

Full wwPDB X-ray Structure Validation Report (i)

Dec 11, 2022 – 12:23 AM EST

PDB ID	:	4DIQ
Title	:	Crystal Structure of human NO66
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Deposited on	:	2012-01-31
Resolution	:	2.40 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Motric	Whole archive	Similar resolution		
IVIEUTIC	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$		
R _{free}	130704	3907 (2.40-2.40)		
Clashscore	141614	4398 (2.40-2.40)		
Ramachandran outliers	138981	4318 (2.40-2.40)		
Sidechain outliers	138945	4319 (2.40-2.40)		
RSRZ outliers	127900	3811 (2.40-2.40)		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	А	489	80%	13%	• 6%
1	В	489	83%	9%	• 7%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7412 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	459	Total	С	Ν	0	\mathbf{S}	0	2	0
	Л		3618	2310	634	660	14	0		
1	В	457	Total	С	Ν	0	S	0	2	0
1	D		3643	2324	639	664	16	0	3	

• Molecule 1 is a protein called Lysine-specific demethylase NO66.

Chain	Residue	Modelled	Actual	Comment	Reference
А	160	LEU	-	expression tag	UNP Q9H6W3
А	161	ARG	-	expression tag	UNP Q9H6W3
А	162	ARG	-	expression tag	UNP Q9H6W3
А	163	ARG	-	expression tag	UNP Q9H6W3
А	164	TYR	-	expression tag	UNP Q9H6W3
А	165	THR	-	expression tag	UNP Q9H6W3
А	166	MET	-	expression tag	UNP Q9H6W3
А	364	ALA	VAL	variant	UNP Q9H6W3
А	642	ALA	-	expression tag	UNP Q9H6W3
А	643	GLU	-	expression tag	UNP Q9H6W3
А	644	ASN	-	expression tag	UNP Q9H6W3
А	645	LEU	-	expression tag	UNP Q9H6W3
А	646	TYR	-	expression tag	UNP Q9H6W3
А	647	PHE	-	expression tag	UNP Q9H6W3
А	648	GLN	-	expression tag	UNP Q9H6W3
В	160	LEU	-	expression tag	UNP Q9H6W3
В	161	ARG	-	expression tag	UNP Q9H6W3
В	162	ARG	-	expression tag	UNP Q9H6W3
В	163	ARG	-	expression tag	UNP Q9H6W3
В	164	TYR	-	expression tag	UNP Q9H6W3
В	165	THR	-	expression tag	UNP Q9H6W3
В	166	MET	-	expression tag	UNP Q9H6W3
В	364	ALA	VAL	variant	UNP Q9H6W3
В	642	ALA	-	expression tag	UNP Q9H6W3
В	643	GLU	-	expression tag	UNP Q9H6W3
				Continue	d on next page

There are 30 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference		
В	644	ASN	-	expression tag	UNP Q9H6W3		
В	645	LEU	-	expression tag	UNP Q9H6W3		
В	646	TYR	-	expression tag	UNP Q9H6W3		
В	647	PHE	-	expression tag	UNP Q9H6W3		
В	648	GLN	-	expression tag	UNP Q9H6W3		

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• Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Ni 1 1	0	0
2	В	1	Total Ni 1 1	0	0

• Molecule 3 is PYRIDINE-2,4-DICARBOXYLIC ACID (three-letter code: PD2) (formula: $C_7H_5NO_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total C N O 12 7 1 4	0	0
3	В	1	Total C N O 12 7 1 4	0	0

• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	В	1	Total 5	0 4	S 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	36	$\begin{array}{cc} \text{Total} & \text{O} \\ 36 & 36 \end{array}$	0	0
5	В	84	Total O 84 84	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: Lysine-specific demethylase NO66



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	78.67Å 149.55Å 105.31Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution (Å)	29.46 - 2.40	Depositor
Resolution (A)	29.46 - 2.40	EDS
% Data completeness	99.7 (29.46-2.40)	Depositor
(in resolution range)	99.8 (29.46-2.40)	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	2.29 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
D D .	0.185 , 0.230	Depositor
n, n_{free}	0.185 , 0.231	DCC
R_{free} test set	1986 reflections (4.03%)	wwPDB-VP
Wilson B-factor $(Å^2)$	46.5	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , 45.4	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7412	wwPDB-VP
Average B, all atoms $(Å^2)$	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: PD2, SO4, NI

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).

Mal Chain		Bo	nd lengths	Bond angles		
1VIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.73	0/3718	0.85	3/5065~(0.1%)	
1	В	0.84	2/3746~(0.1%)	0.89	6/5099~(0.1%)	
All	All	0.79	2/7464~(0.0%)	0.87	9/10164~(0.1%)	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
1	В	223	TRP	CD2-CE2	6.48	1.49	1.41
1	В	309	TRP	CD2-CE2	5.29	1.47	1.41

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	487	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	В	354	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	А	234	ASP	CB-CG-OD2	6.41	124.07	118.30
1	В	201	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	В	187[A]	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	В	187[B]	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	А	456	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	В	201	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	А	231	ARG	NE-CZ-NH2	-5.04	117.78	120.30

All (9) bond angle outliers are listed below:

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	А	3618	0	3495	59	0
1	В	3643	0	3544	52	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	12	0	3	0	0
3	В	12	0	3	1	0
4	В	5	0	0	0	0
5	А	36	0	0	1	0
5	В	84	0	0	1	0
All	All	7412	0	7045	99	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 7.

All (99) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:550:MET:HE1	1:A:598:LEU:HB3	1.33	1.09
1:B:187[B]:ARG:HH11	1:B:187[B]:ARG:HG2	0.97	1.09
1:A:440:VAL:HG21	1:B:436:LEU:HD12	1.45	0.95
1:A:440:VAL:CG2	1:B:436:LEU:CD1	2.49	0.90
1:A:420:LEU:HD23	1:A:421:SER:N	1.86	0.90
1:B:187[B]:ARG:HG2	1:B:187[B]:ARG:NH1	1.76	0.89
1:B:487:ARG:HH11	1:B:487:ARG:HG3	1.41	0.83
1:A:420:LEU:HD23	1:A:420:LEU:C	2.01	0.81
1:B:487:ARG:HH11	1:B:487:ARG:CG	1.94	0.80
1:A:431:PHE:CE2	1:A:435:ILE:CD1	2.65	0.80
1:A:440:VAL:HG21	1:B:436:LEU:CD1	2.12	0.79
1:A:280:ARG:NH1	1:A:282:LEU:HD23	1.98	0.78
1:A:440:VAL:CG2	1:B:436:LEU:HD12	2.11	0.76
1:A:431:PHE:CE2	1:A:435:ILE:HD12	2.21	0.75
1:A:344:ILE:HD12	1:A:344:ILE:O	1.87	0.75
1:B:207:GLU:OE1	5:B:814:HOH:O	2.03	0.75
1:B:344:ILE:O	1:B:344:ILE:HD12	1.86	0.74
1:B:232:ARG:HD2	1:B:394:GLY:O	1.89	0.72



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Atom-1	Atom-2	Interatomic	Clash
		distance (A)	overlap (A)
1:A:232:ARG:HD2	1:A:394:GLY:O	1.89	0.71
1:B:187[B]:ARG:HH11	1:B:187[B]:ARG:CG	1.86	0.71
1:A:436:LEU:HD11	1:B:488:LEU:HD21	1.73	0.70
1:A:436:LEU:HD12	1:B:440:VAL:CG2	2.24	0.68
1:A:250:MET:HE1	1:A:298:LEU:HD21	1.77	0.66
1:A:440:VAL:CG2	1:B:436:LEU:HD11	2.25	0.65
1:A:502:ALA:HB1	1:A:557:ARG:HG2	1.79	0.65
1:A:187[A]:ARG:HG2	1:A:187[A]:ARG:HH11	1.63	0.62
1:A:232:ARG:HD3	1:A:237:TYR:CD1	2.35	0.62
1:A:420:LEU:C	1:A:420:LEU:CD2	2.67	0.61
1:B:232:ARG:HD3	1:B:237:TYR:CD1	2.37	0.60
1:B:480:LYS:HA	1:B:483:VAL:HG12	1.83	0.60
1:B:344:ILE:HD12	1:B:344:ILE:C	2.22	0.59
1:B:420:LEU:C	1:B:420:LEU:HD23	2.24	0.58
1:A:344:ILE:HD12	1:A:344:ILE:C	2.23	0.58
1:A:478:MET:O	1:A:482:ARG:HD3	2.04	0.58
1:A:187[A]:ARG:HH11	1:A:187[A]:ARG:CG	2.17	0.58
1:B:487:ARG:HG3	1:B:487:ARG:NH1	2.11	0.58
1:A:280:ARG:HH11	1:A:282:LEU:HD23	1.67	0.57
1:A:192:LEU:O	1:A:201:ARG:HD3	2.05	0.56
1:A:508:ASP:OD1	1:A:578:HIS:NE2	2.39	0.56
1:B:572:GLU:OE2	1:B:629:LYS:NZ	2.39	0.56
1:A:440:VAL:HG22	1:B:436:LEU:HD11	1.87	0.55
1:A:280:ARG:NH1	5:A:802:HOH:O	2.38	0.55
1:A:431:PHE:HE2	1:A:435:ILE:CD1	2.15	0.55
1:B:250[B]:MET:CE	1:B:304:PHE:HB2	2.36	0.55
1:B:250[B]:MET:HE3	1:B:304:PHE:CB	2.38	0.54
1:A:540:ALA:HB3	1:A:638:LEU:O	2.07	0.54
1:A:550:MET:CE	1:A:598:LEU:HB3	2.22	0.54
1:A:436:LEU:HD12	1:B:440:VAL:HG21	1.89	0.54
1:A:232:ARG:HD3	1:A:237:TYR:CG	2.43	0.53
1:A:274:THR:C	1:A:275:LEU:HD12	2.30	0.51
1:B:250[B]:MET:CE	1:B:298:LEU:HD21	2.41	0.51
1:B:232:ARG:HD3	1:B:237:TYR:CG	2.46	0.51
1:B:192:LEU:O	1:B:201:ARG:HD3	2.10	0.51
1:B:297:ARG:HD3	1:B:328:TYR:CE1	2.46	0.50
1:B:250[B]:MET:HE1	1:B:304:PHE:HB2	1.92	0.50
1:B:499:ASP:HB3	1:B:559:VAL:HG13	1.94	0.50
1:A:219:TYR:CE1	1:B:456:ARG:HD3	2.47	0.49
1:A:585:LEU:C	1:A:585:LEU:HD12	2.33	0.49
1:B:480:LYS:HA	1:B:483:VAL:CG1	2.44	0.48



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		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:633:LEU:C	1:B:633:LEU:HD12	2.34	0.47
1:A:210:ILE:O	1:A:213:MET:HB3	2.15	0.47
1:B:250[B]:MET:CE	1:B:304:PHE:CB	2.93	0.47
1:B:250[B]:MET:HE3	1:B:304:PHE:CG	2.50	0.47
1:A:354:ARG:HB2	1:A:413:VAL:HG21	1.98	0.46
1:B:358:ARG:NH2	1:B:406:GLN:NE2	2.63	0.46
1:A:553:ASP:HB2	1:A:602:TYR:CE1	2.51	0.45
1:B:448:VAL:HG22	1:B:448:VAL:O	2.16	0.45
1:A:556:ALA:O	1:A:557:ARG:HD2	2.17	0.45
1:B:187[B]:ARG:NH1	1:B:187[B]:ARG:CG	2.57	0.45
1:A:362:PRO:HD3	1:A:403:PHE:CE2	2.52	0.45
1:B:344:ILE:C	1:B:344:ILE:CD1	2.85	0.45
1:B:487:ARG:CG	1:B:487:ARG:NH1	2.60	0.44
1:B:210:ILE:O	1:B:213:MET:HB3	2.18	0.44
1:A:436:LEU:CD1	1:B:488:LEU:HD21	2.46	0.44
1:B:362:PRO:HD3	1:B:403:PHE:CE2	2.52	0.44
1:A:344:ILE:C	1:A:344:ILE:CD1	2.85	0.44
1:A:451:ARG:NH1	1:B:368:GLU:O	2.47	0.43
1:A:435:ILE:HG13	1:A:497:VAL:HG21	2.01	0.43
1:A:414:HIS:ND1	1:A:414:HIS:C	2.72	0.43
1:A:310:GLN:HA	1:A:513:VAL:HG21	2.00	0.43
1:B:585:LEU:HD12	1:B:585:LEU:C	2.39	0.43
1:B:355:LYS:HG2	1:B:407:ALA:HB1	2.01	0.43
1:A:399:PHE:HA	1:A:400:PRO:HD3	1.89	0.42
1:A:550:MET:HE1	1:A:598:LEU:CB	2.25	0.42
1:A:214:PRO:HA	1:A:215:PRO:HD3	1.94	0.42
1:B:340:HIS:CD2	3:B:702:PD2:H6	2.54	0.42
1:A:301:PRO:HG3	1:A:327:VAL:HG23	2.00	0.42
1:B:301:PRO:HG2	1:B:325:SER:OG	2.20	0.42
1:A:555:ILE:O	1:A:569:TYR:HA	2.20	0.41
1:A:250:MET:HE3	1:A:250:MET:HB3	1.84	0.41
1:A:608:VAL:HG11	1:A:620:LEU:HD23	2.01	0.41
1:B:185:LEU:CD2	1:B:241:LEU:HB2	2.50	0.41
1:A:301:PRO:HG2	1:A:325:SER:OG	2.21	0.41
1:B:210:ILE:HD12	1:B:213:MET:HG3	2.02	0.41
1:B:399:PHE:HA	1:B:400:PRO:HD3	1.89	0.41
1:A:275:LEU:HD12	1:A:275:LEU:N	2.35	0.40
1:A:187[B]:ARG:HH11	1:A:187[B]:ARG:HG3	1.87	0.40
1:A:611:LEU:HD23	1:A:611:LEU:HA	1.95	0.40
1:A:329:LEU:HD13	1:A:416:LEU:HD13	2.04	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	Perce	ntiles
1	А	457/489~(94%)	452 (99%)	5(1%)	0	100	100
1	В	456/489~(93%)	451 (99%)	5(1%)	0	100	100
All	All	913/978~(93%)	903~(99%)	10 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	А	373/416~(90%)	361~(97%)	12 (3%)	39 59
1	В	381/416~(92%)	370~(97%)	11 (3%)	42 62
All	All	754/832~(91%)	731~(97%)	23~(3%)	43 60

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

Mol	Chain	\mathbf{Res}	Type
1	А	187[A]	ARG
1	А	187[B]	ARG
1	А	188	VAL
1	А	232	ARG
1	А	260	GLN
1	А	272	ARG
1	А	277	PRO
1	А	340	HIS



Mol	Chain	Res	Type
1	А	408	GLU
1	А	414	HIS
1	А	435	ILE
1	А	482	ARG
1	В	232	ARG
1	В	250[A]	MET
1	В	250[B]	MET
1	В	260	GLN
1	В	268	ILE
1	В	272	ARG
1	В	340	HIS
1	В	408	GLU
1	В	414	HIS
1	В	487	ARG
1	В	488	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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



Mol Turo	Turne	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Dec	Tink	Bond lengths			Bond angles		
IVI01	Moi Type Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2								
3	PD2	А	701	2	12,12,12	1.10	0	16, 16, 16	2.05	6 (37%)							
3	PD2	В	702	2	12,12,12	1.91	4 (33%)	16,16,16	2.08	5 (31%)							
4	SO4	В	703	-	4,4,4	0.40	0	6,6,6	0.84	0							

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).

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	PD2	А	701	2	-	0/8/8/8	0/1/1/1
3	PD2	В	702	2	-	0/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
3	В	702	PD2	C2-C21	-5.02	1.43	1.50
3	В	702	PD2	O42-C41	2.19	1.29	1.22
3	В	702	PD2	O41-C41	-2.03	1.24	1.30
3	В	702	PD2	O22-C21	-2.01	1.24	1.30

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	701	PD2	C6-N1-C2	4.37	122.60	116.93
3	В	702	PD2	O22-C21-C2	-3.96	105.67	114.69
3	В	702	PD2	C5-C4-C3	-3.57	115.02	119.24
3	В	702	PD2	O22-C21-O21	3.47	131.05	123.35
3	В	702	PD2	C6-C5-C4	3.38	122.74	119.05
3	А	701	PD2	C5-C6-N1	-3.32	119.83	123.96
3	А	701	PD2	C3-C2-N1	-3.06	119.34	123.19
3	А	701	PD2	O21-C21-C2	2.59	126.49	121.24
3	А	701	PD2	O41-C41-C4	2.55	121.47	114.85
3	А	701	PD2	C3-C2-C21	2.21	124.33	119.57
3	В	702	PD2	C5-C6-N1	-2.05	121.41	123.96

There are no chirality outliers.

There are no torsion outliers.



There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	702	PD2	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^{th} 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	L>2	$OWAB(Å^2)$	Q<0.9
1	А	459/489~(93%)	-0.02	21 (4%) 32	2 31	27, 54, 90, 124	0
1	В	457/489~(93%)	-0.25	11 (2%) 59) 57	26, 40, 74, 104	0
All	All	916/978~(93%)	-0.13	32 (3%) 44	43	26, 48, 85, 124	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	640	LEU	3.9
1	А	639	ALA	3.7
1	А	532	ALA	3.6
1	В	468	ASP	3.5
1	А	530	TRP	3.3
1	А	578	HIS	3.2
1	А	615	SER	3.1
1	В	418	LEU	3.1
1	А	419	THR	3.0
1	А	577	TYR	2.9
1	В	416	LEU	2.8
1	А	543	THR	2.6
1	А	381	ASP	2.6
1	А	411	ASP	2.6
1	В	419	THR	2.6
1	А	616	VAL	2.5
1	А	420	LEU	2.5
1	В	563	GLY	2.5
1	В	420	LEU	2.5
1	В	536	VAL	2.5
1	А	555	ILE	2.4
1	А	349	LEU	2.3
1	A	539	GLY	2.2
1	В	562	GLY	2.2



Mol	Chain	Res	Type	RSRZ
1	В	417	HIS	2.2
1	А	413	VAL	2.1
1	А	609	GLY	2.1
1	В	328	TYR	2.1
1	А	579	LEU	2.1
1	В	327	VAL	2.1
1	А	516	ASP	2.0
1	А	418	LEU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides 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^{th} 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	${f B} ext{-factors}({ m \AA}^2)$	Q < 0.9
4	SO4	В	703	5/5	0.90	0.20	59,72,116,161	0
3	PD2	А	701	12/12	0.97	0.22	32,46,66,79	0
3	PD2	В	702	12/12	0.98	0.20	14,23,32,42	0
2	NI	А	700	1/1	0.99	0.09	49,49,49,49	0
2	NI	В	701	1/1	1.00	0.10	33,33,33,33	0

6.5 Other polymers (i)

There are no such residues in this entry.

