



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:24 PM GMT

PDB ID : 1K4Y  
Title : Crystal Structure of Rabbit Liver Carboxylesterase in Complex with 4-piperidino-piperidine  
Authors : Bencharit, S.; Morton, C.L.; Howard-Williams, E.L.; Danks, M.K.; Potter, P.M.; Redinbo, M.R.  
Deposited on : 2001-10-09  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

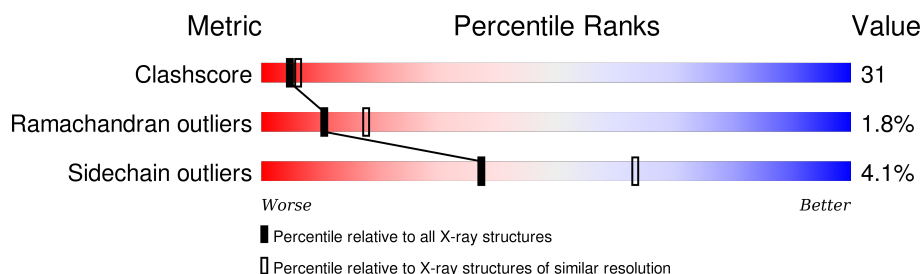
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	534	

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	NAG	A	1080	X	-	-	-
3	NAG	A	1390	X	-	X	-
3	MAN	A	1391	X	-	X	-
3	MAN	A	1392	X	-	-	-
4	4PN	A	2001	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4379 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 LIVER CARBOXYLESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			3895	2506	650	721	18			

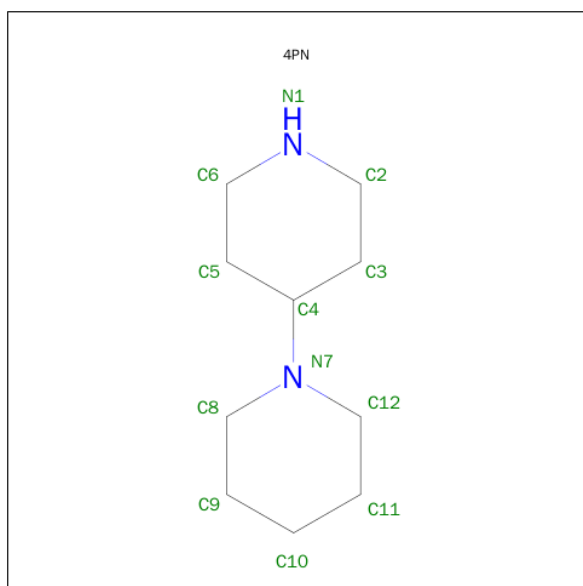
- Molecule 2 is a polymer of unknown type called SUGAR (NAG-NAG).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is a polymer of unknown type called SUGAR (NAG-NAG-MAN-MAN-MAN).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 4 is 4-PIPERIDINO-PIPERIDINE (three-letter code: 4PN) (formula: C<sub>10</sub>H<sub>20</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			12	10	2		

- Molecule 5 is water.

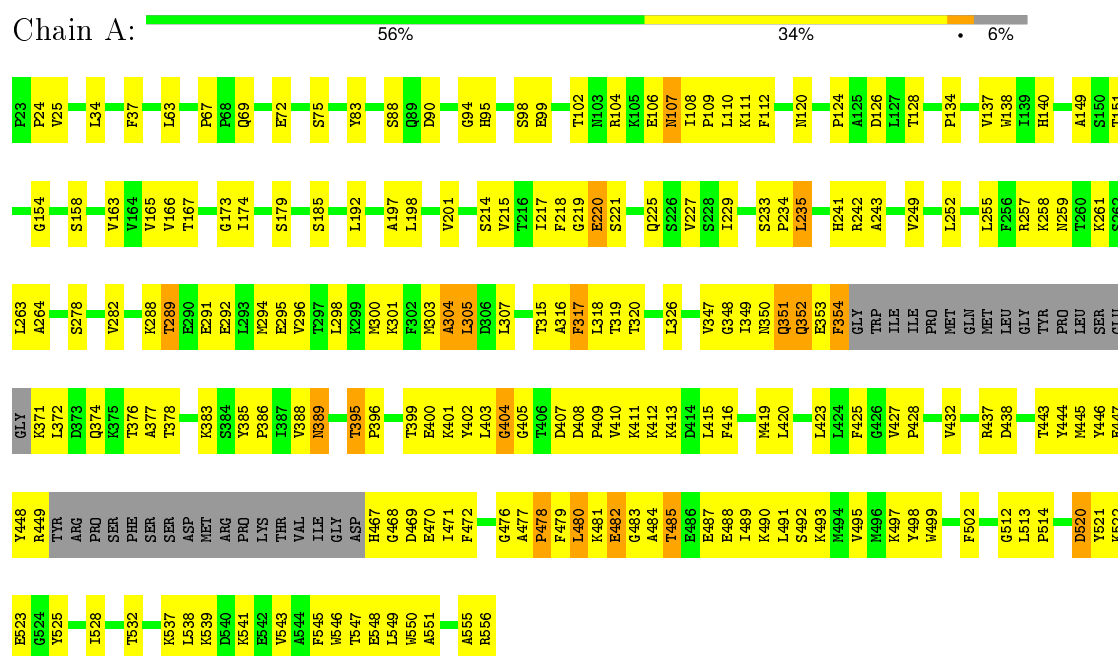
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	383	Total	O	0	0
			383	383		

### 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.

Note EDS was not executed.

#### • Molecule 1: LIVER CARBOXYLESTERASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.23Å 110.23Å 282.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	98.0 (20.00-2.50)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.229 , 0.294	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4379	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

## 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: 4PN, NAG, MAN

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	0.35	0/3991	0.61	0/5413

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
2	A	1	0
3	A	3	0
All	All	4	0

There are no bond length outliers.

There are no bond angle outliers.

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1080	NAG	C1
3	A	1390	NAG	C1
3	A	1391	MAN	C1
3	A	1392	MAN	C1

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3895	0	3886	223	0
2	A	28	0	25	3	0
3	A	61	0	52	17	0
4	A	12	0	20	17	0
5	A	383	0	0	24	0
All	All	4379	0	3983	251	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 31.

All (251) 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)
4:A:2001:4PN:C4	4:A:2001:4PN:C12	2.03	1.35
4:A:2001:4PN:H4	4:A:2001:4PN:C12	1.60	1.32
4:A:2001:4PN:C8	4:A:2001:4PN:C4	2.10	1.26
4:A:2001:4PN:N7	4:A:2001:4PN:C3	2.07	1.17
4:A:2001:4PN:N7	4:A:2001:4PN:C5	2.09	1.15
1:A:108:ILE:HD12	1:A:108:ILE:H	1.21	1.02
1:A:523:GLU:HG3	1:A:537:LYS:HD3	1.43	0.99
1:A:371:LYS:HD2	1:A:411:LYS:HD3	1.46	0.96
1:A:371:LYS:HB2	1:A:410:VAL:HG12	1.48	0.95
1:A:399:THR:HG23	1:A:403:LEU:HD12	1.50	0.94
1:A:388:VAL:HG11	1:A:423:LEU:HD13	1.50	0.94
4:A:2001:4PN:H4	4:A:2001:4PN:H121	1.45	0.94
1:A:215:VAL:H	1:A:241:HIS:HD2	1.14	0.94
1:A:412:LYS:HE2	1:A:412:LYS:HA	1.50	0.92
4:A:2001:4PN:N7	4:A:2001:4PN:C4	0.77	0.92
1:A:480:LEU:H	1:A:480:LEU:HD23	1.31	0.92
3:A:1391:MAN:O4	3:A:1392:MAN:H2	1.69	0.91
4:A:2001:4PN:H4	4:A:2001:4PN:N7	1.24	0.90
3:A:1389:NAG:O3	3:A:1390:NAG:N2	2.07	0.88
1:A:403:LEU:HD13	1:A:413:LYS:HZ2	1.37	0.88
3:A:1390:NAG:H2	4:A:2001:4PN:H121	1.53	0.87
1:A:289:THR:HB	1:A:292:GLU:HG3	1.57	0.85
1:A:215:VAL:H	1:A:241:HIS:CD2	1.95	0.85
1:A:374:GLN:HG2	1:A:413:LYS:HZ3	1.41	0.84
1:A:523:GLU:HB2	1:A:537:LYS:H	1.42	0.84
1:A:403:LEU:HD22	1:A:413:LYS:HD3	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:LEU:O	1:A:413:LYS:HG3	1.79	0.83
1:A:350:ASN:HB3	1:A:352:GLN:HE21	1.42	0.83
1:A:374:GLN:HG2	1:A:413:LYS:NZ	1.96	0.81
1:A:220:GLU:HG2	1:A:471:ILE:HD11	1.63	0.81
1:A:371:LYS:CD	1:A:411:LYS:HD3	2.10	0.80
1:A:134:PRO:HG2	1:A:163:VAL:HG12	1.63	0.80
3:A:1389:NAG:H2	4:A:2001:4PN:H1	1.46	0.79
1:A:108:ILE:CD1	1:A:108:ILE:H	1.96	0.79
1:A:259:ASN:ND2	1:A:261:LYS:H	1.82	0.76
1:A:372:LEU:HD12	1:A:376:THR:HG22	1.68	0.75
3:A:1391:MAN:C4	3:A:1392:MAN:H2	2.16	0.75
1:A:478:PRO:HB3	1:A:489:ILE:HG12	1.69	0.74
1:A:479:PHE:CE2	1:A:493:LYS:HE3	2.23	0.74
1:A:371:LYS:HG2	5:A:3381:HOH:O	1.89	0.72
1:A:469:ASP:HA	1:A:472:PHE:CD1	2.24	0.72
1:A:479:PHE:HE2	1:A:493:LYS:HE3	1.55	0.72
1:A:469:ASP:HA	1:A:472:PHE:HD1	1.54	0.71
1:A:257:ARG:CZ	1:A:315:THR:HG21	2.20	0.71
1:A:349:ILE:C	1:A:350:ASN:HD22	1.95	0.71
1:A:255:LEU:C	1:A:319:THR:OG1	2.29	0.70
1:A:395:THR:HB	1:A:396:PRO:HD3	1.72	0.70
2:A:1079:NAG:H61	2:A:1080:NAG:C1	2.22	0.69
1:A:108:ILE:HD12	1:A:108:ILE:N	2.04	0.69
1:A:259:ASN:HD21	1:A:261:LYS:H	1.39	0.69
1:A:259:ASN:OD1	1:A:261:LYS:HG3	1.93	0.69
1:A:374:GLN:HA	1:A:413:LYS:HZ1	1.58	0.68
1:A:497:LYS:HB3	1:A:513:LEU:HD11	1.76	0.67
1:A:259:ASN:HB2	5:A:3001:HOH:O	1.94	0.67
1:A:448:TYR:HA	1:A:528:ILE:HG23	1.76	0.67
1:A:289:THR:HG22	1:A:291:GLU:N	2.10	0.66
2:A:1079:NAG:H61	2:A:1080:NAG:O5	1.96	0.66
1:A:487:GLU:O	1:A:490:LYS:HG2	1.96	0.66
1:A:99:GLU:HG2	1:A:107:ASN:OD1	1.97	0.65
1:A:215:VAL:N	1:A:241:HIS:HD2	1.90	0.65
1:A:242:ARG:HH11	1:A:242:ARG:HG2	1.63	0.64
1:A:528:ILE:HD12	1:A:532:THR:OG1	1.97	0.64
1:A:523:GLU:CG	1:A:537:LYS:HD3	2.25	0.63
1:A:388:VAL:HG12	1:A:388:VAL:O	1.99	0.63
1:A:354:PHE:N	1:A:354:PHE:HD2	1.97	0.63
1:A:220:GLU:CG	1:A:471:ILE:HD11	2.28	0.62
1:A:523:GLU:HB2	1:A:537:LYS:N	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:LEU:HD11	1:A:326:LEU:HD12	1.82	0.61
3:A:1390:NAG:O3	3:A:1391:MAN:H61	2.00	0.61
1:A:319:THR:HG23	1:A:320:THR:O	1.99	0.61
1:A:104:ARG:HD2	1:A:108:ILE:HD11	1.83	0.61
1:A:258:LYS:HE3	5:A:3216:HOH:O	1.99	0.61
1:A:350:ASN:ND2	1:A:448:TYR:HB3	2.16	0.60
1:A:539:LYS:O	1:A:543:VAL:HG23	2.01	0.60
1:A:95:HIS:O	1:A:99:GLU:HG3	2.01	0.60
1:A:550:TRP:CB	4:A:2001:4PN:H91	2.32	0.60
1:A:403:LEU:HD21	1:A:416:PHE:N	2.17	0.60
1:A:403:LEU:HB3	1:A:413:LYS:NZ	2.17	0.60
1:A:403:LEU:HD23	1:A:415:LEU:HB2	1.82	0.60
1:A:354:PHE:N	1:A:354:PHE:CD2	2.69	0.60
1:A:427:VAL:HB	1:A:428:PRO:HD3	1.83	0.60
1:A:352:GLN:HB2	1:A:354:PHE:CD2	2.37	0.59
1:A:479:PHE:HZ	1:A:493:LYS:HG3	1.67	0.59
3:A:1390:NAG:H2	4:A:2001:4PN:C12	2.27	0.59
1:A:402:TYR:CD2	1:A:419:MET:HB3	2.38	0.59
1:A:249:VAL:HB	1:A:432:VAL:HG21	1.85	0.59
1:A:405:GLY:HA3	5:A:3283:HOH:O	2.02	0.58
3:A:1391:MAN:O4	3:A:1392:MAN:C2	2.48	0.58
1:A:477:ALA:N	1:A:478:PRO:CD	2.66	0.58
1:A:378:THR:OG1	1:A:399:THR:HG21	2.03	0.58
1:A:278:SER:O	1:A:282:VAL:HG23	2.04	0.58
1:A:388:VAL:HG13	1:A:423:LEU:HB3	1.84	0.58
1:A:470:GLU:HG2	1:A:471:ILE:N	2.18	0.58
3:A:1391:MAN:H3	5:A:3225:HOH:O	2.04	0.57
1:A:24:PRO:HD3	1:A:37:PHE:CE1	2.38	0.57
1:A:378:THR:CG2	1:A:395:THR:HG22	2.35	0.57
1:A:249:VAL:H	1:A:252:LEU:HD13	1.68	0.57
3:A:1390:NAG:O7	3:A:1390:NAG:H3	2.03	0.57
3:A:1391:MAN:H62	3:A:1393:MAN:O6	2.04	0.57
1:A:403:LEU:HD22	1:A:413:LYS:CD	2.31	0.57
1:A:378:THR:HG23	1:A:395:THR:HG22	1.86	0.57
1:A:480:LEU:N	1:A:480:LEU:HD23	2.12	0.57
1:A:137:VAL:HG21	1:A:198:LEU:HD21	1.85	0.57
1:A:137:VAL:HG12	1:A:166:VAL:HB	1.87	0.56
1:A:289:THR:HG22	1:A:291:GLU:H	1.71	0.56
1:A:354:PHE:HZ	5:A:3294:HOH:O	1.88	0.56
1:A:543:VAL:O	1:A:547:THR:HG22	2.06	0.56
1:A:512:GLY:O	1:A:513:LEU:HD23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:LYS:HD2	5:A:3223:HOH:O	2.05	0.56
1:A:469:ASP:HB2	5:A:3294:HOH:O	2.05	0.56
1:A:348:GLY:HA3	1:A:446:TYR:CE1	2.40	0.55
1:A:354:PHE:CE2	1:A:467:HIS:HB2	2.41	0.55
1:A:468:GLY:HA2	1:A:471:ILE:HD12	1.89	0.55
1:A:102:THR:HA	1:A:151:THR:O	2.06	0.55
1:A:257:ARG:NE	1:A:315:THR:HG21	2.21	0.55
1:A:106:GLU:CD	1:A:106:GLU:H	2.10	0.55
1:A:25:VAL:HG22	1:A:34:LEU:HD23	1.88	0.55
1:A:491:LEU:O	1:A:495:VAL:HG23	2.06	0.55
1:A:225:GLN:O	1:A:229:ILE:HD13	2.07	0.54
1:A:289:THR:HG21	5:A:3197:HOH:O	2.06	0.54
1:A:408:ASP:N	1:A:409:PRO:CD	2.71	0.54
1:A:403:LEU:HB3	1:A:413:LYS:HZ3	1.73	0.53
1:A:468:GLY:O	1:A:471:ILE:HB	2.08	0.53
1:A:305:LEU:HD11	5:A:3297:HOH:O	2.09	0.53
1:A:225:GLN:HG2	1:A:255:LEU:HD12	1.89	0.53
1:A:550:TRP:HB3	4:A:2001:4PN:H91	1.89	0.53
1:A:400:GLU:HA	1:A:404:GLY:HA2	1.90	0.53
1:A:437:ARG:NH1	1:A:523:GLU:OE1	2.42	0.52
1:A:372:LEU:HD11	1:A:377:ALA:HA	1.92	0.52
1:A:385:TYR:N	1:A:386:PRO:HD2	2.25	0.52
1:A:385:TYR:HA	5:A:3142:HOH:O	2.10	0.51
2:A:1080:NAG:H5	5:A:3093:HOH:O	2.09	0.51
1:A:255:LEU:O	1:A:319:THR:OG1	2.27	0.51
1:A:173:GLY:C	1:A:318:LEU:HD13	2.30	0.51
1:A:354:PHE:HE1	1:A:469:ASP:OD2	1.94	0.51
1:A:476:GLY:HA2	1:A:492:SER:OG	2.11	0.51
3:A:1390:NAG:C4	3:A:1391:MAN:H61	2.40	0.51
1:A:126:ASP:OD1	1:A:128:THR:HB	2.11	0.51
1:A:88:SER:HB3	1:A:294:MET:CE	2.41	0.51
1:A:347:VAL:O	1:A:445:MET:HA	2.09	0.51
1:A:403:LEU:HD21	1:A:416:PHE:CA	2.41	0.51
1:A:242:ARG:NH1	1:A:242:ARG:HG2	2.26	0.50
1:A:401:LYS:HG3	1:A:545:PHE:CE1	2.46	0.50
1:A:352:GLN:HB2	1:A:354:PHE:CE2	2.47	0.50
1:A:372:LEU:HD12	1:A:376:THR:CG2	2.37	0.49
1:A:481:LYS:O	1:A:483:GLY:N	2.45	0.49
1:A:24:PRO:HD3	1:A:37:PHE:CD1	2.47	0.49
1:A:149:ALA:HB1	1:A:167:THR:HB	1.94	0.49
1:A:412:LYS:HA	1:A:412:LYS:CE	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:TYR:HA	1:A:528:ILE:CG2	2.41	0.49
1:A:137:VAL:CG2	1:A:217:ILE:HG22	2.43	0.48
1:A:541:LYS:O	1:A:541:LYS:HD2	2.13	0.48
1:A:83:TYR:OH	1:A:104:ARG:NH1	2.37	0.48
1:A:67:PRO:HB3	1:A:192:LEU:HD13	1.95	0.48
1:A:354:PHE:HE1	1:A:469:ASP:CG	2.15	0.48
1:A:72:GLU:HG3	5:A:3243:HOH:O	2.14	0.48
1:A:480:LEU:H	1:A:480:LEU:CD2	2.12	0.48
1:A:140:HIS:HE1	5:A:3123:HOH:O	1.96	0.48
1:A:477:ALA:HB3	1:A:478:PRO:HD3	1.96	0.47
1:A:108:ILE:HA	1:A:109:PRO:HD3	1.72	0.47
1:A:354:PHE:CE2	1:A:467:HIS:N	2.82	0.47
1:A:303:MET:O	1:A:304:ALA:HB2	2.14	0.47
1:A:179:SER:O	1:A:264:ALA:HB2	2.14	0.47
1:A:289:THR:HB	1:A:292:GLU:CG	2.38	0.47
1:A:485:THR:C	1:A:487:GLU:N	2.67	0.47
1:A:292:GLU:O	1:A:295:GLU:HB3	2.15	0.47
1:A:407:ASP:C	1:A:409:PRO:HD2	2.35	0.47
3:A:1389:NAG:H2	4:A:2001:4PN:N1	2.22	0.47
1:A:403:LEU:HD21	1:A:416:PHE:HB2	1.97	0.47
1:A:350:ASN:N	1:A:350:ASN:HD22	2.12	0.47
1:A:289:THR:CG2	1:A:291:GLU:H	2.27	0.47
1:A:555:ALA:O	1:A:556:ARG:C	2.54	0.46
1:A:548:GLU:O	1:A:551:ALA:HB3	2.14	0.46
1:A:221:SER:HB3	5:A:3002:HOH:O	2.16	0.46
1:A:138:TRP:CZ3	1:A:219:GLY:HA2	2.51	0.46
1:A:98:SER:O	1:A:102:THR:HG23	2.16	0.46
1:A:154:GLY:HA3	1:A:165:VAL:HG11	1.98	0.46
1:A:350:ASN:O	1:A:352:GLN:N	2.46	0.46
3:A:1389:NAG:O3	3:A:1390:NAG:C2	2.65	0.45
1:A:296:VAL:O	1:A:300:MET:HG2	2.16	0.45
1:A:217:ILE:CD1	1:A:227:VAL:HG13	2.46	0.45
1:A:353:GLU:C	1:A:354:PHE:HD2	2.19	0.45
1:A:425:PHE:C	1:A:428:PRO:HD2	2.36	0.45
1:A:227:VAL:CG1	1:A:243:ALA:HB1	2.47	0.45
1:A:385:TYR:O	1:A:389:ASN:N	2.37	0.45
1:A:233:SER:HA	1:A:234:PRO:HD3	1.79	0.45
1:A:353:GLU:O	1:A:354:PHE:C	2.54	0.45
1:A:399:THR:C	1:A:401:LYS:H	2.21	0.45
1:A:174:ILE:N	1:A:318:LEU:HD13	2.31	0.44
1:A:120:ASN:HB2	1:A:167:THR:OG1	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:VAL:CG1	1:A:423:LEU:HB3	2.46	0.44
1:A:289:THR:N	1:A:292:GLU:OE2	2.50	0.44
1:A:88:SER:HB3	1:A:294:MET:HE1	1.98	0.44
1:A:389:ASN:OD1	4:A:2001:4PN:H62	2.18	0.44
1:A:498:TYR:OH	1:A:514:PRO:HG2	2.17	0.44
1:A:307:LEU:O	1:A:383:LYS:HD2	2.17	0.44
1:A:481:LYS:HG2	1:A:482:GLU:H	1.83	0.43
1:A:399:THR:O	1:A:403:LEU:N	2.51	0.43
1:A:124:PRO:HD3	1:A:158:SER:HB2	2.00	0.43
1:A:63:LEU:HA	1:A:63:LEU:HD23	1.79	0.43
1:A:395:THR:CB	1:A:396:PRO:HD3	2.44	0.43
1:A:255:LEU:C	1:A:319:THR:HG1	2.16	0.43
1:A:110:LEU:HD23	1:A:112:PHE:CZ	2.54	0.43
1:A:485:THR:O	1:A:488:GLU:HG2	2.19	0.43
1:A:447:GLU:OE2	1:A:449:ARG:HD3	2.18	0.43
1:A:403:LEU:O	1:A:404:GLY:O	2.36	0.43
1:A:214:SER:HA	1:A:241:HIS:CD2	2.54	0.43
1:A:401:LYS:HG3	1:A:545:PHE:CZ	2.54	0.43
1:A:301:LYS:HE2	1:A:304:ALA:CB	2.49	0.43
1:A:110:LEU:HD12	1:A:110:LEU:N	2.34	0.43
1:A:388:VAL:CG1	1:A:388:VAL:O	2.67	0.43
1:A:351:GLN:C	1:A:352:GLN:CG	2.87	0.43
1:A:289:THR:HG22	1:A:292:GLU:H	1.84	0.43
4:A:2001:4PN:C5	4:A:2001:4PN:C8	2.83	0.43
1:A:354:PHE:HE2	1:A:467:HIS:N	2.17	0.43
1:A:478:PRO:CB	1:A:489:ILE:HA	2.49	0.43
1:A:472:PHE:HZ	5:A:3230:HOH:O	2.02	0.42
1:A:288:LYS:HA	1:A:288:LYS:HD3	1.84	0.42
1:A:479:PHE:CZ	1:A:493:LYS:HE3	2.55	0.42
1:A:549:LEU:HD12	5:A:3229:HOH:O	2.19	0.42
1:A:197:ALA:O	1:A:201:VAL:HG23	2.18	0.42
1:A:396:PRO:O	1:A:400:GLU:HG2	2.19	0.42
1:A:403:LEU:CD1	1:A:413:LYS:HZ2	2.20	0.42
1:A:482:GLU:HG3	1:A:483:GLY:N	2.35	0.42
1:A:467:HIS:HA	5:A:3292:HOH:O	2.20	0.41
1:A:490:LYS:HG3	1:A:491:LEU:N	2.35	0.41
1:A:546:TRP:HB3	1:A:550:TRP:CZ3	2.54	0.41
1:A:257:ARG:NE	1:A:315:THR:CG2	2.83	0.41
1:A:90:ASP:O	1:A:94:GLY:N	2.52	0.41
1:A:352:GLN:NE2	1:A:354:PHE:CZ	2.88	0.41
1:A:525:TYR:CD2	1:A:538:LEU:HB2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:THR:HG22	1:A:444:TYR:N	2.36	0.41
1:A:520:ASP:HB2	1:A:521:TYR:H	1.74	0.41
1:A:249:VAL:HG13	5:A:3189:HOH:O	2.20	0.41
1:A:318:LEU:HD23	1:A:318:LEU:HA	1.91	0.41
3:A:1391:MAN:C4	3:A:1392:MAN:C2	2.87	0.41
1:A:107:ASN:HD22	1:A:107:ASN:HA	1.59	0.41
1:A:104:ARG:HB2	5:A:3059:HOH:O	2.21	0.41
1:A:427:VAL:HG13	1:A:543:VAL:HG22	2.02	0.41
1:A:110:LEU:CD1	1:A:110:LEU:H	2.34	0.41
1:A:242:ARG:HD3	1:A:502:PHE:O	2.21	0.41
1:A:419:MET:HG3	1:A:420:LEU:N	2.36	0.40
1:A:407:ASP:CG	1:A:409:PRO:HD2	2.41	0.40
1:A:303:MET:HG3	5:A:3331:HOH:O	2.21	0.40
1:A:111:LYS:HE2	5:A:3312:HOH:O	2.20	0.40
1:A:411:LYS:HB2	5:A:3362:HOH:O	2.21	0.40
1:A:389:ASN:OD1	3:A:1389:NAG:O5	2.38	0.40
1:A:484:ALA:HB3	1:A:488:GLU:OE2	2.21	0.40
3:A:1390:NAG:O3	4:A:2001:4PN:H112	2.21	0.40
1:A:315:THR:O	1:A:317:PHE:N	2.50	0.40
1:A:69:GLN:NE2	5:A:3052:HOH:O	2.53	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	495/534 (93%)	447 (90%)	39 (8%)	9 (2%)	11 18

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	482	GLU

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Mol	Chain	Res	Type
1	A	404	GLY
1	A	351	GLN
1	A	389	ASN
1	A	185	SER
1	A	304	ALA
1	A	478	PRO
1	A	316	ALA
1	A	395	THR

### 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	417/446 (94%)	400 (96%)	17 (4%)	37 63

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	SER
1	A	107	ASN
1	A	218	PHE
1	A	220	GLU
1	A	235	LEU
1	A	263	LEU
1	A	289	THR
1	A	298	LEU
1	A	305	LEU
1	A	317	PHE
1	A	352	GLN
1	A	354	PHE
1	A	438	ASP
1	A	480	LEU
1	A	485	THR
1	A	499	TRP
1	A	520	ASP

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	140	HIS
1	A	162	ASN
1	A	241	HIS
1	A	259	ASN
1	A	287	GLN
1	A	314	ASN
1	A	350	ASN
1	A	351	GLN
1	A	352	GLN
1	A	431	ASN
1	A	435	HIS
1	A	536	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

7 carbohydrates 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	NAG	A	1079	1,2	14,14,15	1.00	1 (7%)	15,19,21	0.93	1 (6%)
2	NAG	A	1080	2	14,14,15	1.27	1 (7%)	15,19,21	1.01	1 (6%)
3	NAG	A	1389	1,3	14,14,15	0.72	0	15,19,21	1.30	3 (20%)
3	NAG	A	1390	3	14,14,15	1.14	1 (7%)	15,19,21	1.21	1 (6%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	MAN	A	1391	3	11,11,12	0.95	0	14,15,17	1.14	1 (7%)
3	MAN	A	1392	3	11,11,12	0.63	0	14,15,17	1.10	1 (7%)
3	MAN	A	1393	3	11,11,12	0.55	0	14,15,17	0.77	1 (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	NAG	A	1079	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	1080	2	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	A	1389	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	1390	3	1/1/5/7	0/6/23/26	0/1/1/1
3	MAN	A	1391	3	1/1/4/5	0/2/19/22	1/1/1/1
3	MAN	A	1392	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	A	1393	3	-	0/2/19/22	1/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1079	NAG	O4-C4	2.17	1.48	1.43
3	A	1390	NAG	C4-C5	2.65	1.58	1.53
2	A	1080	NAG	C1-C2	4.10	1.58	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1079	NAG	C2-N2-C7	-2.82	119.42	123.04
2	A	1080	NAG	C2-N2-C7	-2.53	119.79	123.04
3	A	1389	NAG	C2-N2-C7	-2.36	120.00	123.04
3	A	1389	NAG	C4-C3-C2	-2.15	107.89	111.23
3	A	1393	MAN	C1-O5-C5	2.65	115.61	112.25
3	A	1389	NAG	O4-C4-C3	2.82	116.70	110.34
3	A	1392	MAN	C1-O5-C5	2.99	116.04	112.25
3	A	1391	MAN	C1-O5-C5	3.07	116.15	112.25
3	A	1390	NAG	C3-C4-C5	3.54	116.37	110.20

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1392	MAN	C1
3	A	1390	NAG	C1
3	A	1391	MAN	C1
2	A	1080	NAG	C1

There are no torsion outliers.

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1393	MAN	C1-C2-C3-C4-C5-O5
3	A	1391	MAN	C1-C2-C3-C4-C5-O5

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1079	NAG	2	0
2	A	1080	NAG	3	0
3	A	1389	NAG	5	0
3	A	1390	NAG	8	0
3	A	1391	MAN	8	0
3	A	1392	MAN	4	0
3	A	1393	MAN	1	0

## 5.6 Ligand geometry

1 ligand is 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
4	4PN	A	2001	-	13,13,13	7.77	6 (46%)	16,16,16	2.93	8 (50%)

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
4	4PN	A	2001	-	-	0/4/20/20	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2001	4PN	C4-N7	-27.11	0.77	1.48
4	A	2001	4PN	C11-C12	2.13	1.58	1.51
4	A	2001	4PN	C5-C4	2.14	1.58	1.52
4	A	2001	4PN	C3-C4	2.72	1.59	1.52
4	A	2001	4PN	C8-N7	3.12	1.53	1.47
4	A	2001	4PN	C12-N7	3.87	1.55	1.47

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2001	4PN	C3-C4-C5	-2.18	106.10	111.22
4	A	2001	4PN	C6-C5-C4	2.29	114.28	110.80
4	A	2001	4PN	C10-C9-C8	2.46	116.12	111.26
4	A	2001	4PN	C3-C4-N7	2.56	118.35	112.57
4	A	2001	4PN	C10-C11-C12	2.79	116.78	111.26
4	A	2001	4PN	C12-N7-C4	3.21	118.67	112.37
4	A	2001	4PN	C5-C4-N7	3.89	121.33	112.57
4	A	2001	4PN	C8-N7-C4	8.31	128.65	112.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2001	4PN	17	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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.