



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 12:48 PM GMT

PDB ID : 4JH0  
Title : Crystal structure of dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2) (DPP-IV-WT) complex with bms-767778 AKA 2-(3-(aminomethyl)-4-(2,4-dichlorophenyl)-2-methyl-5-oxo-5,7-dihydro-6h-pyrrolo[3,4-b]pyridin-6-yl)-n,n-dimethylacetamide  
Authors : Klei, H.E.  
Deposited on : 2013-03-04  
Resolution : 2.35 Å(reported)

This is a full wwPDB validation 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 <http://wwpdb.org/ValidationPDFNotes.html>

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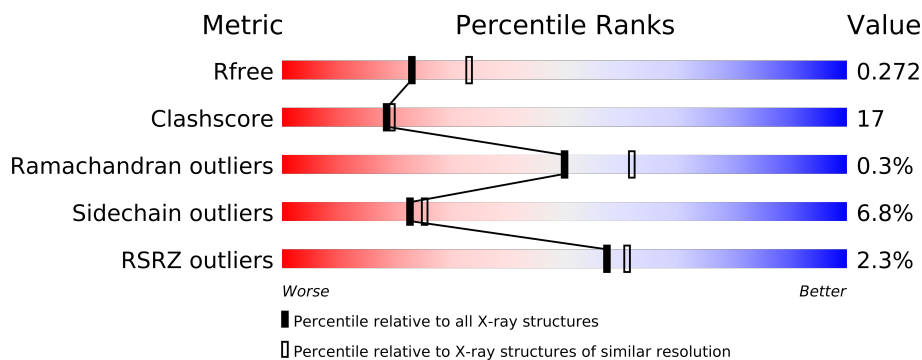
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
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) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.35 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))
$R_{free}$	66092	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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  $\geq 3$ , 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	728	
1	B	728	

## 2 Entry composition i

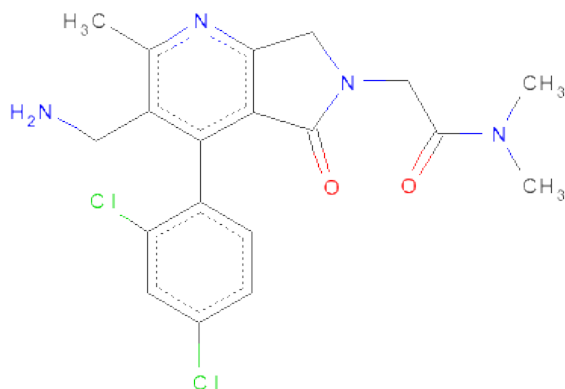
There are 3 unique types of molecules in this entry. The entry contains 12054 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			
1	B	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			

- Molecule 2 is 2-[3-(AMINOMETHYL)-4-(2,4-DICHLOROPHENYL)-2-METHYL-5-OXO-5,7-DIHYDRO-6H-PYRROLO[3,4-B]PYRIDIN-6-YL]-N,N-DIMETHYLACETAMIDE (three-letter code: 1MD) (formula: C<sub>19</sub>H<sub>20</sub>Cl<sub>2</sub>N<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			27	19	2	4	2		
2	B	1	Total	C	Cl	N	O	0	0
			27	19	2	4	2		

- Molecule 3 is water.

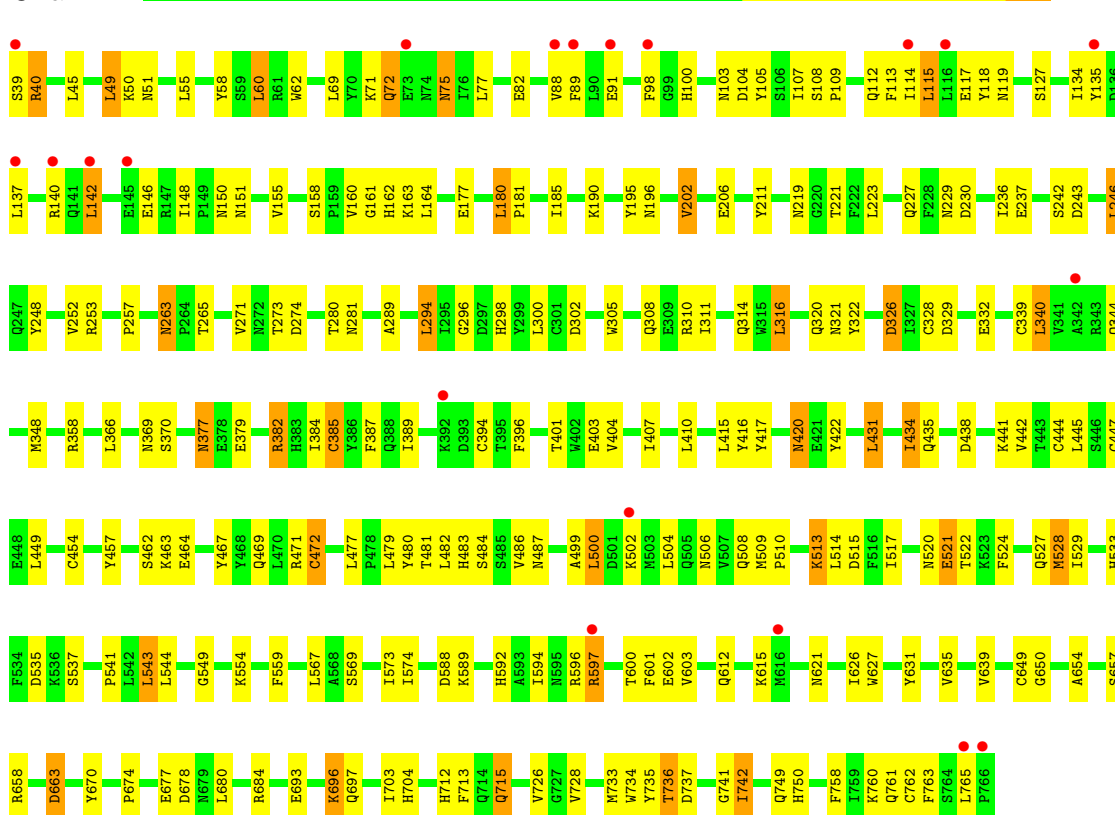
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	34	Total 34	O 34	0	0
3	B	40	Total 40	O 40	0	0

### 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: Dipeptidyl peptidase 4

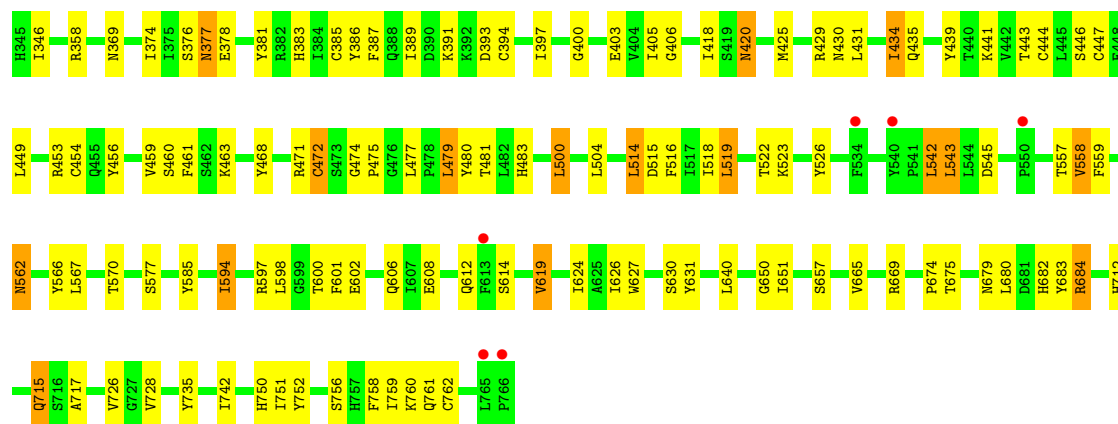
Chain A:



#### • Molecule 1: Dipeptidyl peptidase 4

Chain B:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.31Å 67.11Å 423.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.95 – 2.35 47.95 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.7 (47.95-2.35) 91.8 (47.95-2.35)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 2.34Å)	Xtriage
Refinement program	CNX 2005	Depositor
R, $R_{free}$	0.243 , 0.272 0.240 , 0.272	Depositor DCC
$R_{free}$ test set	1546 reflections (2.17%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.1	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 18.8	EDS
Estimated twinning fraction	0.075 for k,h,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 72726 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12054	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: 1MD

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	0.37	0/6135	0.53	0/8344
1	B	0.35	0/6135	0.52	0/8344
All	All	0.36	0/12270	0.53	0/16688

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	110	ASP	Peptide

### 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	5963	0	5695	209	0
1	B	5963	0	5695	187	0
2	A	27	0	20	0	0
2	B	27	0	20	0	0
3	A	34	0	0	6	0
3	B	40	0	0	9	0
All	All	12054	0	11430	386	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 17.

All (386) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:340:LEU:H	1:A:340:LEU:HD12	1.25	0.99
1:A:434:ILE:HD13	1:A:434:ILE:H	1.35	0.92
1:A:658:ARG:NH2	1:A:684:ARG:HE	1.71	0.88
1:B:328:CYS:HG	1:B:339:CYS:HG	1.12	0.88
1:A:454:CYS:HG	1:A:472:CYS:HG	1.00	0.86
1:A:431:LEU:HD13	1:A:445:LEU:HD12	1.58	0.86
1:A:444:CYS:HG	1:A:447:CYS:HG	0.85	0.85
1:B:403:GLU:H	1:B:420:ASN:HD21	1.26	0.83
1:A:253:ARG:HH22	1:B:253:ARG:NH1	1.80	0.80
1:A:649:CYS:HG	1:A:762:CYS:HG	0.81	0.79
1:B:163:LYS:HD3	1:B:273:THR:HG21	1.63	0.78
1:B:320:GLN:OE1	1:B:669:ARG:HD3	1.84	0.78
1:A:597:ARG:HD3	1:A:600:THR:HG21	1.65	0.78
1:A:434:ILE:HG22	1:A:442:VAL:HG22	1.66	0.77
1:A:693:GLU:O	1:A:696:LYS:HG3	1.85	0.76
1:B:331:ASP:HB3	1:B:334:SER:HB3	1.68	0.76
1:A:567:LEU:HD22	1:A:573:ILE:HD12	1.65	0.76
1:A:377:ASN:C	1:A:377:ASN:HD22	1.90	0.75
1:A:415:LEU:HB3	1:A:434:ILE:HD11	1.67	0.74
1:A:89:PHE:HE2	1:A:107:ILE:HD13	1.51	0.73
1:A:508:GLN:HE21	1:A:533:HIS:HE1	1.37	0.72
1:A:658:ARG:HH21	1:A:684:ARG:HE	1.38	0.72
1:B:726:VAL:HG13	1:B:728:VAL:HG23	1.71	0.71
1:A:177:GLU:HB2	1:A:180:LEU:HB2	1.72	0.70
1:A:750:HIS:HE1	1:B:728:VAL:O	1.75	0.70
1:A:734:TRP:HE1	1:A:736:THR:HG22	1.57	0.69
1:B:139:LYS:O	1:B:140:ARG:HG3	1.91	0.69
1:A:735:TYR:OH	1:A:750:HIS:HD2	1.76	0.69
1:A:385:CYS:HG	1:A:394:CYS:HG	1.39	0.69
1:A:734:TRP:NE1	1:A:736:THR:HG22	2.08	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:508:GLN:HE21	1:A:533:HIS:CE1	2.11	0.69
1:A:328:CYS:HG	1:A:339:CYS:HG	0.68	0.68
1:B:562:ASN:HD22	1:B:562:ASN:C	1.95	0.68
1:A:221:THR:O	1:A:273:THR:HB	1.94	0.68
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.77	0.67
1:B:306:ALA:HB3	1:B:310:ARG:HG2	1.75	0.67
1:A:658:ARG:NH2	1:A:684:ARG:NE	2.40	0.67
1:A:736:THR:HG21	1:B:717:ALA:O	1.96	0.66
1:B:377:ASN:HD22	1:B:377:ASN:C	1.97	0.66
1:A:696:LYS:HD2	1:A:697:GLN:HG3	1.79	0.65
1:B:159:PRO:HB2	3:B:929:HOH:O	1.96	0.65
1:A:736:THR:O	1:A:737:ASP:HB2	1.95	0.65
1:A:280:THR:HG22	1:A:281:ASN:O	1.95	0.65
1:A:55:LEU:HD21	1:A:559:PHE:HE2	1.60	0.64
1:B:110:ASP:HB2	3:B:904:HOH:O	1.96	0.64
1:A:596:ARG:NH2	1:A:678:ASP:OD1	2.31	0.64
1:B:218:PRO:HA	3:B:929:HOH:O	1.97	0.64
1:A:340:LEU:H	1:A:340:LEU:CD1	2.05	0.63
1:B:543:LEU:HD21	1:B:627:TRP:HD1	1.61	0.63
1:A:657:SER:H	1:A:715:GLN:NE2	1.96	0.63
1:A:403:GLU:H	1:A:420:ASN:HD21	1.45	0.63
1:A:358:ARG:HB3	1:A:358:ARG:NH1	2.13	0.63
1:B:231:THR:HG22	1:B:232:GLU:HG2	1.80	0.63
1:A:734:TRP:CD1	1:A:736:THR:HG22	2.33	0.63
1:A:40:ARG:HA	1:A:40:ARG:HE	1.65	0.62
1:A:206:GLU:OE1	1:A:206:GLU:HA	2.00	0.62
1:A:305:TRP:CZ3	1:A:311:ILE:HG12	2.35	0.62
1:B:657:SER:H	1:B:715:GLN:NE2	1.98	0.62
1:B:477:LEU:HD22	1:B:500:LEU:HD13	1.82	0.62
1:B:435:GLN:HE22	1:B:441:LYS:HD2	1.64	0.61
1:B:453:ARG:O	1:B:475:PRO:HD2	1.99	0.61
1:A:758:PHE:O	1:A:761:GLN:HG3	2.00	0.61
1:B:726:VAL:O	1:B:726:VAL:HG22	2.00	0.61
1:A:340:LEU:N	1:A:340:LEU:HD12	2.08	0.61
1:B:459:VAL:HG22	1:B:460:SER:N	2.16	0.61
1:A:219:ASN:HB2	1:A:308:GLN:OE1	2.00	0.61
1:A:658:ARG:HH21	1:A:684:ARG:NE	1.97	0.61
1:A:289:ALA:HB3	1:A:294:LEU:HD13	1.83	0.61
1:B:420:ASN:C	1:B:420:ASN:HD22	2.04	0.60
1:A:382:ARG:H	1:A:403:GLU:HG2	1.67	0.60
1:A:302:ASP:HB3	1:A:314:GLN:HB2	1.83	0.60
1:B:137:LEU:C	1:B:139:LYS:H	2.04	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:471:ARG:HG3	1:A:480:TYR:CE2	2.36	0.60
1:A:635:VAL:O	1:A:639:VAL:HG23	2.02	0.60
1:B:63:ILE:HD11	1:B:69:LEU:HD12	1.84	0.59
1:B:369:ASN:O	1:B:389:ILE:HG12	2.03	0.59
1:B:461:PHE:CD1	1:B:468:TYR:HB3	2.37	0.59
1:B:403:GLU:H	1:B:420:ASN:ND2	1.97	0.58
1:B:386:TYR:HB2	1:B:397:ILE:HD11	1.85	0.58
1:A:508:GLN:NE2	1:A:533:HIS:HE1	2.01	0.58
1:A:316:LEU:HD22	1:A:320:GLN:HG2	1.86	0.58
1:A:510:PRO:HD3	1:A:569:SER:HB2	1.85	0.57
1:A:529:ILE:HD12	1:A:529:ILE:N	2.19	0.57
1:B:111:GLY:O	1:B:137:LEU:HD12	2.05	0.57
1:A:358:ARG:HH11	1:A:358:ARG:HB3	1.70	0.57
1:A:481:THR:OG1	1:A:483:HIS:HE1	1.87	0.57
1:B:627:TRP:HB2	1:B:651:ILE:HB	1.87	0.57
1:A:142:LEU:HD12	1:A:142:LEU:H	1.70	0.57
1:B:341:VAL:HG13	1:B:344:GLN:NE2	2.20	0.57
1:A:434:ILE:HD13	1:A:434:ILE:N	2.13	0.56
1:A:499:ALA:O	1:A:502:LYS:HG3	2.05	0.56
1:B:237:GLU:OE2	1:B:253:ARG:HD3	2.05	0.56
1:A:696:LYS:HB3	1:A:728:VAL:HG22	1.88	0.56
1:A:40:ARG:NE	1:A:40:ARG:HA	2.21	0.56
1:A:384:ILE:HG13	1:A:404:VAL:HG21	1.88	0.56
1:A:377:ASN:ND2	1:A:377:ASN:C	2.58	0.56
1:A:520:ASN:O	1:A:521:GLU:HG3	2.07	0.55
1:B:288:THR:HG22	1:B:289:ALA:O	2.06	0.55
1:A:370:SER:HB2	1:A:387:PHE:O	2.07	0.55
1:B:42:THR:HG23	1:B:570:THR:OG1	2.06	0.55
1:B:42:THR:CG2	1:B:570:THR:OG1	2.55	0.55
1:B:474:GLY:HA3	1:B:558:VAL:HA	1.88	0.55
1:A:477:LEU:HD22	1:A:500:LEU:HD13	1.87	0.55
1:A:596:ARG:HA	1:A:670:TYR:O	2.07	0.54
1:A:60:LEU:HD13	1:A:60:LEU:H	1.71	0.54
1:B:500:LEU:CD2	1:B:504:LEU:HG	2.38	0.54
1:B:142:LEU:HD12	1:B:142:LEU:H	1.72	0.54
1:B:518:ILE:O	1:B:519:LEU:HD13	2.08	0.54
1:B:179:ASN:OD1	1:B:180:LEU:HD13	2.06	0.54
1:A:326:ASP:OD1	1:A:344:GLN:HG2	2.08	0.54
1:B:542:LEU:HD23	1:B:624:ILE:HG23	1.90	0.54
1:A:486:VAL:HG23	1:A:487:ASN:N	2.22	0.54
1:A:434:ILE:H	1:A:434:ILE:CD1	2.14	0.53
1:A:435:GLN:NE2	1:A:441:LYS:HD3	2.22	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:387:PHE:CD2	1:A:394:CYS:HB3	2.43	0.53
1:B:562:ASN:ND2	1:B:562:ASN:C	2.62	0.53
1:A:253:ARG:HH12	1:B:253:ARG:HH12	1.56	0.53
1:B:57:LEU:N	1:B:57:LEU:HD12	2.24	0.53
1:A:296:GLY:O	1:A:298:HIS:HD2	1.92	0.53
1:A:377:ASN:ND2	1:A:379:GLU:H	2.07	0.53
1:A:602:GLU:HG2	1:A:603:VAL:N	2.24	0.53
1:A:253:ARG:HH22	1:B:253:ARG:HH12	1.57	0.53
1:A:195:TYR:O	1:A:227:GLN:HA	2.09	0.53
1:B:514:LEU:HD12	1:B:557:THR:HG22	1.91	0.53
1:A:60:LEU:O	1:A:60:LEU:HD22	2.08	0.52
1:A:60:LEU:N	1:A:60:LEU:HD13	2.24	0.52
1:B:127:SER:HA	1:B:211:TYR:CD2	2.44	0.52
1:B:296:GLY:O	1:B:298:HIS:HD2	1.93	0.52
1:B:330:TYR:HB2	1:B:337:TRP:CH2	2.45	0.52
1:A:55:LEU:HD23	1:A:500:LEU:CD1	2.39	0.52
1:B:429:ARG:NE	3:B:911:HOH:O	2.43	0.52
1:A:127:SER:HB3	1:A:211:TYR:CD1	2.45	0.52
1:A:146:GLU:OE2	1:A:181:PRO:HG3	2.09	0.52
1:B:55:LEU:HD23	1:B:500:LEU:HD12	1.92	0.52
1:A:594:ILE:CD1	1:A:601:PHE:HB2	2.39	0.52
1:B:516:PHE:CE1	1:B:523:LYS:HE2	2.46	0.51
1:B:377:ASN:HD21	1:B:381:TYR:H	1.58	0.51
1:A:486:VAL:HG23	1:A:487:ASN:H	1.76	0.51
1:B:600:THR:OG1	1:B:601:PHE:N	2.43	0.51
1:B:331:ASP:CB	1:B:334:SER:HB3	2.39	0.51
1:A:221:THR:HG23	1:A:274:ASP:OD2	2.10	0.51
1:A:58:TYR:HD1	1:A:60:LEU:HD12	1.76	0.51
1:A:741:GLY:O	1:A:742:ILE:C	2.48	0.51
1:A:535:ASP:OD1	1:A:537:SER:HB3	2.09	0.51
1:B:418:ILE:HD13	1:B:431:LEU:HA	1.92	0.51
1:A:726:VAL:HG22	1:A:726:VAL:O	2.11	0.51
1:B:481:THR:OG1	1:B:483:HIS:HE1	1.94	0.51
1:B:680:LEU:HD13	1:B:680:LEU:C	2.31	0.51
1:A:253:ARG:HH22	1:B:253:ARG:HH11	1.54	0.51
1:A:196:ASN:OD1	1:A:227:GLN:HG3	2.11	0.51
1:B:751:ILE:HG23	1:B:752:TYR:N	2.25	0.50
1:B:219:ASN:ND2	3:B:934:HOH:O	2.44	0.50
1:A:89:PHE:HE2	1:A:107:ILE:CD1	2.21	0.50
1:A:242:SER:OG	1:A:243:ASP:N	2.44	0.50
1:B:459:VAL:HG22	1:B:460:SER:H	1.75	0.50
1:B:341:VAL:HA	1:B:344:GLN:HG3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:219:ASN:N	1:B:308:GLN:OE1	2.42	0.50
1:A:242:SER:HB3	1:A:246:LEU:HD12	1.93	0.49
1:A:50:LYS:O	1:A:51:ASN:HB2	2.12	0.49
1:A:88:VAL:HG21	1:A:91:GLU:HG3	1.94	0.49
1:B:597:ARG:HA	1:B:682:HIS:CE1	2.47	0.49
1:B:640:LEU:HD11	1:B:650:GLY:CA	2.42	0.49
1:A:369:ASN:O	1:A:389:ILE:HG12	2.12	0.49
1:A:431:LEU:CD1	1:A:445:LEU:HD12	2.37	0.49
1:B:675:THR:C	1:B:680:LEU:HB2	2.33	0.49
1:A:454:CYS:CB	1:A:472:CYS:HG	2.24	0.49
1:B:434:ILE:O	1:B:434:ILE:HG23	2.12	0.49
1:B:200:ASP:OD2	1:B:264:PRO:HG3	2.13	0.49
1:A:71:LYS:HG3	1:A:71:LYS:O	2.11	0.49
1:A:109:PRO:CB	1:A:160:VAL:HA	2.42	0.49
1:A:734:TRP:HE1	1:A:736:THR:CG2	2.25	0.49
1:B:756:SER:O	1:B:760:LYS:HG3	2.12	0.49
1:A:517:ILE:HD12	1:A:612:GLN:HG3	1.95	0.49
1:B:657:SER:H	1:B:715:GLN:HE21	1.60	0.49
1:B:58:TYR:HD1	1:B:60:LEU:HD12	1.77	0.49
1:A:543:LEU:HD12	1:A:567:LEU:CD1	2.43	0.48
1:B:434:ILE:HD11	1:B:439:TYR:HA	1.95	0.48
1:A:112:GLN:O	1:A:137:LEU:HB2	2.13	0.48
1:B:229:ASN:ND2	3:B:901:HOH:O	2.39	0.48
1:B:377:ASN:C	1:B:377:ASN:ND2	2.65	0.48
1:A:457:TYR:HA	1:A:471:ARG:O	2.14	0.48
1:A:69:LEU:HD13	1:A:107:ILE:HD12	1.96	0.48
1:A:160:VAL:HG22	1:A:161:GLY:N	2.29	0.48
1:B:627:TRP:HA	1:B:651:ILE:O	2.13	0.48
1:A:529:ILE:N	1:A:529:ILE:CD1	2.76	0.48
1:A:522:THR:N	3:A:931:HOH:O	2.43	0.48
1:B:236:ILE:HD12	1:B:712:HIS:CD2	2.49	0.48
1:B:191:GLU:O	1:B:192:ASP:HB2	2.13	0.48
1:B:155:VAL:O	1:B:156:THR:HG23	2.13	0.48
1:A:109:PRO:HD2	1:A:161:GLY:O	2.14	0.47
1:B:299:TYR:CZ	1:B:665:VAL:HG22	2.49	0.47
1:A:98:PHE:CE2	1:A:100:HIS:HB2	2.49	0.47
1:B:177:GLU:CB	1:B:180:LEU:HD22	2.44	0.47
1:A:596:ARG:N	1:A:670:TYR:O	2.47	0.47
1:A:55:LEU:HD23	1:A:500:LEU:HD12	1.95	0.47
1:B:543:LEU:HD21	1:B:627:TRP:CD1	2.44	0.47
1:B:651:ILE:HD11	1:B:759:ILE:HD13	1.96	0.47
1:A:703:ILE:HA	1:A:733:MET:O	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:594:ILE:HD11	1:B:602:GLU:H	1.79	0.47
1:B:154:TRP:CE2	1:B:212:SER:HB2	2.49	0.47
1:A:543:LEU:HD12	1:A:567:LEU:HD13	1.97	0.47
1:B:735:TYR:OH	1:B:750:HIS:HD2	1.98	0.47
1:A:69:LEU:CD1	1:A:107:ILE:HD12	2.45	0.47
1:A:506:ASN:HD22	1:A:506:ASN:N	2.12	0.47
1:B:518:ILE:C	1:B:519:LEU:HD13	2.35	0.47
1:B:479:LEU:HD22	1:B:480:TYR:N	2.30	0.47
1:A:115:LEU:HD11	1:A:155:VAL:HG11	1.97	0.47
1:A:420:ASN:C	1:A:420:ASN:HD22	2.18	0.47
1:B:434:ILE:C	1:B:434:ILE:HD13	2.34	0.47
1:A:58:TYR:CD1	1:A:60:LEU:HD12	2.50	0.47
1:B:300:LEU:HD13	1:B:300:LEU:C	2.35	0.47
1:A:513:LYS:HE2	1:A:515:ASP:HB2	1.97	0.47
1:B:235:LEU:HD23	1:B:255:PRO:N	2.30	0.47
1:A:98:PHE:HD2	1:A:100:HIS:O	1.97	0.46
1:B:305:TRP:CZ3	1:B:311:ILE:HG12	2.50	0.46
1:B:377:ASN:ND2	1:B:381:TYR:H	2.13	0.46
1:B:324:VAL:HG22	1:B:346:ILE:HG12	1.98	0.46
1:A:103:ASN:HB3	1:A:117:GLU:O	2.15	0.46
1:A:39:SER:HB2	1:A:508:GLN:HG3	1.95	0.46
1:A:219:ASN:HB2	3:A:915:HOH:O	2.14	0.46
1:A:407:ILE:HG23	1:A:415:LEU:HD21	1.98	0.46
1:B:137:LEU:C	1:B:139:LYS:N	2.68	0.46
1:B:49:LEU:HA	1:B:49:LEU:HD12	1.72	0.46
1:B:89:PHE:CE2	1:B:107:ILE:HD13	2.50	0.46
1:A:573:ILE:HD11	1:A:765:LEU:CD1	2.46	0.46
1:A:104:ASP:OD1	1:A:105:TYR:N	2.47	0.46
1:B:444:CYS:HG	1:B:447:CYS:HG	0.53	0.46
1:A:377:ASN:HB3	1:A:396:PHE:CE1	2.51	0.46
1:A:592:HIS:HE1	3:A:929:HOH:O	1.98	0.45
1:B:95:PHE:C	1:B:97:GLU:N	2.70	0.45
1:B:454:CYS:CB	1:B:472:CYS:HG	2.29	0.45
1:B:177:GLU:HB2	1:B:180:LEU:HD22	1.98	0.45
1:B:429:ARG:NH1	1:B:456:TYR:OH	2.50	0.45
1:A:612:GLN:O	1:A:615:LYS:HB2	2.17	0.45
1:B:269:PHE:CE1	1:B:286:GLN:HB2	2.52	0.45
1:B:387:PHE:CD2	1:B:394:CYS:HB3	2.51	0.45
1:A:221:THR:HG23	1:A:274:ASP:CG	2.36	0.45
1:B:453:ARG:C	1:B:475:PRO:HD2	2.37	0.45
1:A:520:ASN:N	3:A:931:HOH:O	2.49	0.45
1:B:316:LEU:HD12	1:B:323:SER:HB3	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:405:ILE:HG12	1:B:429:ARG:NE	2.32	0.45
1:A:202:VAL:HG22	1:A:257:PRO:HD2	1.98	0.45
1:B:289:ALA:HB2	1:B:315:TRP:CH2	2.51	0.45
1:B:61:ARG:O	1:B:61:ARG:HG3	2.16	0.45
1:B:374:ILE:HD11	1:B:406:GLY:HA2	1.98	0.45
1:A:434:ILE:N	1:A:434:ILE:CD1	2.79	0.45
1:A:422:TYR:CD1	1:A:447:CYS:SG	3.10	0.45
1:A:588:ASP:HB3	1:A:592:HIS:CD2	2.52	0.45
1:B:751:ILE:CG2	1:B:752:TYR:N	2.80	0.45
1:A:45:LEU:HG	1:A:49:LEU:HD22	1.99	0.45
1:A:321:ASN:O	1:A:348:MET:HA	2.17	0.45
1:B:614:SER:HA	1:B:619:VAL:CG2	2.46	0.45
1:A:158:SER:OG	1:A:163:LYS:HB2	2.17	0.44
1:A:463:LYS:O	1:A:464:GLU:HB2	2.17	0.44
1:A:72:GLN:HB2	1:A:77:LEU:HD22	1.99	0.44
1:A:40:ARG:CA	1:A:40:ARG:HE	2.29	0.44
1:B:434:ILE:HD11	1:B:439:TYR:HD1	1.82	0.44
1:B:143:ILE:HG13	1:B:143:ILE:O	2.18	0.44
1:A:554:LYS:HE2	1:A:554:LYS:HB3	1.69	0.44
1:A:263:ASN:HA	1:A:263:ASN:HD22	1.61	0.44
1:A:60:LEU:HD11	1:A:469:GLN:NE2	2.32	0.44
1:B:471:ARG:HD3	1:B:480:TYR:HE2	1.82	0.44
1:A:134:ILE:HD11	1:A:148:ILE:HD11	2.00	0.44
1:A:415:LEU:HD23	1:A:416:TYR:N	2.32	0.44
1:B:63:ILE:HD11	1:B:69:LEU:CD1	2.47	0.44
1:B:142:LEU:HD12	1:B:142:LEU:N	2.33	0.44
1:A:109:PRO:HB2	1:A:160:VAL:HA	2.00	0.44
1:A:703:ILE:HG12	1:A:733:MET:HB3	1.99	0.44
1:B:95:PHE:C	1:B:97:GLU:H	2.19	0.44
1:B:170:ASN:O	1:B:196:ASN:HB2	2.18	0.44
1:A:177:GLU:HG3	1:A:180:LEU:HD22	1.99	0.43
1:B:680:LEU:O	1:B:683:TYR:HB2	2.18	0.43
1:A:366:LEU:HD23	1:A:366:LEU:HA	1.88	0.43
1:B:651:ILE:CD1	1:B:759:ILE:HD13	2.48	0.43
1:A:49:LEU:HG	1:A:749:GLN:HG2	2.01	0.43
1:B:184:ARG:HD3	1:B:187:TRP:CH2	2.52	0.43
1:B:403:GLU:OE1	1:B:585:TYR:HA	2.18	0.43
1:A:377:ASN:HB3	1:A:396:PHE:CZ	2.53	0.43
1:B:208:PHE:HZ	1:B:300:LEU:HD12	1.83	0.43
1:A:401:THR:HG22	1:A:401:THR:O	2.18	0.43
1:A:434:ILE:CG2	1:A:442:VAL:HG22	2.42	0.43
1:B:759:ILE:HG22	1:B:760:LYS:N	2.32	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:513:LYS:O	1:A:527:GLN:HA	2.19	0.43
1:A:185:ILE:HD12	1:A:271:VAL:HG11	2.00	0.43
1:B:55:LEU:HD21	1:B:559:PHE:CE2	2.54	0.43
1:A:549:GLY:HA2	1:A:631:TYR:CE1	2.53	0.43
1:A:541:PRO:HB2	1:A:763:PHE:CE2	2.54	0.43
1:B:109:PRO:HG2	1:B:158:SER:O	2.18	0.43
1:A:654:ALA:HA	1:A:704:HIS:ND1	2.34	0.43
1:B:680:LEU:HD13	1:B:684:ARG:HD2	2.01	0.43
1:A:105:TYR:HA	1:A:115:LEU:O	2.18	0.43
1:A:107:ILE:HG12	1:A:114:ILE:HD12	2.01	0.43
1:B:110:ASP:O	1:B:112:GLN:HG3	2.19	0.43
1:B:742:ILE:HG22	1:B:742:ILE:O	2.18	0.43
1:B:64:SER:HA	1:B:463:LYS:HD2	2.00	0.43
1:A:89:PHE:CE2	1:A:107:ILE:HD13	2.42	0.43
1:A:180:LEU:HD12	1:A:180:LEU:HA	1.73	0.43
1:B:459:VAL:CG2	1:B:460:SER:N	2.81	0.43
1:B:327:ILE:O	1:B:327:ILE:HG22	2.19	0.43
1:A:567:LEU:CD2	1:A:573:ILE:HD12	2.42	0.42
1:B:137:LEU:O	1:B:139:LYS:N	2.52	0.42
1:B:306:ALA:CB	1:B:310:ARG:HG2	2.47	0.42
1:B:397:ILE:HG23	1:B:439:TYR:CD1	2.54	0.42
1:A:508:GLN:NE2	1:A:533:HIS:CE1	2.81	0.42
1:A:522:THR:HB	1:A:524:PHE:CE2	2.55	0.42
1:B:471:ARG:HD3	1:B:480:TYR:CE2	2.54	0.42
1:B:545:ASP:OD1	1:B:545:ASP:C	2.57	0.42
1:A:417:TYR:HE1	1:A:434:ILE:HG23	1.84	0.42
1:B:446:SER:HA	1:B:449:LEU:CD1	2.49	0.42
1:A:113:PHE:HE2	1:A:162:HIS:ND1	2.17	0.42
1:A:504:LEU:HD22	1:A:509:MET:SD	2.60	0.42
1:B:102:ILE:HD13	1:B:116:LEU:HD22	2.01	0.42
1:A:712:HIS:O	1:A:713:PHE:C	2.58	0.42
1:A:382:ARG:HH11	1:A:382:ARG:HG2	1.84	0.42
1:B:715:GLN:HB3	1:B:715:GLN:HE21	1.66	0.42
1:B:289:ALA:HB2	1:B:315:TRP:CZ3	2.55	0.42
1:A:236:ILE:HG12	1:A:712:HIS:CE1	2.54	0.42
1:B:223:LEU:HD23	1:B:223:LEU:HA	1.88	0.42
1:B:276:LEU:HD23	1:B:282:ALA:HB2	2.02	0.42
1:B:429:ARG:NH2	3:B:911:HOH:O	2.53	0.42
1:B:236:ILE:HD13	1:B:238:TYR:HD1	1.85	0.42
1:A:62:TRP:CG	1:A:462:SER:HA	2.55	0.42
1:B:55:LEU:HD21	1:B:559:PHE:HE2	1.85	0.42
1:B:602:GLU:O	1:B:606:GLN:HG2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:71:LYS:HD3	1:B:105:TYR:HE2	1.84	0.42
1:B:522:THR:HG22	1:B:523:LYS:N	2.34	0.42
1:A:150:ASN:O	1:A:151:ASN:HB2	2.19	0.42
1:A:237:GLU:HA	1:A:252:VAL:O	2.20	0.42
1:A:39:SER:HB3	1:A:506:ASN:O	2.20	0.41
1:B:614:SER:HA	1:B:619:VAL:HG22	2.01	0.41
1:A:229:ASN:HB3	1:A:265:THR:OG1	2.19	0.41
1:B:608:GLU:O	1:B:612:GLN:HG2	2.20	0.41
1:A:573:ILE:HD11	1:A:765:LEU:HD11	2.02	0.41
1:B:626:ILE:O	1:B:650:GLY:HA2	2.20	0.41
1:B:461:PHE:CE1	1:B:468:TYR:HB3	2.55	0.41
1:B:418:ILE:HA	1:B:430:ASN:O	2.21	0.41
1:A:82:GLU:HB2	1:A:467:TYR:OH	2.21	0.41
1:A:528:MET:HG2	1:A:574:ILE:CG2	2.50	0.41
1:B:543:LEU:HD12	1:B:567:LEU:HD13	2.02	0.41
1:B:425:MET:CE	1:B:514:LEU:HD13	2.50	0.41
1:A:528:MET:HB2	1:A:528:MET:HE2	1.72	0.41
1:B:62:TRP:CE3	1:B:68:TYR:HB3	2.55	0.41
1:B:758:PHE:O	1:B:761:GLN:HG3	2.20	0.41
1:A:594:ILE:HG23	1:A:594:ILE:O	2.20	0.41
1:A:246:LEU:HD23	1:A:246:LEU:HA	1.77	0.41
1:B:334:SER:C	1:B:336:ARG:H	2.24	0.41
1:B:358:ARG:NH2	3:B:912:HOH:O	2.53	0.41
1:B:515:ASP:HB3	1:B:526:TYR:CZ	2.56	0.41
1:B:383:HIS:HE1	1:B:400:GLY:O	2.04	0.41
1:B:263:ASN:HD22	1:B:263:ASN:HA	1.63	0.41
1:B:304:THR:HB	1:B:312:SER:OG	2.20	0.41
1:A:219:ASN:ND2	3:A:908:HOH:O	2.54	0.41
1:B:58:TYR:CD1	1:B:60:LEU:HD12	2.55	0.41
1:A:118:TYR:O	1:A:119:ASN:HB2	2.21	0.41
1:A:253:ARG:NH2	1:B:253:ARG:NH1	2.59	0.41
1:B:454:CYS:HB3	1:B:472:CYS:HB2	2.03	0.41
1:B:598:LEU:O	1:B:682:HIS:HE1	2.04	0.41
1:A:150:ASN:ND2	3:A:919:HOH:O	2.46	0.41
1:A:449:LEU:HA	1:A:449:LEU:HD23	1.75	0.41
1:B:118:TYR:O	1:B:119:ASN:HB2	2.21	0.41
1:A:310:ARG:HG3	1:A:329:ASP:OD1	2.21	0.41
1:A:253:ARG:NH1	1:B:253:ARG:HH12	2.19	0.41
1:B:110:ASP:O	1:B:112:GLN:N	2.48	0.41
1:B:393:ASP:HB3	1:B:394:CYS:H	1.74	0.40
1:A:163:LYS:HZ2	1:A:273:THR:HG21	1.86	0.40
1:A:206:GLU:OE2	1:A:663:ASP:OD2	2.39	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:674:PRO:O	1:B:680:LEU:HD23	2.21	0.40
1:A:248:TYR:CZ	1:B:234:PRO:HB2	2.56	0.40
1:A:626:ILE:O	1:A:650:GLY:CA	2.69	0.40
1:A:114:ILE:CG2	1:A:135:TYR:HB3	2.51	0.40
1:A:39:SER:O	1:A:40:ARG:HB2	2.21	0.40
1:B:429:ARG:CZ	3:B:911:HOH:O	2.69	0.40
1:A:592:HIS:C	1:A:594:ILE:H	2.24	0.40
1:A:728:VAL:O	1:B:750:HIS:HE1	2.03	0.40
1:A:654:ALA:HA	1:A:704:HIS:CE1	2.57	0.40
1:B:248:TYR:HA	1:B:249:PRO:HD3	1.99	0.40
1:A:435:GLN:HE22	1:A:441:LYS:HD3	1.85	0.40
1:A:322:TYR:HD2	1:A:348:MET:HG2	1.86	0.40
1:B:276:LEU:CD2	1:B:282:ALA:HB2	2.50	0.40
1:A:75:ASN:N	1:A:75:ASN:OD1	2.54	0.40
1:A:164:LEU:HA	1:A:164:LEU:HD23	1.85	0.40
1:A:674:PRO:O	1:A:680:LEU:HB2	2.21	0.40
1:B:626:ILE:O	1:B:650:GLY:CA	2.70	0.40
1:B:680:LEU:C	1:B:680:LEU:CD1	2.90	0.40
1:B:158:SER:HA	1:B:216:TRP:CD1	2.57	0.40
1:B:630:SER:OG	1:B:631:TYR:N	2.55	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	726/728 (100%)	672 (93%)	51 (7%)	3 (0%)	43	52
1	B	726/728 (100%)	687 (95%)	37 (5%)	2 (0%)	50	62
All	All	1452/1456 (100%)	1359 (94%)	88 (6%)	5 (0%)	50	62

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	521	GLU
1	A	742	ILE
1	B	138	ASN
1	B	140	ARG
1	A	438	ASP

### 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	653/653 (100%)	604 (92%)	49 (8%)	19	21
1	B	653/653 (100%)	613 (94%)	40 (6%)	26	31
All	All	1306/1306 (100%)	1217 (93%)	89 (7%)	22	25

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	49	LEU
1	A	60	LEU
1	A	72	GLN
1	A	75	ASN
1	A	108	SER
1	A	115	LEU
1	A	140	ARG
1	A	142	LEU
1	A	180	LEU
1	A	190	LYS
1	A	202	VAL
1	A	223	LEU
1	A	230	ASP
1	A	246	LEU
1	A	263	ASN
1	A	294	LEU
1	A	300	LEU
1	A	316	LEU
1	A	326	ASP
1	A	332	GLU

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Mol	Chain	Res	Type
1	A	340	LEU
1	A	377	ASN
1	A	382	ARG
1	A	385	CYS
1	A	410	LEU
1	A	420	ASN
1	A	431	LEU
1	A	434	ILE
1	A	472	CYS
1	A	479	LEU
1	A	482	LEU
1	A	484	SER
1	A	500	LEU
1	A	513	LYS
1	A	514	LEU
1	A	528	MET
1	A	543	LEU
1	A	544	LEU
1	A	589	LYS
1	A	597	ARG
1	A	621	ASN
1	A	627	TRP
1	A	663	ASP
1	A	677	GLU
1	A	696	LYS
1	A	715	GLN
1	A	736	THR
1	A	760	LYS
1	B	40	ARG
1	B	41	LYS
1	B	42	THR
1	B	49	LEU
1	B	57	LEU
1	B	60	LEU
1	B	78	VAL
1	B	91	GLU
1	B	144	THR
1	B	214	LEU
1	B	223	LEU
1	B	236	ILE
1	B	246	LEU
1	B	326	ASP

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Mol	Chain	Res	Type
1	B	336	ARG
1	B	376	SER
1	B	377	ASN
1	B	378	GLU
1	B	385	CYS
1	B	391	LYS
1	B	420	ASN
1	B	434	ILE
1	B	443	THR
1	B	472	CYS
1	B	479	LEU
1	B	500	LEU
1	B	514	LEU
1	B	519	LEU
1	B	542	LEU
1	B	543	LEU
1	B	558	VAL
1	B	562	ASN
1	B	566	TYR
1	B	577	SER
1	B	594	ILE
1	B	619	VAL
1	B	679	ASN
1	B	684	ARG
1	B	715	GLN
1	B	762	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	141	GLN
1	A	247	GLN
1	A	263	ASN
1	A	298	HIS
1	A	363	HIS
1	A	377	ASN
1	A	420	ASN
1	A	435	GLN
1	A	483	HIS
1	A	506	ASN
1	A	508	GLN

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Mol	Chain	Res	Type
1	A	533	HIS
1	A	586	GLN
1	A	592	HIS
1	A	612	GLN
1	A	679	ASN
1	A	715	GLN
1	A	750	HIS
1	A	757	HIS
1	B	66	HIS
1	B	169	ASN
1	B	263	ASN
1	B	298	HIS
1	B	377	ASN
1	B	383	HIS
1	B	420	ASN
1	B	435	GLN
1	B	483	HIS
1	B	562	ASN
1	B	612	GLN
1	B	679	ASN
1	B	682	HIS
1	B	715	GLN
1	B	750	HIS

### 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 ⓘ

2 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	1MD	A	801	-	29,29,29	1.84	9 (31%)	43,43,43	2.01	10 (23%)
2	1MD	B	801	-	29,29,29	1.91	10 (34%)	43,43,43	2.39	15 (34%)

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	1MD	A	801	-	-	0/13/26/26	0/1/3/3
2	1MD	B	801	-	-	0/13/26/26	0/1/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	1MD	C18-C17	4.14	1.46	1.38
2	A	801	1MD	C20-C19	4.02	1.45	1.38
2	A	801	1MD	C2-C3	3.47	1.44	1.38
2	B	801	1MD	C19-CL2	-3.40	1.66	1.74
2	B	801	1MD	C2-C3	3.34	1.43	1.38
2	A	801	1MD	C18-C17	3.31	1.45	1.38
2	A	801	1MD	C18-C19	2.99	1.43	1.38
2	B	801	1MD	C14-C21	2.86	1.44	1.40
2	B	801	1MD	C20-C21	2.79	1.43	1.38
2	A	801	1MD	C14-C21	2.74	1.44	1.40
2	B	801	1MD	C3-N4	2.73	1.38	1.34
2	A	801	1MD	C20-C21	2.72	1.43	1.38
2	B	801	1MD	C7-N2	2.65	1.38	1.34
2	A	801	1MD	C7-N2	2.59	1.38	1.34
2	B	801	1MD	C18-C19	2.57	1.43	1.38
2	B	801	1MD	C17-C14	2.35	1.43	1.40
2	A	801	1MD	C17-C14	2.21	1.43	1.40
2	B	801	1MD	C5-C6	2.11	1.55	1.50
2	A	801	1MD	C4-C9	-2.06	1.46	1.49

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	1MD	C10-N1-C9	-6.29	117.14	123.47
2	B	801	1MD	C20-C21-C14	6.20	126.19	121.82
2	A	801	1MD	C20-C21-C14	5.84	125.93	121.82
2	B	801	1MD	C10-N1-C9	-5.36	118.08	123.47
2	B	801	1MD	C20-C21-CL1	-4.47	111.52	118.55
2	A	801	1MD	C21-C20-C19	-4.44	113.53	118.67
2	B	801	1MD	C21-C20-C19	-4.12	113.90	118.67
2	B	801	1MD	C15-C2-C3	-3.93	116.10	119.83
2	B	801	1MD	C3-N4-C6	-3.88	114.22	119.56
2	B	801	1MD	C5-N1-C10	3.57	128.34	123.23
2	B	801	1MD	C20-C19-CL2	-3.53	114.79	119.14
2	B	801	1MD	C7-C10-N1	3.39	116.70	110.89
2	B	801	1MD	C13-C3-C2	-2.96	116.80	122.60
2	A	801	1MD	C20-C21-CL1	-2.85	114.07	118.55
2	B	801	1MD	C4-C6-N4	-2.81	124.76	126.71
2	B	801	1MD	C4-C1-C2	-2.76	114.84	118.01
2	A	801	1MD	C13-C3-N4	-2.53	112.37	116.42
2	A	801	1MD	C3-N4-C6	-2.49	116.14	119.56
2	A	801	1MD	O2-C7-N2	2.38	125.99	121.67
2	A	801	1MD	C8-N2-C7	-2.17	115.37	121.70
2	A	801	1MD	C5-N1-C10	2.15	126.30	123.23
2	B	801	1MD	C15-C2-C1	2.14	124.36	120.99
2	A	801	1MD	C10-C7-N2	-2.13	113.32	116.76
2	B	801	1MD	C1-C14-C21	-2.07	119.94	122.10
2	B	801	1MD	C18-C19-C20	2.07	124.40	121.54

There are no chirality outliers.

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, 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	728/728 (100%)	0.01	20 (2%)	52	55	20, 36, 80, 152	0
1	B	728/728 (100%)	0.18	13 (1%)	65	68	21, 41, 81, 144	0
All	All	1456/1456 (100%)	0.10	33 (2%)	57	61	20, 39, 81, 152	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	766	PRO	6.1
1	A	39	SER	4.1
1	A	766	PRO	3.7
1	B	39	SER	3.7
1	A	765	LEU	3.0
1	A	91	GLU	3.0
1	A	73	GLU	2.9
1	A	88	VAL	2.8
1	A	98	PHE	2.7
1	A	502	LYS	2.7
1	B	41	LYS	2.6
1	B	534	PHE	2.5
1	B	550	PRO	2.5
1	A	142	LEU	2.5
1	B	279	VAL	2.5
1	A	392	LYS	2.5
1	A	116	LEU	2.4
1	B	765	LEU	2.4
1	A	114	ILE	2.4
1	B	140	ARG	2.3
1	B	90	LEU	2.2
1	B	540	TYR	2.2
1	B	97	GLU	2.1
1	A	342	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	140	ARG	2.1
1	B	613	PHE	2.1
1	A	137	LEU	2.1
1	A	616	MET	2.1
1	B	273	THR	2.1
1	A	145	GLU	2.1
1	A	89	PHE	2.1
1	A	135	TYR	2.1
1	A	597	ARG	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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	1MD	A	801	27/27	0.14	0.69	21,21,21,21	0
2	1MD	B	801	27/27	0.15	0.18	21,21,21,21	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.