



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 02:11 AM UTC

PDB ID : 2OBE / pdb\_00002obe  
Title : Crystal Structure of Chimpanzee Adenovirus (Type 68/Simian 25) Major Coat Protein Hexon  
Authors : Xue, F.; Rux, J.J.; Burnett, R.M.  
Deposited on : 2006-12-18  
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

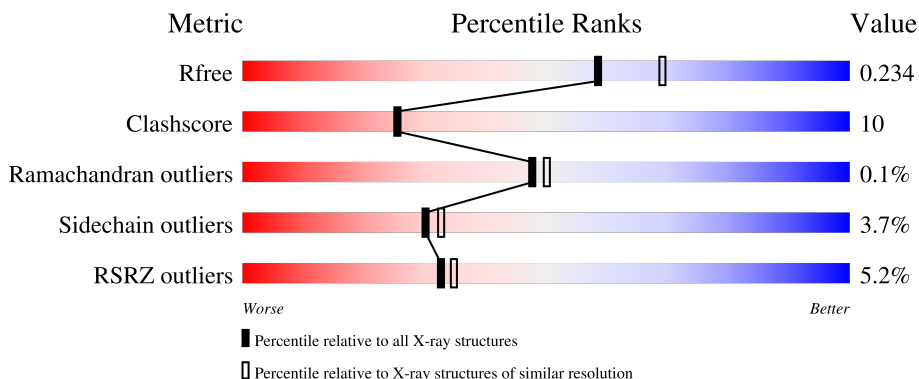
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	932	 3% 81% 14% ..
1	B	932	 3% 80% 14% ..
1	C	932	 9% 76% 17% ...

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	2HP	A	1610	-	X	-	-
2	2HP	A	1619	-	X	-	-
2	2HP	B	1605	-	X	-	-
2	2HP	B	1607	-	X	-	-
2	2HP	B	1609	-	X	-	-
2	2HP	B	1615	-	X	-	-
2	2HP	B	1622	-	X	-	-
2	2HP	C	1618	-	X	-	-
3	MPD	A	1704	X	-	X	-
3	MPD	A	1717	X	-	-	-
3	MPD	A	1720	X	-	X	-
3	MPD	B	1703	-	-	X	-
3	MPD	B	1709	-	-	X	-
3	MPD	B	1711	-	-	X	-
3	MPD	B	1718	X	-	-	-
3	MPD	B	1719	X	-	-	-
3	MPD	B	1721	X	-	-	-
3	MPD	B	1722	X	-	-	-
3	MPD	B	1724	X	-	-	-
3	MPD	C	1713	X	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23334 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.

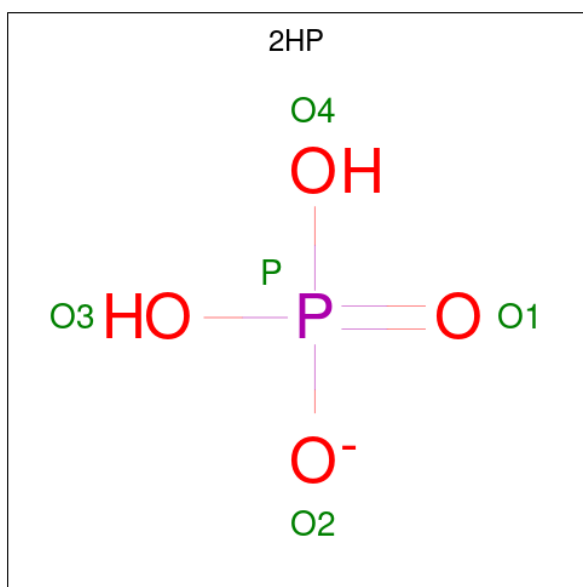
- Molecule 1 is a protein called Hexon protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	915	7208	4582	1217	1377	32	2	0	0
1	B	906	7169	4562	1206	1369	32	2	0	0
1	C	909	7134	4540	1201	1361	32	2	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	825	ASN	UNK	conflict	UNP Q8UY79
A	921	LEU	UNK	conflict	UNP Q8UY79
B	825	ASN	UNK	conflict	UNP Q8UY79
B	921	LEU	UNK	conflict	UNP Q8UY79
C	825	ASN	UNK	conflict	UNP Q8UY79
C	921	LEU	UNK	conflict	UNP Q8UY79

- Molecule 2 is DIHYDROGENPHOSPHATE ION (CCD ID: 2HP) (formula: H<sub>2</sub>O<sub>4</sub>P).



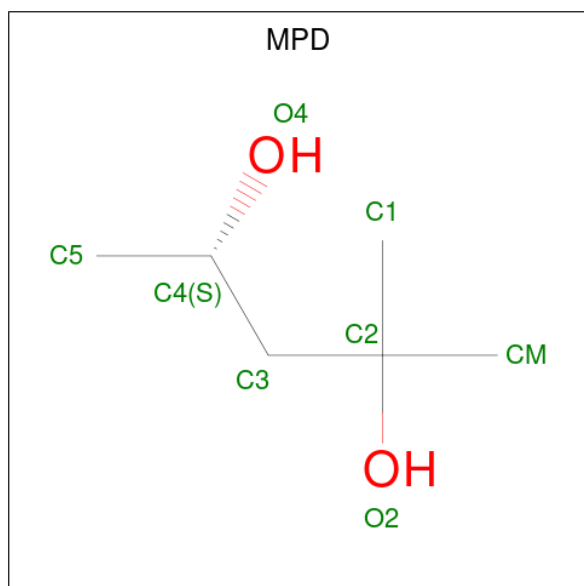
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0
3	A	1	Total C O 8 6 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		

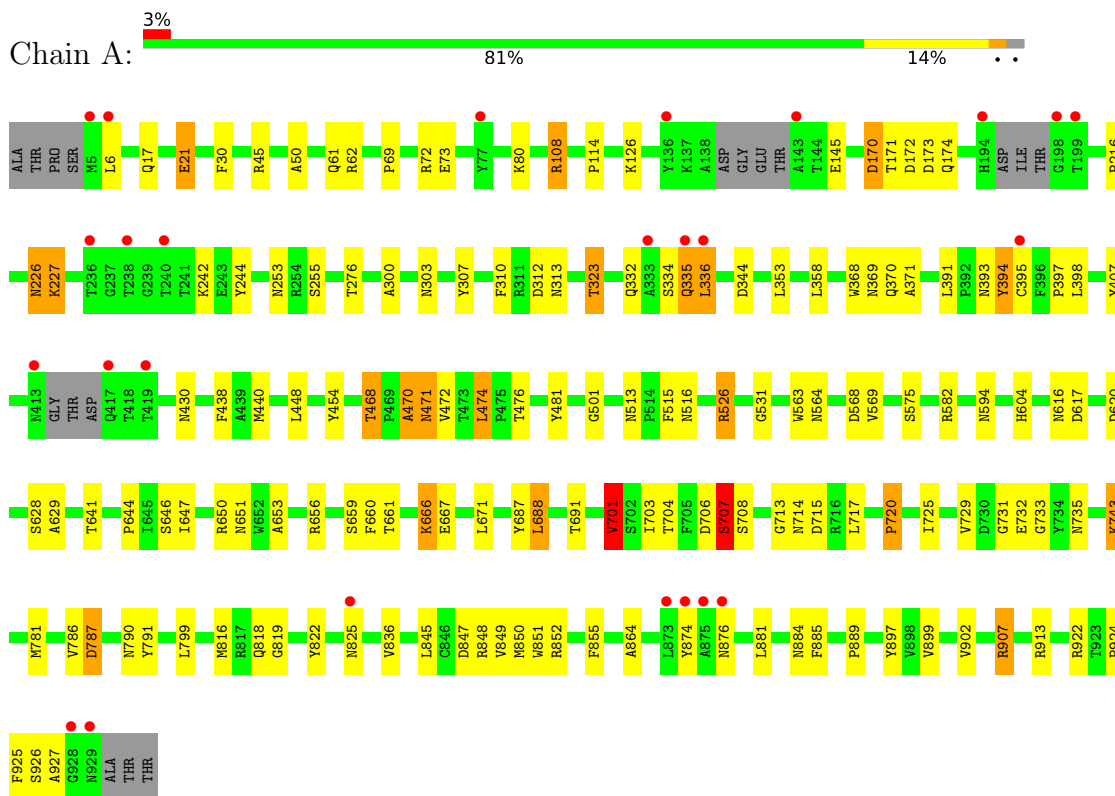
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	542	Total 542	O 542	0	0
4	B	563	Total 563	O 563	0	0
4	C	416	Total 416	O 416	0	0

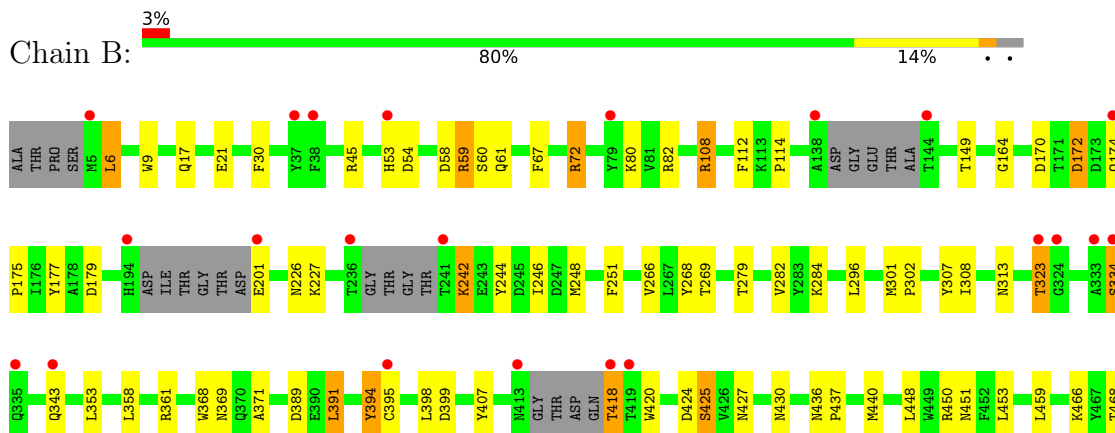
### 3 Residue-property plots [i](#)

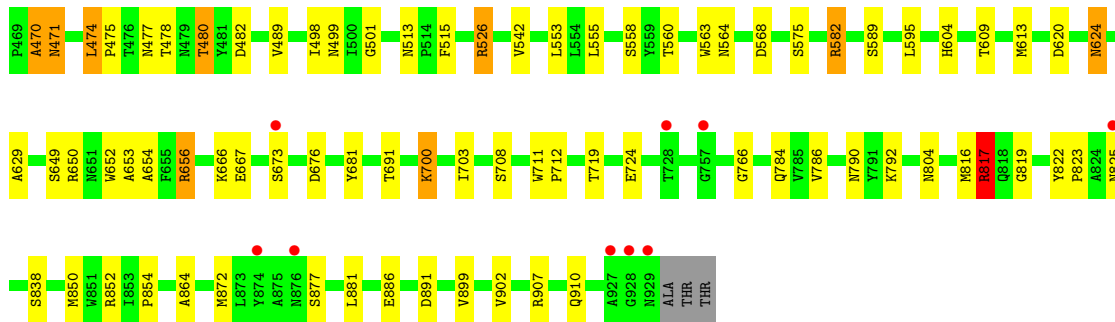
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Hexon protein

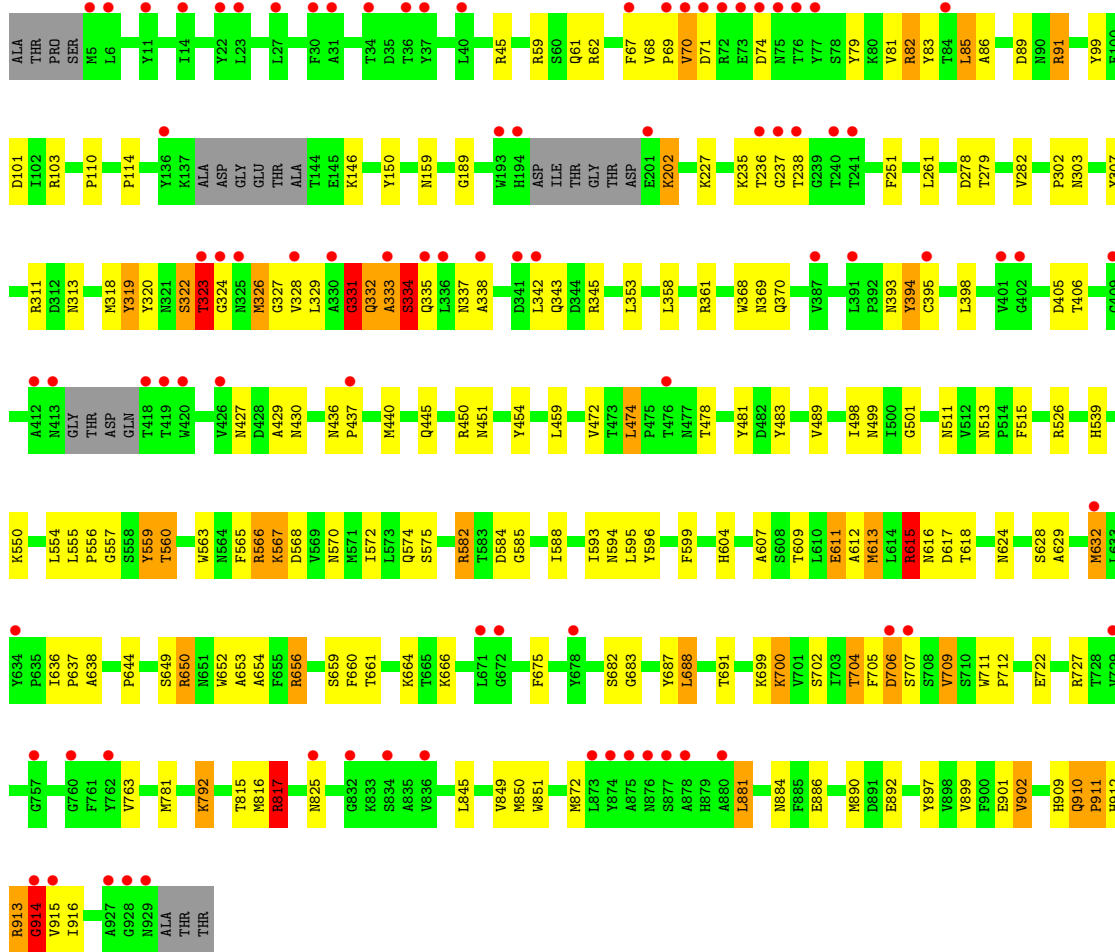
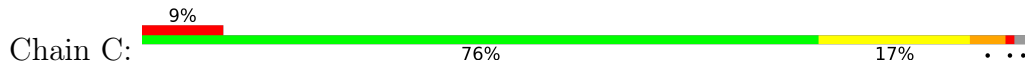


- Molecule 1: Hexon protein





● Molecule 1: Hexon protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.80Å 433.00Å 159.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.27 – 2.10 49.27 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.27-2.10) 93.8 (49.27-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.63 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.2.0019, CNS	Depositor
R, $R_{free}$	0.169 , 0.210 0.168 , 0.234	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtrriage
Anisotropy	0.703	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	23334	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2HP, MPD

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	1.14	20/7404 (0.3%)	1.11	29/10090 (0.3%)
1	B	1.15	9/7364 (0.1%)	1.12	26/10034 (0.3%)
1	C	1.53	61/7328 (0.8%)	1.22	39/9991 (0.4%)
All	All	1.29	90/22096 (0.4%)	1.15	94/30115 (0.3%)

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
1	B	0	1
1	C	0	5
All	All	0	7

The worst 5 of 90 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	825	ASN	CG-OD1	-35.11	0.56	1.23
1	C	328	VAL	C-O	30.06	1.58	1.24
1	B	825	ASN	CG-OD1	-27.97	0.70	1.23
1	C	615	ARG	NE-CZ	26.81	1.62	1.33
1	C	914	GLY	C-O	21.56	1.54	1.23

The worst 5 of 94 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	825	ASN	OD1-CG-ND2	34.57	157.17	122.60
1	B	825	ASN	OD1-CG-ND2	26.22	148.82	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	825	ASN	CB-CG-ND2	-25.41	78.28	116.40
1	A	825	ASN	OD1-CG-ND2	24.07	146.67	122.60
1	B	825	ASN	CB-CG-ND2	-21.05	84.83	116.40

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	849	VAL	Peptide
1	B	817	ARG	Sidechain
1	C	236	THR	Peptide
1	C	323	THR	Peptide
1	C	331	GLY	Mainchain

## 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	7208	0	6804	118	0
1	B	7169	0	6783	150	0
1	C	7134	0	6705	144	0
2	A	25	0	0	1	0
2	B	60	0	0	2	0
2	C	25	0	0	0	0
3	A	56	0	98	33	0
3	B	96	0	168	54	0
3	C	40	0	70	9	0
4	A	542	0	0	2	0
4	B	563	0	0	10	0
4	C	416	0	0	5	0
All	All	23334	0	20628	405	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 10.

The worst 5 of 405 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:913:ARG:C	1:C:913:ARG:CA	1.76	1.52
1:C:567:LYS:NZ	1:C:567:LYS:CE	1.74	1.48
1:B:425:SER:CB	1:B:425:SER:OG	1.65	1.41
1:B:227:LYS:H	3:B:1703:MPD:C1	1.53	1.19
3:B:1711:MPD:H11	3:B:1711:MPD:C5	1.72	1.17

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	907/932 (97%)	873 (96%)	32 (4%)	2 (0%)	43	44
1	B	896/932 (96%)	858 (96%)	38 (4%)	0	100	100
1	C	901/932 (97%)	858 (95%)	41 (5%)	2 (0%)	43	44
All	All	2704/2796 (97%)	2589 (96%)	111 (4%)	4 (0%)	48	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	707	SER
1	A	335	GLN
1	C	334	SER
1	C	238	THR

#### 5.3.2 Protein sidechains [i](#)

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	764/799 (96%)	736 (96%)	28 (4%)	30	33
1	B	764/799 (96%)	733 (96%)	31 (4%)	27	29
1	C	750/799 (94%)	724 (96%)	26 (4%)	32	35
All	All	2278/2397 (95%)	2193 (96%)	85 (4%)	30	33

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	708	SER
1	C	398	LEU
1	C	45	ARG
1	C	332	GLN
1	C	624	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	393	ASN
1	C	651	ASN
1	B	604	HIS
1	C	616	ASN
1	C	884	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

46 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
3	MPD	A	1706	-	7,7,7	0.34	0	9,10,10	0.95	0
3	MPD	A	1705	-	7,7,7	0.36	0	9,10,10	0.73	0
3	MPD	C	1701	-	7,7,7	0.37	0	9,10,10	0.80	0
3	MPD	C	1715	-	7,7,7	0.33	0	9,10,10	0.33	0
2	2HP	A	1610	-	4,4,4	5.50	2 (50%)	6,6,6	1.89	2 (33%)
2	2HP	B	1622	-	4,4,4	5.27	3 (75%)	6,6,6	1.77	1 (16%)
2	2HP	B	1614	-	4,4,4	5.91	2 (50%)	6,6,6	1.30	1 (16%)
3	MPD	B	1724	-	7,7,7	0.33	0	9,10,10	0.65	0
2	2HP	A	1602	-	4,4,4	5.91	2 (50%)	6,6,6	1.40	1 (16%)
2	2HP	C	1611	-	4,4,4	6.12	2 (50%)	6,6,6	1.01	0
3	MPD	B	1722	-	7,7,7	0.57	0	9,10,10	0.49	0
3	MPD	B	1723	-	7,7,7	0.44	0	9,10,10	0.66	0
3	MPD	C	1713	-	7,7,7	0.57	0	9,10,10	1.31	1 (11%)
3	MPD	A	1716	-	7,7,7	1.05	0	9,10,10	1.13	0
3	MPD	A	1704	-	7,7,7	0.75	0	9,10,10	0.76	1 (11%)
3	MPD	B	1707	-	7,7,7	0.41	0	9,10,10	0.43	0
3	MPD	A	1720	-	7,7,7	0.36	0	9,10,10	0.85	0
3	MPD	A	1702	-	7,7,7	0.48	0	9,10,10	1.90	4 (44%)
2	2HP	B	1608	-	4,4,4	6.15	2 (50%)	6,6,6	1.14	1 (16%)
3	MPD	B	1709	-	7,7,7	1.16	1 (14%)	9,10,10	1.13	1 (11%)
2	2HP	C	1617	-	4,4,4	6.43	2 (50%)	6,6,6	1.51	1 (16%)
2	2HP	B	1605	-	4,4,4	6.02	2 (50%)	6,6,6	1.64	2 (33%)
2	2HP	A	1620	-	4,4,4	6.05	2 (50%)	6,6,6	0.94	0
2	2HP	C	1604	-	4,4,4	5.32	2 (50%)	6,6,6	1.47	1 (16%)
2	2HP	C	1613	-	4,4,4	6.02	2 (50%)	6,6,6	1.47	1 (16%)
2	2HP	C	1618	-	4,4,4	5.79	2 (50%)	6,6,6	1.53	2 (33%)
2	2HP	B	1615	-	4,4,4	6.55	2 (50%)	6,6,6	1.73	3 (50%)
3	MPD	A	1717	-	7,7,7	0.58	0	9,10,10	0.86	0
2	2HP	B	1616	-	4,4,4	6.43	2 (50%)	6,6,6	0.82	0
3	MPD	C	1712	-	7,7,7	0.62	0	9,10,10	0.96	0
3	MPD	B	1703	-	7,7,7	0.72	0	9,10,10	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	2HP	A	1619	-	4,4,4	6.52	2 (50%)	6,6,6	1.55	2 (33%)
2	2HP	A	1603	-	4,4,4	5.57	2 (50%)	6,6,6	1.16	0
3	MPD	B	1718	-	7,7,7	0.89	0	9,10,10	1.50	2 (22%)
2	2HP	B	1612	-	4,4,4	6.17	2 (50%)	6,6,6	1.14	0
3	MPD	B	1719	-	7,7,7	0.38	0	9,10,10	0.84	0
3	MPD	C	1714	-	7,7,7	0.43	0	9,10,10	0.30	0
3	MPD	B	1721	-	7,7,7	0.33	0	9,10,10	0.60	0
2	2HP	B	1609	-	4,4,4	4.64	2 (50%)	6,6,6	2.27	3 (50%)
3	MPD	B	1711	-	7,7,7	0.39	0	9,10,10	0.97	0
3	MPD	B	1708	-	7,7,7	0.37	0	9,10,10	0.44	0
2	2HP	B	1601	-	4,4,4	5.25	2 (50%)	6,6,6	1.41	1 (16%)
2	2HP	B	1621	-	4,4,4	6.20	2 (50%)	6,6,6	0.99	0
2	2HP	B	1606	-	4,4,4	5.56	2 (50%)	6,6,6	0.91	0
3	MPD	B	1710	-	7,7,7	0.59	0	9,10,10	0.61	0
2	2HP	B	1607	-	4,4,4	5.71	2 (50%)	6,6,6	1.87	2 (33%)

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
3	MPD	A	1706	-	-	0/5/5/5	-
3	MPD	A	1705	-	-	2/5/5/5	-
3	MPD	C	1701	-	-	3/5/5/5	-
3	MPD	C	1715	-	-	0/5/5/5	-
3	MPD	B	1724	-	1/1/2/2	2/5/5/5	-
3	MPD	B	1722	-	1/1/2/2	3/5/5/5	-
3	MPD	B	1723	-	-	0/5/5/5	-
3	MPD	C	1713	-	1/1/2/2	4/5/5/5	-
3	MPD	A	1704	-	1/1/2/2	5/5/5/5	-
3	MPD	B	1707	-	-	5/5/5/5	-
3	MPD	A	1720	-	1/1/2/2	5/5/5/5	-
3	MPD	A	1702	-	-	0/5/5/5	-
3	MPD	B	1709	-	-	2/5/5/5	-
3	MPD	A	1717	-	1/1/2/2	3/5/5/5	-
3	MPD	C	1712	-	-	4/5/5/5	-
3	MPD	B	1703	-	-	0/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MPD	B	1718	-	1/1/2/2	3/5/5/5	-
3	MPD	B	1719	-	1/1/2/2	2/5/5/5	-
3	MPD	C	1714	-	-	1/5/5/5	-
3	MPD	B	1721	-	1/1/2/2	1/5/5/5	-
3	MPD	B	1711	-	-	4/5/5/5	-
3	MPD	B	1708	-	-	0/5/5/5	-
3	MPD	A	1716	-	-	4/5/5/5	-
3	MPD	B	1710	-	-	1/5/5/5	-

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1615	2HP	P-O4	10.18	1.84	1.54
2	C	1617	2HP	P-O3	9.60	1.82	1.54
2	B	1616	2HP	P-O3	9.42	1.82	1.54
2	A	1619	2HP	P-O4	9.22	1.81	1.54
2	A	1619	2HP	P-O3	9.20	1.81	1.54

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1610	2HP	O2-P-O1	3.90	124.74	110.95
2	B	1609	2HP	O4-P-O2	-3.39	97.38	107.91
2	B	1622	2HP	O4-P-O3	3.26	118.06	107.91
2	B	1607	2HP	O2-P-O1	3.07	121.80	110.95
3	B	1709	MPD	O4-C4-C5	3.05	122.59	109.45

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1704	MPD	C4
3	A	1717	MPD	C4
3	A	1720	MPD	C4
3	B	1718	MPD	C4
3	B	1719	MPD	C4

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1704	MPD	CM-C2-C3-C4
3	A	1705	MPD	C2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
3	A	1716	MPD	C2-C3-C4-O4
3	A	1716	MPD	C2-C3-C4-C5
3	A	1717	MPD	C2-C3-C4-O4

There are no ring outliers.

20 monomers are involved in 99 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1705	MPD	2	0
2	A	1610	2HP	1	0
3	B	1722	MPD	3	0
3	B	1723	MPD	5	0
3	C	1713	MPD	8	0
3	A	1716	MPD	5	0
3	A	1704	MPD	10	0
3	B	1707	MPD	4	0
3	A	1720	MPD	11	0
3	A	1702	MPD	1	0
3	B	1709	MPD	12	0
3	A	1717	MPD	4	0
2	B	1616	2HP	1	0
3	B	1703	MPD	13	0
3	B	1718	MPD	4	0
3	B	1719	MPD	4	0
3	C	1714	MPD	1	0
3	B	1721	MPD	1	0
3	B	1711	MPD	8	0
2	B	1606	2HP	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	915/932 (98%)	0.28	25 (2%) 56 59	24, 36, 52, 73	1 (0%)
1	B	906/932 (97%)	0.34	31 (3%) 48 50	25, 36, 49, 73	1 (0%)
1	C	909/932 (97%)	0.86	85 (9%) 14 14	24, 36, 50, 73	1 (0%)
All	All	2730/2796 (97%)	0.49	141 (5%) 33 35	24, 36, 50, 73	3 (0%)

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	928	GLY	9.5
1	C	418	THR	6.1
1	C	413	ASN	5.9
1	C	929	ASN	5.1
1	A	929	ASN	4.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MPD	B	1722	8/8	0.56	0.20	95,95,95,95	0
3	MPD	A	1717	8/8	0.57	0.24	67,69,70,70	0
3	MPD	B	1703	8/8	0.69	0.20	61,62,63,64	0
3	MPD	A	1720	8/8	0.70	0.17	63,65,66,66	0
2	2HP	B	1612	5/5	0.73	0.14	77,78,79,79	0
2	2HP	B	1621	5/5	0.79	0.12	72,72,73,74	0
3	MPD	B	1723	8/8	0.81	0.20	70,74,75,76	0
3	MPD	C	1701	8/8	0.81	0.18	55,55,57,57	0
3	MPD	A	1716	8/8	0.82	0.16	33,36,41,44	0
3	MPD	A	1704	8/8	0.82	0.15	35,39,41,46	0
3	MPD	B	1711	8/8	0.82	0.17	55,55,56,57	0
3	MPD	C	1712	8/8	0.82	0.15	42,45,46,49	0
3	MPD	C	1714	8/8	0.82	0.16	54,55,56,57	0
3	MPD	B	1721	8/8	0.83	0.18	61,62,63,64	0
2	2HP	A	1619	5/5	0.83	0.12	59,60,60,61	0
3	MPD	C	1713	8/8	0.83	0.16	39,42,44,44	0
3	MPD	B	1718	8/8	0.83	0.16	34,37,44,44	0
2	2HP	B	1608	5/5	0.84	0.14	78,78,79,79	0
3	MPD	B	1708	8/8	0.84	0.17	71,72,72,73	0
3	MPD	B	1709	8/8	0.84	0.15	28,33,39,42	0
3	MPD	A	1705	8/8	0.86	0.14	58,58,58,59	0
2	2HP	C	1611	5/5	0.86	0.21	54,54,55,56	0
2	2HP	C	1617	5/5	0.86	0.23	46,50,52,53	0
2	2HP	A	1620	5/5	0.86	0.12	69,71,71,71	0
3	MPD	A	1702	8/8	0.88	0.13	41,45,46,48	0
2	2HP	B	1605	5/5	0.88	0.15	53,55,56,56	0
3	MPD	A	1706	8/8	0.89	0.15	60,61,62,63	0
2	2HP	C	1618	5/5	0.89	0.12	56,57,58,59	0
2	2HP	C	1604	5/5	0.90	0.17	51,52,53,53	0
2	2HP	B	1616	5/5	0.90	0.11	58,59,61,61	0
3	MPD	B	1710	8/8	0.90	0.12	44,45,47,47	0
2	2HP	A	1610	5/5	0.90	0.13	51,51,53,54	0
2	2HP	B	1622	5/5	0.90	0.22	34,37,46,46	0
3	MPD	B	1707	8/8	0.90	0.12	49,52,54,54	0
3	MPD	C	1715	8/8	0.90	0.16	64,66,67,67	0
3	MPD	B	1724	8/8	0.91	0.14	58,60,61,61	0
3	MPD	B	1719	8/8	0.91	0.12	44,47,49,49	0
2	2HP	C	1613	5/5	0.91	0.14	49,51,52,52	0
2	2HP	B	1614	5/5	0.93	0.08	60,60,61,62	0
2	2HP	B	1615	5/5	0.93	0.18	41,41,42,42	0
2	2HP	A	1603	5/5	0.94	0.20	42,43,44,45	0
2	2HP	B	1607	5/5	0.94	0.12	45,45,48,48	0
2	2HP	B	1606	5/5	0.95	0.11	52,52,55,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	2HP	B	1609	5/5	0.96	0.12	35,35,37,38	0
2	2HP	A	1602	5/5	0.96	0.12	36,39,43,45	0
2	2HP	B	1601	5/5	0.96	0.09	37,38,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.