	0	0
2	C	29	0	35	2	0
2	D	29	0	35	1	0
3	B	27	0	12	3	0
3	D	27	0	12	1	0
4	A	66	0	0	0	0
4	B	79	0	0	0	0
4	C	67	0	0	1	0
4	D	75	0	0	0	0
All	All	12022	0	11849	87	0

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

All (87) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:828:LYS:H	1:B:828:LYS:HD2	1.19	1.08
1:B:828:LYS:N	1:B:828:LYS:HD2	1.99	0.74
1:B:555:MET:HE3	1:B:563:VAL:HG22	1.71	0.73
1:A:529:ASN:ND2	3:B:101:ADP:H2	1.88	0.72
1:A:581:SER:OG	1:A:840:ARG:HD2	1.94	0.67
1:B:828:LYS:H	1:B:828:LYS:CD	1.90	0.66
1:A:683:VAL:HG11	2:A:2:114:H221	1.77	0.66
1:A:529:ASN:HD22	3:B:101:ADP:H2	1.40	0.66
1:A:655:MET:SD	1:A:657:MET:HG2	2.36	0.66
1:D:596:LEU:HD13	1:D:602:SER:HA	1.81	0.63
1:D:595:ARG:HD2	1:D:679:GLN:OE1	1.98	0.63
1:C:518:ASN:HD21	1:C:521:LEU:HD13	1.64	0.60
1:A:542:GLY:H	1:A:567:ASN:ND2	2.00	0.59
1:A:636:THR:CG2	1:A:643:LEU:HD11	2.34	0.58
1:A:529:ASN:ND2	3:B:101:ADP:C2	2.72	0.57
1:A:625:THR:CG2	1:A:666:LYS:HG3	2.33	0.57
1:A:590:ARG:NH2	1:A:657:MET:HE3	2.20	0.56
1:A:817:CYS:HA	1:A:820:MET:HE3	1.87	0.56
1:A:523:MET:HE1	1:A:530:VAL:HG21	1.88	0.56
1:A:656:GLY:O	1:A:660:ILE:HG12	2.07	0.55
1:C:850:GLU:O	1:C:854:MET:HG2	2.07	0.54
1:A:811:LEU:HB2	1:A:814:GLN:HG2	1.91	0.53
1:A:632:GLN:NE2	1:A:650:ARG:HG2	2.23	0.53
1:C:658:ASN:O	1:C:662:LYS:HG3	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:542:GLY:H	1:A:567:ASN:HD22	1.57	0.52
1:A:683:VAL:CG1	2:A:2:114:H221	2.39	0.52
1:D:850:GLU:O	1:D:854:MET:HG2	2.09	0.52
1:B:446:GLU:O	1:B:449:LEU:HG	2.09	0.52
1:B:649:SER:HB3	1:B:660:ILE:CD1	2.40	0.51
1:C:596:LEU:HD13	1:C:602:SER:HA	1.92	0.51
1:C:518:ASN:ND2	1:C:521:LEU:HD13	2.27	0.50
1:A:625:THR:HG22	1:A:666:LYS:HG3	1.92	0.50
1:A:781:MET:CE	1:A:854:MET:HG3	2.42	0.50
1:D:606:LYS:HG3	1:D:636:THR:OG1	2.12	0.50
1:D:715:LYS:HG3	1:D:718:ARG:NH2	2.26	0.49
1:A:485:ILE:CG2	1:A:486:GLU:N	2.76	0.49
1:C:523:MET:HE1	4:C:1172:HOH:O	2.13	0.49
1:A:477:PRO:O	1:A:478:ALA:HB3	2.13	0.49
1:A:441:GLU:N	1:A:442:PRO:CD	2.76	0.48
1:A:754:ALA:HA	1:A:775:SER:OG	2.14	0.48
1:C:606:LYS:HG3	1:C:636:THR:OG1	2.14	0.48
1:C:683:VAL:HG11	2:C:4:114:H221	1.95	0.47
1:B:485:ILE:HD13	1:B:494:ILE:HD12	1.94	0.47
1:C:715:LYS:HG3	1:C:718:ARG:NH2	2.29	0.47
1:D:683:VAL:HG11	2:D:3:114:H221	1.95	0.47
1:A:480:LYS:O	1:A:483:THR:HG22	2.15	0.47
1:D:715:LYS:HB3	1:D:715:LYS:NZ	2.29	0.47
1:C:715:LYS:HB3	1:C:715:LYS:NZ	2.30	0.47
1:B:498:LEU:O	1:B:501:LYS:HG2	2.14	0.47
1:A:484:LEU:HD22	1:A:485:ILE:HD12	1.97	0.46
1:B:850:GLU:O	1:B:854:MET:HG2	2.16	0.46
1:D:590:ARG:HA	1:D:590:ARG:HD3	1.75	0.45
1:C:517:TYR:HE2	1:C:522:VAL:HG21	1.82	0.45
1:B:811:LEU:O	1:B:815:GLN:HG3	2.17	0.45
1:A:850:GLU:O	1:A:854:MET:HG2	2.17	0.45
1:A:629:ALA:O	1:A:630:ARG:HD2	2.16	0.45
1:B:466:GLU:O	1:B:470:LEU:HD13	2.16	0.45
1:B:449:LEU:HD23	1:B:449:LEU:HA	1.82	0.44
1:D:771:ASN:OD1	1:D:775:SER:OG	2.34	0.44
1:C:657:MET:HA	1:C:657:MET:CE	2.47	0.44
1:B:447:GLU:C	1:B:449:LEU:H	2.20	0.44
1:A:592:PRO:HD2	1:A:645:ILE:O	2.17	0.44
1:A:590:ARG:HD3	1:A:590:ARG:HA	1.61	0.43
1:A:479:TYR:HB3	1:A:529:ASN:HD21	1.84	0.43
1:B:732:ASN:HA	1:B:854:MET:HE1	2.01	0.43
1:C:560:GLY:O	1:C:561:CYS:HB2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:629:ALA:C	1:A:630:ARG:HD2	2.39	0.43
1:C:590:ARG:HB2	1:C:660:ILE:HG22	2.00	0.43
1:C:772:VAL:HG23	1:D:771:ASN:ND2	2.34	0.43
1:B:677:GLU:CD	1:B:677:GLU:H	2.21	0.43
1:A:630:ARG:O	1:A:632:GLN:NE2	2.52	0.43
1:C:771:ASN:OD1	1:C:775:SER:OG	2.36	0.43
1:A:463:SER:OG	1:A:466:GLU:HG3	2.19	0.43
1:C:590:ARG:HA	1:C:590:ARG:HD3	1.72	0.42
1:A:649:SER:HB3	1:A:660:ILE:HD12	2.01	0.41
1:D:493:SER:O	1:D:497:GLN:HG3	2.19	0.41
1:C:523:MET:CE	1:C:523:MET:HA	2.50	0.41
1:D:656:GLY:HA2	3:D:102:ADP:O1B	2.21	0.41
1:A:781:MET:HE3	1:A:854:MET:HG3	2.01	0.41
1:B:625:THR:HG21	1:B:663:GLY:HA2	2.01	0.41
1:A:811:LEU:O	1:A:815:GLN:HG3	2.21	0.41
1:A:637:SER:HB2	1:A:687:TYR:OH	2.21	0.41
1:A:808:GLY:O	1:A:814:GLN:HG3	2.22	0.40
1:B:796:THR:HG21	1:C:638:ILE:O	2.20	0.40
1:B:443:ARG:HA	1:B:444:PRO:HD3	1.95	0.40
1:D:560:GLY:O	1:D:561:CYS:HB2	2.20	0.40
1:C:683:VAL:CG1	2:C:4:114:H221	2.52	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	398/467 (85%)	381 (96%)	14 (4%)	3 (1%)	27	20
1	B	406/467 (87%)	389 (96%)	17 (4%)	0	100	100
1	C	371/467 (79%)	359 (97%)	12 (3%)	0	100	100
1	D	370/467 (79%)	356 (96%)	14 (4%)	0	100	100
All	All	1545/1868 (83%)	1485 (96%)	57 (4%)	3 (0%)	56	57

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	478	ALA
1	A	486	GLU
1	A	444	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	323/375 (86%)	316 (98%)	7 (2%)	64	68
1	B	328/375 (88%)	318 (97%)	10 (3%)	53	55
1	C	294/375 (78%)	288 (98%)	6 (2%)	68	72
1	D	294/375 (78%)	285 (97%)	9 (3%)	52	54
All	All	1239/1500 (83%)	1207 (97%)	32 (3%)	59	62

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	498	LEU
1	A	509	LEU
1	A	512	LEU
1	A	634	LEU
1	A	669	SER
1	A	752	HIS
1	A	814	GLN
1	B	484	LEU
1	B	486	GLU
1	B	487	THR
1	B	505	GLU
1	B	523	MET
1	B	634	LEU
1	B	688	CYS
1	B	752	HIS
1	B	828	LYS
1	B	829	ASP
1	C	523	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	595	ARG
1	C	596	LEU
1	C	657	MET
1	C	669	SER
1	C	752	HIS
1	D	500	SER
1	D	509	LEU
1	D	595	ARG
1	D	596	LEU
1	D	627	ARG
1	D	634	LEU
1	D	657	MET
1	D	660	ILE
1	D	752	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	HIS
1	A	518	ASN
1	A	529	ASN
1	A	567	ASN
1	A	632	GLN
1	B	472	ASN
1	B	488	HIS
1	B	510	GLN
1	B	635	HIS
1	D	642	ASN
1	D	672	HIS
1	D	788	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

6 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	114	A	2	-	30,30,30	1.80	9 (30%)	41,41,41	1.20	4 (9%)
2	114	B	1	-	30,30,30	1.77	8 (26%)	41,41,41	1.24	4 (9%)
3	ADP	B	101	-	29,29,29	1.37	3 (10%)	45,45,45	0.76	0
2	114	C	4	-	30,30,30	1.74	7 (23%)	41,41,41	1.21	4 (9%)
3	ADP	D	102	-	29,29,29	1.51	6 (20%)	45,45,45	0.92	2 (4%)
2	114	D	3	-	30,30,30	1.80	6 (20%)	41,41,41	1.14	3 (7%)

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	114	A	2	-	1/1/10/13	0/23/50/50	0/2/2/2
2	114	B	1	-	-	0/23/50/50	0/2/2/2
3	ADP	B	101	-	-	0/16/32/32	0/3/3/3
2	114	C	4	-	-	0/23/50/50	0/2/2/2
3	ADP	D	102	-	-	0/16/32/32	0/3/3/3
2	114	D	3	-	-	0/23/50/50	0/2/2/2

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	3	114	C9-C8	4.59	1.59	1.54
2	B	1	114	C9-C8	4.35	1.58	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2	114	O1A-C1	4.30	1.37	1.22
2	C	4	114	C9-C8	4.14	1.58	1.54
2	C	4	114	O1A-C1	4.14	1.36	1.22
2	A	2	114	C9-C8	3.97	1.58	1.54
2	D	3	114	O1A-C1	3.95	1.36	1.22
2	B	1	114	O1A-C1	3.88	1.35	1.22
2	D	3	114	C13-C12	3.68	1.57	1.52
2	C	4	114	C13-C12	3.40	1.57	1.52
2	A	2	114	C13-C12	3.23	1.57	1.52
3	B	101	ADP	C8-N7	-3.16	1.28	1.34
3	D	102	ADP	PA-O3A	3.08	1.65	1.59
2	B	1	114	C13-C12	3.06	1.57	1.52
3	D	102	ADP	O4'-C4'	3.02	1.52	1.45
3	D	102	ADP	C8-N7	-3.00	1.28	1.34
3	D	102	ADP	C8-N9	-2.82	1.32	1.36
2	C	4	114	C9-C10	2.64	1.55	1.50
2	C	4	114	C13-C8	2.48	1.58	1.54
2	D	3	114	C11-C12	-2.45	1.36	1.43
3	B	101	ADP	C8-N9	-2.41	1.33	1.36
3	B	101	ADP	O4'-C4'	2.32	1.50	1.45
2	B	1	114	C13-C8	2.31	1.58	1.54
2	A	2	114	C9-C10	2.28	1.54	1.50
2	D	3	114	C9-C10	2.28	1.54	1.50
2	C	4	114	C16-C17	2.26	1.54	1.50
2	A	2	114	C13-C8	2.23	1.58	1.54
2	B	1	114	O14-C18	2.20	1.39	1.34
2	C	4	114	C11-C12	-2.20	1.37	1.43
2	D	3	114	O1B-C1	-2.20	1.22	1.30
2	B	1	114	C11-C12	-2.19	1.37	1.43
2	A	2	114	C11-C12	-2.17	1.37	1.43
2	B	1	114	C15-C14	2.16	1.56	1.52
2	B	1	114	C16-C17	2.11	1.54	1.50
3	D	102	ADP	O4'-C1'	2.09	1.43	1.41
2	A	2	114	C16-C17	2.05	1.54	1.50
2	A	2	114	C15-C14	2.03	1.56	1.52
2	A	2	114	O14-C18	2.03	1.38	1.34
3	D	102	ADP	C5-C4	-2.02	1.35	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	114	O1B-C1-C2	2.91	124.16	114.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	114	O1A-C1-C2	-2.90	112.40	122.60
2	B	1	114	O1B-C1-C2	2.83	123.91	114.20
2	D	3	114	C9A-C9-C10	-2.82	106.33	110.83
2	A	2	114	O1B-C1-C2	2.80	123.79	114.20
2	C	4	114	O1A-C1-C2	-2.79	112.80	122.60
2	A	2	114	O1A-C1-C2	-2.74	112.98	122.60
2	D	3	114	O1A-C1-C2	-2.71	113.09	122.60
2	A	2	114	C9A-C9-C10	-2.67	106.57	110.83
2	D	3	114	O1B-C1-C2	2.67	123.33	114.20
2	C	4	114	C9A-C9-C10	-2.52	106.81	110.83
3	D	102	ADP	O4'-C1'-N9	2.39	113.30	108.10
2	C	4	114	O14-C14-C15	2.39	112.90	108.50
2	B	1	114	C9A-C9-C10	-2.33	107.11	110.83
2	B	1	114	C15-C16-C17	2.02	115.46	111.69
2	A	2	114	C15-C16-C17	2.01	115.44	111.69
3	D	102	ADP	N3-C4-N9	2.00	128.83	125.39

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2	114	C19

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	404/467 (86%)	0.19	29 (7%)	15 17	20, 34, 69, 99	0
1	B	410/467 (87%)	0.02	9 (2%)	59 64	20, 33, 60, 88	0
1	C	373/467 (79%)	0.07	9 (2%)	56 61	20, 33, 54, 80	0
1	D	372/467 (79%)	-0.09	5 (1%)	74 78	21, 32, 50, 61	0
All	All	1559/1868 (83%)	0.05	52 (3%)	44 49	20, 33, 57, 99	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	484	LEU	9.7
1	C	524	GLY	7.0
1	A	470	LEU	4.4
1	A	446	GLU	4.4
1	B	448	CYS	4.4
1	A	829	ASP	4.2
1	A	482	GLU	4.0
1	A	448	CYS	4.0
1	A	485	ILE	3.8
1	A	486	GLU	3.7
1	A	447	GLU	3.6
1	B	449	LEU	3.5
1	B	446	GLU	3.5
1	A	627	ARG	3.4
1	B	485	ILE	3.3
1	A	628	PHE	3.2
1	A	471	VAL	3.1
1	B	461	PHE	3.0
1	B	451	ILE	3.0
1	D	523	MET	3.0
1	A	479	TYR	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	746	ILE	3.0
1	C	627	ARG	2.9
1	A	445	ASN	2.8
1	A	477	PRO	2.7
1	A	464	ASP	2.6
1	A	478	ALA	2.6
1	A	483	THR	2.6
1	A	629	ALA	2.6
1	A	772	VAL	2.6
1	D	490	ARG	2.5
1	A	501	LYS	2.5
1	A	630	ARG	2.5
1	C	548	GLU	2.4
1	C	515	ARG	2.4
1	D	524	GLY	2.3
1	B	460	LYS	2.3
1	A	516	ASP	2.3
1	C	746	ILE	2.3
1	A	480	LYS	2.3
1	B	829	ASP	2.3
1	A	748	GLY	2.2
1	D	516	ASP	2.2
1	A	787	THR	2.2
1	C	518	ASN	2.2
1	C	860	GLY	2.2
1	B	476	ILE	2.2
1	A	828	LYS	2.2
1	A	467	ILE	2.1
1	A	617	VAL	2.1
1	C	497	GLN	2.0
1	C	829	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	ADP	D	102	27/27	0.15	2.88	58,67,80,81	0
2	114	C	4	29/29	0.14	1.25	30,40,47,48	0
3	ADP	B	101	27/27	0.21	0.67	83,90,100,100	0
2	114	A	2	29/29	0.12	0.19	33,40,47,49	0
2	114	B	1	29/29	0.11	0.16	28,36,46,47	0
2	114	D	3	29/29	0.12	-0.07	29,41,49,50	0

6.5 Other polymers

There are no such residues in this entry.