



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:42 AM GMT

PDB ID : 3MSJ
Title : Structure of bace (beta secretase) in complex with inhibitor
Authors : Madden, J.; Kramer, J.; Smith, M.A.; Barker, J.; Godemann, R.
Deposited on : 2010-04-29
Resolution : 1.80 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

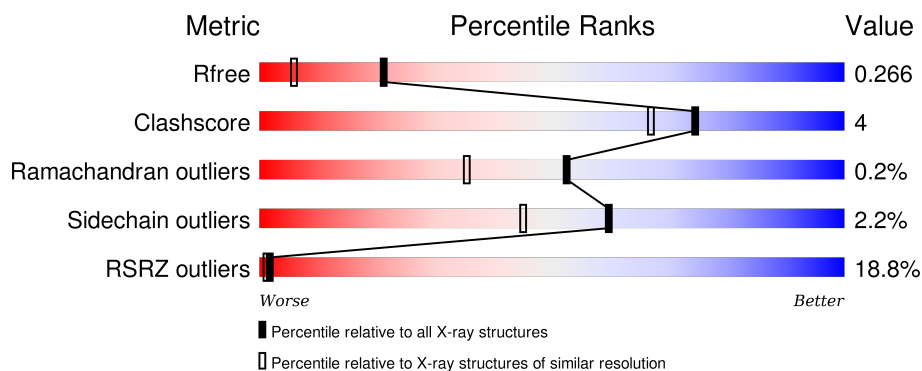
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	411	<div> <div>20%</div> <div>78%</div> <div>11%</div> <div>9%</div> </div>
1	B	411	<div> <div>11%</div> <div>83%</div> <div>7%</div> <div>9%</div> </div>
1	C	411	<div> <div>20%</div> <div>84%</div> <div>6%</div> <div>9%</div> </div>

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
3	GOL	A	395	-	-	-	X
3	GOL	A	396	-	-	-	X
3	GOL	A	399	-	-	-	X
3	GOL	B	394	-	-	X	X
3	GOL	B	395	-	-	-	X
3	GOL	B	397	-	-	-	X
3	GOL	B	398	-	-	-	X
3	GOL	B	400	-	-	-	X
3	GOL	C	394	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9702 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.

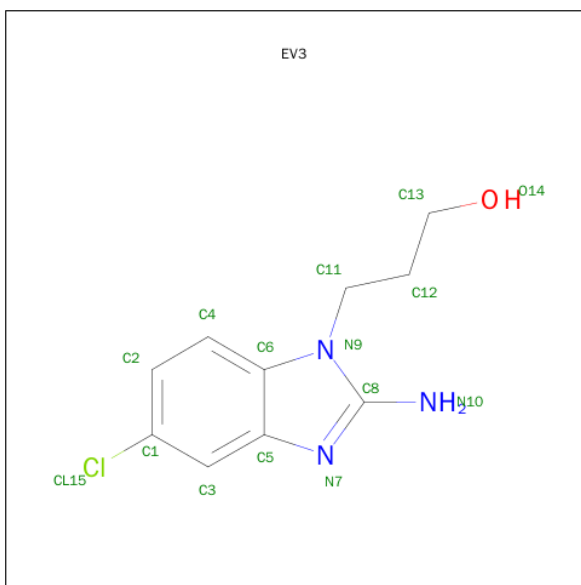
- Molecule 1 is a protein called BETA-SECRETASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	4	0
			2962	1897	493	558	14			
1	B	373	Total	C	N	O	S	0	4	0
			2956	1894	493	555	14			
1	C	375	Total	C	N	O	S	0	6	0
			2987	1912	494	567	14			

There are 6 discrepancies between the modelled and reference sequences:

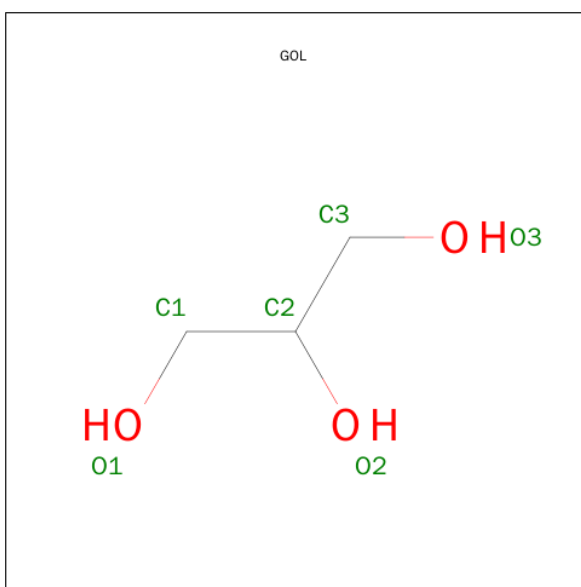
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	LYS	ARG	ENGINEERED MUTATION	UNP P56817
A	-4	THR	ARG	ENGINEERED MUTATION	UNP P56817
B	-5	LYS	ARG	ENGINEERED MUTATION	UNP P56817
B	-4	THR	ARG	ENGINEERED MUTATION	UNP P56817
C	-5	LYS	ARG	ENGINEERED MUTATION	UNP P56817
C	-4	THR	ARG	ENGINEERED MUTATION	UNP P56817

- Molecule 2 is 3-(2-AMINO-5-CHLORO-1H-BENZIMIDAZOL-1-YL)PROPAN-1-OL (three-letter code: EV3) (formula: C₁₀H₁₂ClN₃O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			15	10	1	3	1		
2	B	1	Total	C	Cl	N	O	0	0
			15	10	1	3	1		
2	C	1	Total	C	Cl	N	O	0	0
			15	10	1	3	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	236	Total O 236 236	0	0
4	B	243	Total O 246 246	0	3
4	C	167	Total O 168 168	0	1

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 ($\text{RSRZ} > 2$). 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.

Chain A:

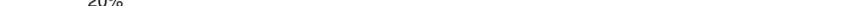
20% 78% 11% 9%

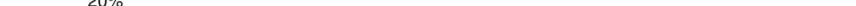
Amino Acid	Count
L287	1
L293	1
R297	1
L298	1
I300	1
V309	1
E310	1
ASP	1
VAL	1
THR	1
THR	1
THR	1
Q316	1
D317	1
K321	1
Q326	1
M333	1
M338	1
E339	1
G340	1
F341	1
F342	1
V343	1
V344	1
F345	1
I352	1
G353	1
F354	1
S357	1
H360	1
E364	1
T367	1
T376	1
L377	1
D378	1
N385	1
ILE	1
PRO	1
GLN	1
THR	1
ASP	1
GLU	1
SER	1
L63	1
V68	1
V69	1
F70	1
W71	1
T72	1
Q73	1
G74	1
K75	1
W76	1
T82	1
G90	1
F91	1
N92	1
V95	1
I99	1
A100	1
A101	1
E104	1
S105	1
D106	1
K107	1
F108	1
F109	1
N110	1
N111	1
G112	1
S113	1
I118	1
L119	1
K238	1
K239	1
V240	1
E241	1
E242	1
A243	1
L248	1
K256	1
D259	1
G260	1
L267	1
Q271	1
A272	1
V282	1
I283	1
S284	1
V285	1
L63	1
V68	1
V69	1
F70	1
W71	1
T72	1
Q73	1
G74	1
K75	1
W76	1
T82	1
G90	1
F91	1
N92	1
V95	1
I99	1
A100	1
A101	1
E104	1
S105	1
D106	1
K107	1
F108	1
F109	1
N110	1
N111	1
G112	1
S113	1
I118	1
L119	1
K238	1
K239	1
V240	1
E241	1
E242	1
A243	1
L248	1
K256	1
D259	1
G260	1
L267	1
Q271	1
A272	1
V282	1
I283	1
S284	1
V285	1
L63	1
V68	1
V69	1
F70	1
W71	1
T72	1
Q73	1
G74	1
K75	1
W76	1
T82	1
G90	1
F91	1
N92	1
V95	1
I99	1
A100	1
A101	1
E104	1
S105	1
D106	1
K107	1
F108	1
F109	1
N110	1
N111	1
G112	1
S113	1
I118	1
L119	1
K238	1
K239	1
V240	1
E241	1
E242	1
A243	1
L248	1
K256	1
D259	1
G260	1
L267	1
Q271	1
A272	1
V282	1
I283	1
S284	1
V285	1
L63	1
V68	1
V69	1
F70	1
W71	1
T72	1
Q73	1
G74	1
K75	1
W76	1
T82	1
G90	1
F91	1
N92	1
V95	1
I99	1
A100	1
A101	1
E104	1
S105	1
D106	1
K107	1
F108	1
F109	1
N110	1
N111	1
G112	1
S113	1
I118	1
L119	1
K238	1
K239	1
V240	1
E241	1
E242	1
A243	1
L248	1
K256	1
D259	1
G260	1
L267	1
Q271	

Chain B:

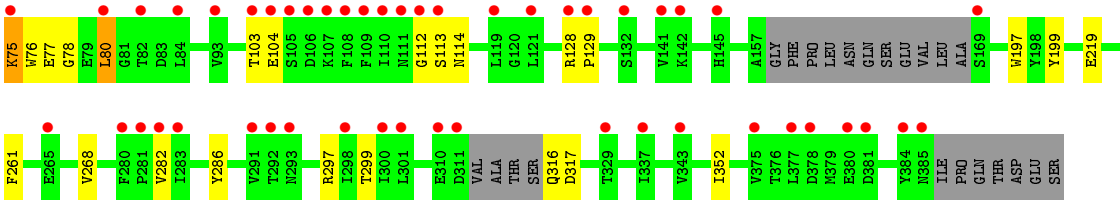
11% 83% 7% 9%

LEU PRO ARG GLU THR ASP GLU PRO GLU PRO GLU PRO GLU LYS T-4 V0 E1 M2 V3 G11 V20 I29 D32 F38 A39 V40 V67 Q73 L80 N92 V95 I99 A100 A101 I102 I110 N111 G112 S113 I118 L119 P129 F136 L140 H145 L152 G156 A157 PHE PRO LEU ASN SER GLU VAL LEU ALA H181 W197 Y198 Y199 I203 V204 R205 Y222 L234 R235 L236 K239 K256 F261 E265 Q266 L267 V268 Q271 A272 F280 P281 V282 L283 S284 L285 Y286 L287

Chain C: 



LEU PRO ARG GLU THR ASP GLU PRO GLU GLY LYS T-4 G-3 G21 S22 P23 P24 Q25 V31 A39 A42 A43 P44 P46 P47 A48 A49 A50 A51 Y52 Q53 R54 Q55 L56 S57 S58 T59 Y60 R61 D62 L63 K64 R65 G66 V67 Y68 V69 Y70 Y71 T72 Q73 C74



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	229.20 Å 98.83 Å 63.13 Å 90.00° 103.36° 90.00°	Depositor
Resolution (Å)	111.80 – 1.80 24.03 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.4 (111.80-1.80) 94.4 (24.03-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.80 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.177 , 0.208 0.247 , 0.266	Depositor DCC
R_{free} test set	1212 reflections (1.02%)	DCC
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.1	EDS
Estimated twinning fraction	0.024 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 119460 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9702	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, EV3

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	0.55	0/3046	0.69	2/4136 (0.0%)
1	B	0.55	0/3039	0.71	1/4127 (0.0%)
1	C	0.50	0/3077	0.65	0/4179
All	All	0.53	0/9162	0.68	3/12442 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	67	VAL	CB-CA-C	-6.05	99.90	111.40
1	A	297	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	A	297	ARG	NE-CZ-NH2	-5.10	117.75	120.30

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	A	2962	0	2875	38	0
1	B	2956	0	2882	21	0
1	C	2987	0	2897	15	0
2	A	15	0	12	3	0
2	B	15	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	15	0	12	0	0
3	A	42	0	56	2	0
3	B	48	0	64	7	0
3	C	12	0	16	0	0
4	A	236	0	0	3	0
4	B	246	0	0	0	0
4	C	168	0	0	0	0
All	All	9702	0	8826	72	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 4.

All (72) 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:A:267:LEU:HD23	1:A:321:LYS:HG3	1.60	0.82
1:C:282:VAL:HG13	1:C:299:THR:HG23	1.68	0.75
1:A:215:MET:HE1	1:A:243:ALA:HB3	1.72	0.69
1:B:0:VAL:H	3:B:394:GOL:H31	1.63	0.63
1:A:309:VAL:HG21	1:A:321:LYS:HD2	1.83	0.61
1:B:0:VAL:HG22	3:B:394:GOL:H32	1.81	0.60
1:C:199:TYR:HB3	1:C:352:ILE:HD11	1.84	0.59
1:A:267:LEU:CD2	1:A:321:LYS:HG3	2.31	0.59
1:C:286:TYR:CZ	1:C:297:ARG:HD3	2.38	0.58
1:A:199:TYR:HB3	1:A:352:ILE:HD11	1.87	0.56
1:C:282:VAL:HG13	1:C:299:THR:CG2	2.34	0.55
1:A:69:VAL:HG21	1:A:76:TRP:CZ2	2.41	0.55
1:B:205:ARG:HA	3:B:400:GOL:H32	1.89	0.55
1:A:2:MET:HE1	1:A:176:ILE:H	1.70	0.55
1:C:67:VAL:HG22	1:C:80:LEU:HD22	1.90	0.54
1:B:199:TYR:HB3	1:B:352:ILE:HD11	1.91	0.52
1:C:69:VAL:HG21	1:C:76:TRP:CZ2	2.45	0.51
1:A:333:MET:HE3	1:A:337:ILE:HG21	1.91	0.51
1:A:215:MET:HE1	1:A:240:VAL:HA	1.93	0.51
1:A:134:GLU:OE2	1:B:1:GLU:OE2	2.28	0.51
1:A:17:GLU:HB3	4:A:607:HOH:O	2.11	0.51
1:A:111:ASN:HD22	1:A:112:GLY:N	2.12	0.47
1:A:213:LEU:HD23	1:A:215:MET:HE3	1.95	0.47
1:B:0:VAL:HG22	3:B:394:GOL:C3	2.45	0.47
1:A:32:ASP:OD2	1:A:118:ILE:HD11	2.13	0.47
2:A:393:EV3:C3	3:A:398:GOL:H2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:MET:CE	1:A:243:ALA:HB3	2.44	0.47
1:A:357:SER:HB3	1:A:360:HIS:HB3	1.97	0.46
1:C:112:GLY:O	1:C:114:ASN:N	2.48	0.46
1:B:95:VAL:HG11	1:B:140:LEU:HD12	1.98	0.46
1:B:333:MET:HE3	1:B:337:ILE:HG21	1.97	0.46
1:B:156:GLY:O	1:B:157:ALA:CB	2.64	0.46
1:A:364:GLU:HB3	4:A:499:HOH:O	2.16	0.45
1:A:215:MET:CE	1:A:240:VAL:HA	2.47	0.45
1:A:32:ASP:OD2	2:A:393:EV3:N7	2.49	0.45
1:C:77:GLU:HG3	1:C:104:GLU:CG	2.47	0.45
1:C:69:VAL:HG22	1:C:128:ARG:HG3	1.98	0.44
1:A:154:LEU:O	1:A:339:GLU:HA	2.18	0.44
1:B:261:PHE:CD1	1:B:268:VAL:HG23	2.52	0.44
1:A:222:TYR:HA	1:A:223:ASP:HA	1.74	0.44
1:A:1:GLU:CD	1:A:1:GLU:H	2.21	0.44
1:B:11:GLY:N	3:B:397:GOL:H2	2.32	0.44
2:A:393:EV3:C5	3:A:398:GOL:H2	2.48	0.44
1:A:92:ASN:C	1:A:92:ASN:HD22	2.21	0.44
1:B:32:ASP:OD2	2:B:393:EV3:N7	2.51	0.44
1:A:238:LYS:NZ	1:A:242:GLU:OE2	2.49	0.43
1:A:2:MET:CE	1:A:90:GLY:HA2	2.48	0.43
1:B:110:ILE:HB	1:B:113:SER:HB3	2.01	0.43
1:B:293:ASN:HA	1:B:376:THR:O	2.19	0.42
1:A:134:GLU:HB2	3:B:394:GOL:H2	2.01	0.42
1:A:333:MET:CE	1:A:337:ILE:HG21	2.50	0.42
1:B:67:VAL:HG13	1:B:129:PRO:HD3	2.01	0.42
1:C:71:TYR:CE1	1:C:75:LYS:HA	2.55	0.42
1:A:197:TRP:CG	1:A:198:TYR:N	2.88	0.42
1:A:211:GLN:NE2	4:A:483:HOH:O	2.53	0.42
1:A:213:LEU:HG	1:A:215:MET:HE2	2.00	0.42
1:B:92:ASN:HD22	3:B:395:GOL:H31	1.85	0.42
1:A:2:MET:CE	1:A:176:ILE:H	2.33	0.41
1:A:238:LYS:HE2	1:A:326:GLN:HE22	1.84	0.41
1:A:95:VAL:HG11	1:A:140:LEU:HA	2.02	0.41
1:A:82:THR:HG21	1:B:0:VAL:HG12	2.02	0.41
1:A:42:ALA:CB	1:A:101:ALA:HB1	2.50	0.41
1:C:65:LYS:NZ	1:C:129:PRO:HG3	2.35	0.41
1:A:63:LEU:O	1:B:181:HIS:HD2	2.04	0.41
1:B:267:LEU:HD21	1:B:309:VAL:HG21	2.02	0.41
1:B:32:ASP:OD2	1:B:118:ILE:HD11	2.21	0.41
1:C:78:GLY:HA2	1:C:103:THR:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:LEU:HD12	1:C:80:LEU:HB3	2.02	0.41
1:B:222:TYR:OH	1:C:219:GLU:OE1	2.26	0.41
1:A:293:ASN:HA	1:A:376:THR:O	2.21	0.40
1:C:261:PHE:CD1	1:C:268:VAL:HG23	2.57	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	371/411 (90%)	362 (98%)	9 (2%)	0	100	100
1	B	371/411 (90%)	364 (98%)	7 (2%)	0	100	100
1	C	375/411 (91%)	364 (97%)	9 (2%)	2 (0%)	34	17
All	All	1117/1233 (91%)	1090 (98%)	25 (2%)	2 (0%)	52	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	-3	GLY
1	C	113	SER

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	322/352 (92%)	313 (97%)	9 (3%)	51	35
1	B	322/352 (92%)	317 (98%)	5 (2%)	70	59
1	C	326/352 (93%)	319 (98%)	7 (2%)	61	47
All	All	970/1056 (92%)	949 (98%)	21 (2%)	60	45

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLU
1	A	72	THR
1	A	92	ASN
1	A	111	ASN
1	A	169	SER
1	A	197	TRP
1	A	259	ASP
1	A	364	GLU
1	A	367	THR
1	B	67	VAL
1	B	73	GLN
1	B	111	ASN
1	B	197	TRP
1	B	239	LYS
1	C	65	LYS
1	C	67	VAL
1	C	75	LYS
1	C	80	LEU
1	C	197	TRP
1	C	316	GLN
1	C	317	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	73	GLN
1	A	92	ASN
1	A	111	ASN
1	A	114	ASN
1	A	211	GLN
1	A	266	GLN
1	A	326	GLN

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Mol	Chain	Res	Type
1	A	362	HIS
1	B	28	ASN
1	B	53	GLN
1	B	92	ASN
1	B	111	ASN
1	B	181	HIS
1	B	362	HIS
1	C	28	ASN
1	C	53	GLN
1	C	73	GLN
1	C	92	ASN
1	C	362	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

20 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	EV3	A	393	-	14,16,16	1.41	2 (14%)	15,22,22	0.94	0
3	GOL	A	394	-	5,5,5	0.35	0	5,5,5	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	395	-	5,5,5	0.61	0	5,5,5	0.46	0
3	GOL	A	396	-	5,5,5	0.49	0	5,5,5	0.57	0
3	GOL	A	397	-	5,5,5	0.31	0	5,5,5	0.36	0
3	GOL	A	398	-	5,5,5	0.33	0	5,5,5	0.40	0
3	GOL	A	399	-	5,5,5	0.35	0	5,5,5	0.71	0
3	GOL	A	400	-	5,5,5	0.36	0	5,5,5	0.14	0
2	EV3	B	393	-	14,16,16	1.44	2 (14%)	15,22,22	0.95	0
3	GOL	B	394	-	5,5,5	0.66	0	5,5,5	1.56	2 (40%)
3	GOL	B	395	-	5,5,5	0.30	0	5,5,5	0.32	0
3	GOL	B	396	-	5,5,5	0.39	0	5,5,5	0.55	0
3	GOL	B	397	-	5,5,5	0.25	0	5,5,5	0.43	0
3	GOL	B	398	-	5,5,5	0.34	0	5,5,5	0.35	0
3	GOL	B	399	-	5,5,5	0.34	0	5,5,5	0.54	0
3	GOL	B	400	-	5,5,5	0.32	0	5,5,5	0.54	0
3	GOL	B	401	-	5,5,5	0.32	0	5,5,5	0.49	0
2	EV3	C	393	-	14,16,16	1.45	2 (14%)	15,22,22	0.87	0
3	GOL	C	394	-	5,5,5	0.39	0	5,5,5	0.49	0
3	GOL	C	395	-	5,5,5	0.39	0	5,5,5	0.35	0

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	EV3	A	393	-	-	0/4/4/4	0/2/2/2
3	GOL	A	394	-	-	0/4/4/4	0/0/0/0
3	GOL	A	395	-	-	0/4/4/4	0/0/0/0
3	GOL	A	396	-	-	0/4/4/4	0/0/0/0
3	GOL	A	397	-	-	0/4/4/4	0/0/0/0
3	GOL	A	398	-	-	0/4/4/4	0/0/0/0
3	GOL	A	399	-	-	0/4/4/4	0/0/0/0
3	GOL	A	400	-	-	0/4/4/4	0/0/0/0
2	EV3	B	393	-	-	0/4/4/4	0/2/2/2
3	GOL	B	394	-	-	0/4/4/4	0/0/0/0
3	GOL	B	395	-	-	0/4/4/4	0/0/0/0
3	GOL	B	396	-	-	0/4/4/4	0/0/0/0
3	GOL	B	397	-	-	0/4/4/4	0/0/0/0
3	GOL	B	398	-	-	0/4/4/4	0/0/0/0
3	GOL	B	399	-	-	0/4/4/4	0/0/0/0
3	GOL	B	400	-	-	0/4/4/4	0/0/0/0
3	GOL	B	401	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EV3	C	393	-	-	0/4/4/4	0/2/2/2
3	GOL	C	394	-	-	0/4/4/4	0/0/0/0
3	GOL	C	395	-	-	0/4/4/4	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	393	EV3	C3-C5	-2.53	1.37	1.41
2	C	393	EV3	C3-C5	-2.40	1.38	1.41
2	B	393	EV3	C3-C5	-2.07	1.38	1.41
2	A	393	EV3	C8-N10	2.97	1.40	1.33
2	C	393	EV3	C8-N10	3.14	1.40	1.33
2	B	393	EV3	C8-N10	3.24	1.40	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	394	GOL	O3-C3-C2	2.14	120.56	110.18
3	B	394	GOL	O1-C1-C2	2.35	121.57	110.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	393	EV3	3	0
3	A	398	GOL	2	0
2	B	393	EV3	1	0
3	B	394	GOL	4	0
3	B	395	GOL	1	0
3	B	397	GOL	1	0
3	B	400	GOL	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	373/411 (90%)	1.08	82 (21%) 1 1	9, 20, 34, 179	5 (1%)
1	B	373/411 (90%)	0.62	47 (12%) 5 4	6, 24, 74, 100	4 (1%)
1	C	375/411 (91%)	1.28	82 (21%) 1 1	11, 20, 37, 618	4 (1%)
All	All	1121/1233 (90%)	0.99	211 (18%) 2 1	6, 21, 58, 618	13 (1%)

All (211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	48	LEU	15.5
1	A	48	LEU	9.5
1	C	45	HIS	7.5
1	A	72	THR	7.4
1	C	73	GLN	7.2
1	C	72	THR	6.9
1	A	73	GLN	6.7
1	C	80	LEU	6.6
1	C	46	PRO	6.2
1	C	71	TYR	5.6
1	C	110	ILE	5.5
1	C	70	PRO	5.4
1	A	43	ALA	5.4
1	C	145	HIS	5.4
1	A	47	PHE	5.3
1	C	47	PHE	5.3
1	A	111	ASN	5.1
1	A	337	ILE	4.9
1	C	64	ARG	4.9
1	C	74	GLY	4.9
1	C	63	LEU	4.8
1	A	-2	SER	4.7
1	A	310	GLU	4.7

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Mol	Chain	Res	Type	RSRZ
1	C	132	SER	4.6
1	B	272	ALA	4.6
1	A	298	ILE	4.5
1	C	103	THR	4.5
1	A	112	GLY	4.5
1	A	203	ILE	4.4
1	A	285	LEU	4.4
1	A	201	VAL	4.4
1	C	377	LEU	4.4
1	A	119	LEU	4.3
1	C	55	GLN	4.3
1	A	110	ILE	4.2
1	A	56	LEU	4.2
1	A	49	HIS	4.1
1	A	352	ILE	4.1
1	A	0	VAL	4.1
1	A	145	HIS	4.1
1	C	112	GLY	4.1
1	C	291	VAL	4.1
1	C	49	HIS	4.0
1	C	68	TYR	4.0
1	C	75	LYS	4.0
1	C	142	LYS	4.0
1	C	111	ASN	4.0
1	C	113	SER	3.9
1	A	10	SER	3.9
1	A	9	LYS	3.8
1	A	316	GLN	3.8
1	A	23	PRO	3.8
1	B	265	GLU	3.8
1	A	354	PHE	3.8
1	A	51	TYR	3.7
1	B	38	PHE	3.7
1	A	55	GLN	3.7
1	C	58	SER	3.7
1	C	378	ASP	3.7
1	A	92	ASN	3.7
1	A	74	GLY	3.6
1	C	311	ASP	3.6
1	C	119	LEU	3.6
1	A	68	TYR	3.6
1	A	287	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	-3	GLY	3.5
1	A	343	VAL	3.5
1	A	169	SER	3.5
1	C	84	LEU	3.5
1	C	298	ILE	3.5
1	A	45	HIS	3.5
1	C	380	GLU	3.4
1	C	43	ALA	3.4
1	A	106	ASP	3.4
1	B	380	GLU	3.4
1	B	145	HIS	3.4
1	B	39	ALA	3.4
1	B	99	ILE	3.4
1	B	73	GLN	3.4
1	B	384	TYR	3.4
1	C	44	PRO	3.4
1	C	56	LEU	3.3
1	C	106	ASP	3.3
1	A	38	PHE	3.3
1	C	265	GLU	3.3
1	C	107	LYS	3.2
1	C	23	PRO	3.2
1	C	310	GLU	3.2
1	A	283	ILE	3.2
1	C	24	PRO	3.2
1	C	300	ILE	3.2
1	A	42	ALA	3.2
1	A	300	ILE	3.2
1	A	-1	PHE	3.1
1	A	191	THR	3.1
1	C	109	PHE	3.1
1	C	31	VAL	3.1
1	C	93	VAL	3.1
1	C	51	TYR	3.1
1	C	292	THR	3.0
1	A	1	GLU	3.0
1	C	60	TYR	3.0
1	C	104	GLU	3.0
1	B	337	ILE	3.0
1	C	381	ASP	3.0
1	B	306	LEU	3.0
1	A	227	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	40	VAL	2.9
1	C	66	GLY	2.9
1	A	71	TYR	2.9
1	C	25	GLN	2.9
1	C	141	VAL	2.9
1	A	271	GLN	2.9
1	A	121	LEU	2.9
1	A	202	ILE	2.9
1	B	203	ILE	2.9
1	B	157	ALA	2.9
1	A	104	GLU	2.9
1	C	385	ASN	2.8
1	C	375	VAL	2.8
1	B	100	ALA	2.8
1	B	378	ASP	2.8
1	B	305	TYR	2.8
1	C	384	TYR	2.8
1	B	271	GLN	2.8
1	A	107	LYS	2.8
1	B	29	ILE	2.8
1	C	21	GLY	2.8
1	B	281	PRO	2.8
1	C	22	SER	2.8
1	C	337	ILE	2.8
1	A	150	PHE	2.8
1	A	333	MET	2.7
1	A	44	PRO	2.7
1	A	344	VAL	2.7
1	B	343	VAL	2.7
1	B	152	LEU	2.7
1	B	285	LEU	2.7
1	C	50	ARG	2.7
1	A	118	ILE	2.6
1	A	206	VAL	2.6
1	B	0	VAL	2.6
1	B	324	ILE	2.6
1	C	282	VAL	2.6
1	A	378	ASP	2.6
1	A	152	LEU	2.6
1	B	169	SER	2.6
1	B	102	ILE	2.6
1	B	280	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	317	ASP	2.6
1	B	331	THR	2.6
1	A	234	LEU	2.5
1	C	301	LEU	2.5
1	A	317	ASP	2.5
1	A	156	GLY	2.5
1	C	39	ALA	2.5
1	C	42	ALA	2.5
1	B	136	PHE	2.5
1	C	108	PHE	2.5
1	A	99	ILE	2.5
1	B	300	ILE	2.5
1	A	53	GLN	2.5
1	C	121	LEU	2.5
1	B	101	ALA	2.4
1	B	283	ILE	2.4
1	C	281	PRO	2.4
1	B	20[A]	VAL	2.4
1	A	4	ASP	2.4
1	A	248	ILE	2.4
1	C	53	GLN	2.4
1	A	20	VAL	2.4
1	A	46	PRO	2.4
1	C	283	ILE	2.3
1	C	129	PRO	2.3
1	B	354	PHE	2.3
1	C	329	THR	2.3
1	B	119	LEU	2.3
1	A	385	ASN	2.3
1	A	272	ALA	2.3
1	A	256	LYS	2.3
1	A	282	VAL	2.3
1	C	293	ASN	2.3
1	A	345	PHE	2.2
1	A	113	SER	2.2
1	B	118	ILE	2.2
1	B	3	VAL	2.2
1	A	39	ALA	2.2
1	A	260	GLY	2.2
1	B	256	LYS	2.2
1	B	375	VAL	2.2
1	A	341	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	280	PHE	2.2
1	B	236	LEU	2.2
1	C	82	THR	2.2
1	C	69	VAL	2.2
1	A	12	GLN	2.1
1	B	316	GLN	2.1
1	A	109	PHE	2.1
1	A	26	THR	2.1
1	C	169	SER	2.1
1	C	128	ARG	2.1
1	C	343	VAL	2.1
1	C	62	ASP	2.1
1	B	80	LEU	2.1
1	C	65	LYS	2.1
1	C	105	SER	2.1
1	B	234	LEU	2.0
1	B	287	LEU	2.0
1	A	58	SER	2.0
1	B	282	VAL	2.0
1	A	338	MET	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	GOL	A	395	6/6	0.81	0.28	9.88	21,31,34,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	B	400	6/6	0.74	0.36	7.40	35,42,43,46	0
3	GOL	A	399	6/6	0.69	0.32	7.11	51,56,57,58	0
3	GOL	B	395	6/6	0.81	0.24	5.40	36,41,44,44	0
3	GOL	B	394	6/6	0.83	0.33	4.54	5,19,31,38	0
3	GOL	B	398	6/6	0.81	0.35	3.74	19,39,42,44	0
3	GOL	C	394	6/6	0.86	0.22	3.18	21,34,35,43	0
3	GOL	B	397	6/6	0.88	0.21	2.37	29,33,33,35	0
3	GOL	A	396	6/6	0.64	0.23	2.16	22,40,41,45	0
3	GOL	B	396	6/6	0.87	0.21	1.59	11,37,42,42	0
3	GOL	B	401	6/6	0.78	0.22	0.95	51,54,56,58	0
2	EV3	B	393	15/15	0.79	0.17	0.50	38,42,44,44	0
2	EV3	C	393	15/15	0.66	0.21	0.24	62,72,72,72	0
2	EV3	A	393	15/15	0.84	0.13	-0.01	27,31,34,36	0
3	GOL	B	399	6/6	0.78	0.16	-0.20	31,40,42,43	0
3	GOL	A	398	6/6	0.68	0.14	-0.21	50,53,55,58	0
3	GOL	A	400	6/6	0.74	0.21	-	51,52,54,56	0
3	GOL	A	397	6/6	0.84	0.15	-	47,47,48,49	0
3	GOL	A	394	6/6	0.76	0.17	-	46,51,52,53	0
3	GOL	C	395	6/6	0.78	0.26	-	43,47,49,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.