Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 07:05 AM EDT

PDB ID	:	3O9M
Title	:	Co-crystallization studies of full length recombinant BChE with cocaine offers insights into cocaine detoxification
Authors	:	Asojo, O.A.; Ngamelue, M.N.; Homma, K.; Lockridge, O.
Deposited on	:	2010-08-04
Resolution	:	2.98 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 (i)) were used in the production of this report:

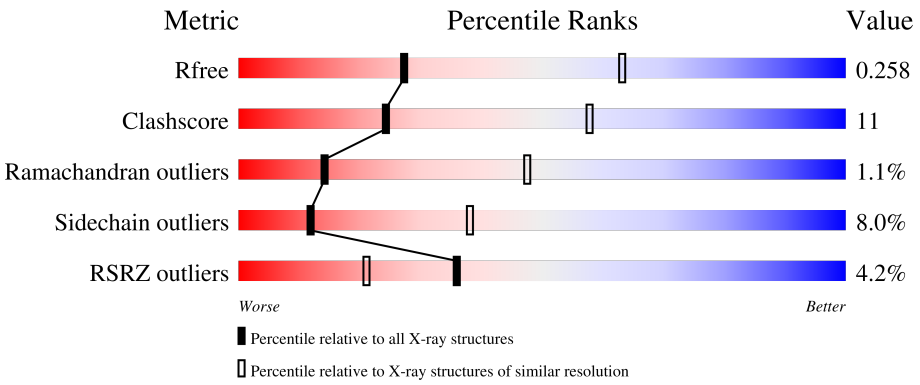
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	130704	2754 (3.00-2.96)
Clashscore	141614	3103 (3.00-2.96)
Ramachandran outliers	138981	2993 (3.00-2.96)
Sidechain outliers	138945	2996 (3.00-2.96)
RSRZ outliers	127900	2644 (3.00-2.96)

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	A	574	4% 74% 15% • • 7%
1	B	574	4% 67% 21% • • 7%

2 Entry composition (i)

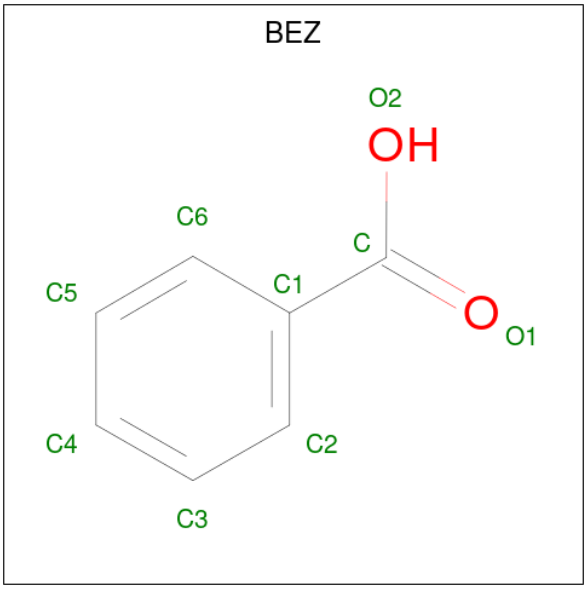
There are 3 unique types of molecules in this entry. The entry contains 8472 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	531	4226	2726	710	774	16	0	0	0
1	B	531	4226	2726	710	774	16	0	0	0

- Molecule 2 is BENZOIC ACID (three-letter code: BEZ) (formula: $C_7H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	9	7	2	0	0
2	B	1	9	7	2	0	0

- Molecule 3 is water.

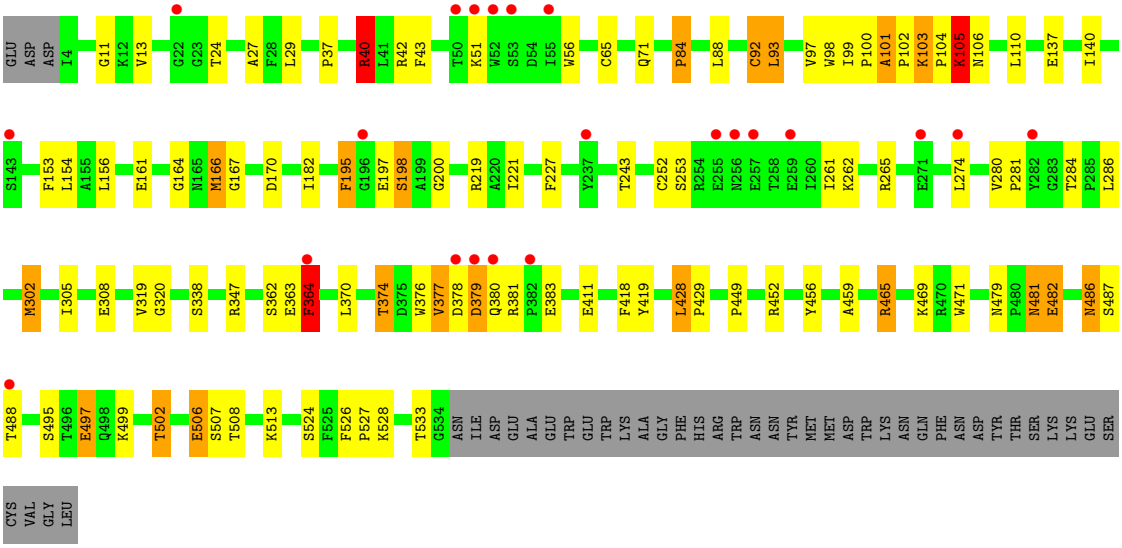
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	1	1	1	0	0
			Total	O		
3	B	1	1	1	0	0

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.

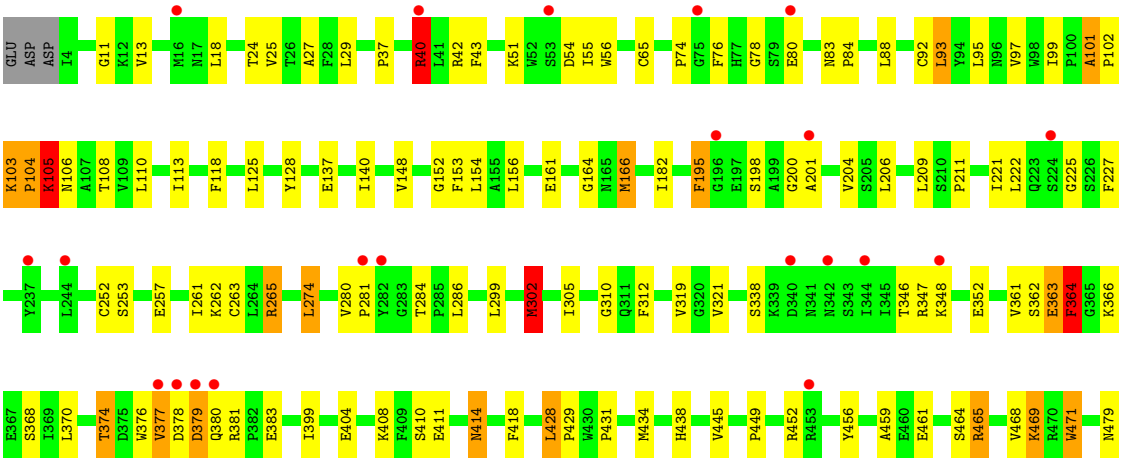
- Molecule 1: Cholinesterase

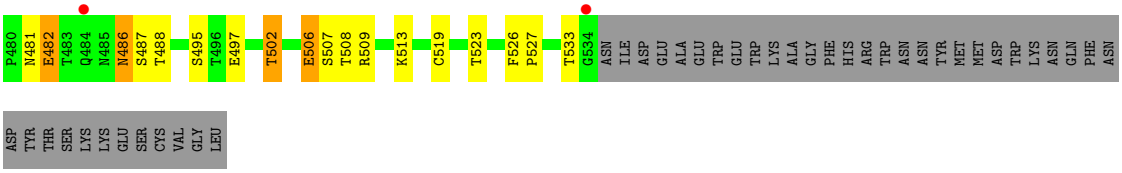
Chain A:



- Molecule 1: Cholinesterase

Chain B:




P480
N481
E482
T483
Q484
N485
N486
S487
T488
S495
T496
E497
T502
E506
S507
T508
R509
K513
C519
T523
F526
P527
T533
G534
ASN
ILE
ASP
GLU
ALA
GLU
TRP
GLU
TRP
LYS
ALA
GLY
PHE
HIS
ARG
TRP
ASN
ASN
TYR
MET
MET
ASP
TRP
LYS
ASN
GLN
PHE
ASN
ASP
TYR
THR
SER
LYS
LYS
GLU
SER
CYS
VAL
GLY
LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α, β, γ	150.39Å 150.39Å 142.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	142.45 – 2.98 31.73 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.7 (142.45-2.98) 99.8 (31.73-2.98)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	14.22 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.223 , 0.262 0.217 , 0.258	Depositor DCC
R_{free} test set	1720 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	60.3	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 30.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8472	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.96% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: BEZ

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	0.86	4/4345 (0.1%)	0.85	11/5900 (0.2%)
1	B	0.86	4/4345 (0.1%)	0.84	11/5900 (0.2%)
All	All	0.86	8/8690 (0.1%)	0.84	22/11800 (0.2%)

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

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	364	PHE	CB-CG	-7.85	1.38	1.51
1	A	40	ARG	CZ-NH2	7.26	1.42	1.33
1	B	105	LYS	CD-CE	7.04	1.68	1.51
1	B	364	PHE	CB-CG	-7.01	1.39	1.51
1	A	92	CYS	CB-SG	-6.86	1.70	1.82
1	B	404	GLU	CG-CD	5.61	1.60	1.51
1	A	101	ALA	C-O	-5.38	1.13	1.23
1	B	40	ARG	CZ-NH2	-5.07	1.26	1.33

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	40	ARG	NE-CZ-NH2	-8.38	116.11	120.30
1	B	40	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	A	302	MET	CG-SD-CE	7.20	111.72	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	105	LYS	CB-CA-C	7.05	124.50	110.40
1	B	104	PRO	C-N-CA	6.49	137.93	121.70
1	A	364	PHE	CB-CG-CD1	-6.42	116.30	120.80
1	A	465	ARG	NE-CZ-NH1	-6.12	117.24	120.30
1	A	101	ALA	C-N-CA	-5.92	97.15	122.00
1	B	302	MET	CA-CB-CG	5.90	123.33	113.30
1	A	101	ALA	C-N-CD	5.81	140.60	128.40
1	A	40	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	B	364	PHE	N-CA-CB	-5.55	100.61	110.60
1	B	263	CYS	CA-CB-SG	5.53	123.95	114.00
1	B	286	LEU	CA-CB-CG	5.53	128.01	115.30
1	B	101	ALA	C-N-CD	-5.38	108.77	120.60
1	A	302	MET	CB-CG-SD	5.31	128.32	112.40
1	B	110	LEU	CA-CB-CG	5.28	127.44	115.30
1	A	219	ARG	NE-CZ-NH1	-5.24	117.68	120.30
1	A	286	LEU	CA-CB-CG	5.24	127.36	115.30
1	A	481	ASN	CB-CA-C	5.17	120.75	110.40
1	B	105	LYS	CB-CA-C	5.14	120.69	110.40
1	B	104	PRO	CA-C-N	5.09	128.40	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	104	PRO	Peptide

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	4226	0	4131	79	0
1	B	4226	0	4131	107	0
2	A	9	0	5	2	0
2	B	9	0	5	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	8472	0	8272	184	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 11.

All (184) 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:B:105:LYS:HE2	1:B:106:ASN:H	1.07	1.11
1:B:40:ARG:HH11	1:B:40:ARG:HB2	1.02	1.07
1:B:105:LYS:HE2	1:B:106:ASN:N	1.74	1.02
1:B:105:LYS:CE	1:B:106:ASN:H	1.78	0.96
1:A:164:GLY:C	1:A:166:MET:HE2	1.91	0.90
1:B:40:ARG:HB2	1:B:40:ARG:NH1	1.88	0.89
1:A:370:LEU:O	1:A:374:THR:HB	1.73	0.88
1:B:370:LEU:O	1:B:374:THR:HB	1.79	0.82
1:B:164:GLY:C	1:B:166:MET:HE2	2.03	0.79
1:A:24:THR:O	1:A:101:ALA:HB2	1.83	0.78
1:B:302:MET:HB3	1:B:305:ILE:HD12	1.66	0.78
1:A:497:GLU:OE2	1:A:499:LYS:HE3	1.87	0.74
1:B:40:ARG:HH11	1:B:40:ARG:CB	1.91	0.73
1:A:449:PRO:HA	1:A:456:TYR:CD1	2.23	0.73
1:A:506:GLU:HG2	1:A:507:SER:H	1.53	0.73
1:B:449:PRO:HA	1:B:456:TYR:CD1	2.24	0.72
1:A:506:GLU:CG	1:A:507:SER:H	2.01	0.72
1:B:506:GLU:HG2	1:B:507:SER:H	1.52	0.72
1:A:377:VAL:HG22	1:A:377:VAL:O	1.90	0.71
1:B:506:GLU:CG	1:B:507:SER:H	2.03	0.70
1:B:319:VAL:O	1:B:418:PHE:HA	1.93	0.69
1:B:164:GLY:CA	1:B:166:MET:HE2	2.22	0.69
1:A:40:ARG:HB2	1:A:40:ARG:NH1	2.08	0.68
1:A:302:MET:HB2	1:A:305:ILE:HD12	1.76	0.68
1:B:13:VAL:HG12	1:B:56:TRP:HB3	1.76	0.67
1:A:164:GLY:CA	1:A:166:MET:HE2	2.24	0.66
1:B:40:ARG:HA	1:B:265:ARG:HH21	1.60	0.65
1:B:379:ASP:OD2	1:B:381:ARG:HG3	1.97	0.65
1:A:377:VAL:HG23	1:B:459:ALA:HB2	1.79	0.64
1:A:37:PRO:HD3	1:A:93:LEU:HD22	1.78	0.64
1:B:105:LYS:HB3	1:B:105:LYS:NZ	2.13	0.64
1:A:319:VAL:O	1:A:418:PHE:HA	1.98	0.63
1:A:42:ARG:O	1:A:43:PHE:HB2	1.98	0.63
1:A:97:VAL:HG12	1:A:99:ILE:CD1	2.29	0.63
1:B:482:GLU:O	1:B:486:ASN:HB3	1.99	0.63
1:B:321:VAL:HG21	1:B:399:ILE:HG12	1.81	0.62
1:A:482:GLU:O	1:A:486:ASN:HB3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:LEU:HD12	1:B:128:TYR:CE2	2.36	0.60
1:B:37:PRO:HD3	1:B:93:LEU:HD22	1.82	0.60
1:A:379:ASP:OD2	1:A:381:ARG:HG3	2.02	0.59
1:B:156:LEU:HD12	1:B:261:ILE:CD1	2.33	0.59
1:A:13:VAL:HG12	1:A:56:TRP:HB3	1.84	0.59
1:B:24:THR:O	1:B:101:ALA:CB	2.51	0.59
1:B:84:PRO:HG2	1:B:88:LEU:HD11	1.83	0.58
1:B:377:VAL:HG22	1:B:377:VAL:O	2.02	0.58
1:A:40:ARG:HA	1:A:265:ARG:HH21	1.68	0.58
1:A:105:LYS:NZ	1:A:106:ASN:H	2.02	0.58
1:B:97:VAL:HG12	1:B:99:ILE:CD1	2.35	0.57
1:A:164:GLY:CA	1:A:166:MET:CE	2.84	0.56
1:A:97:VAL:HG12	1:A:99:ILE:HD11	1.87	0.55
1:A:102:PRO:O	1:A:103:LYS:C	2.44	0.55
1:B:198:SER:OG	2:B:999:BEZ:H6	2.07	0.55
1:B:27:ALA:HB1	1:B:29:LEU:HD13	1.89	0.55
1:A:105:LYS:CE	1:A:106:ASN:H	2.20	0.55
1:A:198:SER:HG	2:A:999:BEZ:H6	1.72	0.55
1:B:24:THR:O	1:B:101:ALA:HB2	2.07	0.55
1:A:153:PHE:HA	1:A:166:MET:HE3	1.89	0.54
1:B:507:SER:O	1:B:508:THR:CG2	2.55	0.54
1:A:198:SER:OG	2:A:999:BEZ:H6	2.07	0.54
1:A:156:LEU:HD12	1:A:261:ILE:CD1	2.38	0.54
1:B:156:LEU:HD12	1:B:261:ILE:HD11	1.89	0.54
1:B:43:PHE:CE1	1:B:154:LEU:HD22	2.44	0.53
1:B:11:GLY:HA2	1:B:51:LYS:NZ	2.24	0.53
1:B:97:VAL:HG12	1:B:99:ILE:HD11	1.89	0.53
1:B:221:ILE:C	1:B:222:LEU:HD12	2.29	0.53
1:B:431:PRO:HD2	1:B:434:MET:SD	2.48	0.53
1:B:469:LYS:HG2	1:B:482:GLU:HG2	1.90	0.53
1:A:105:LYS:HZ3	1:A:106:ASN:H	1.55	0.53
1:B:140:ILE:HG21	1:B:182:ILE:HD11	1.89	0.53
1:A:459:ALA:HB2	1:B:377:VAL:HG23	1.89	0.53
1:B:161:GLU:HB3	1:B:261:ILE:HG21	1.91	0.53
1:B:506:GLU:HG2	1:B:507:SER:N	2.23	0.53
1:A:164:GLY:HA2	1:A:166:MET:CE	2.39	0.52
1:A:486:ASN:C	1:A:486:ASN:OD1	2.47	0.52
1:A:98:TRP:C	1:A:99:ILE:HD12	2.30	0.52
1:A:140:ILE:HG21	1:A:182:ILE:HD11	1.90	0.52
1:A:469:LYS:HG2	1:A:482:GLU:HG2	1.92	0.52
1:A:164:GLY:HA2	1:A:166:MET:HE1	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:ASP:OD1	1:B:54:ASP:N	2.43	0.51
1:B:152:GLY:O	1:B:166:MET:HE3	2.10	0.51
1:B:166:MET:HE3	1:B:166:MET:H	1.75	0.51
1:B:137:GLU:OE2	1:B:469:LYS:HE3	2.11	0.51
1:B:479:ASN:OD1	1:B:481:ASN:ND2	2.44	0.51
1:A:378:ASP:C	1:A:380:GLN:N	2.64	0.51
1:A:156:LEU:HD12	1:A:261:ILE:HD11	1.92	0.50
1:B:166:MET:H	1:B:166:MET:CE	2.24	0.50
1:A:506:GLU:HG2	1:A:507:SER:N	2.23	0.50
1:A:227:PHE:CD1	1:A:227:PHE:C	2.85	0.49
1:B:153:PHE:HA	1:B:166:MET:HE3	1.93	0.49
1:B:164:GLY:HA2	1:B:166:MET:CE	2.41	0.49
1:A:154:LEU:HD11	1:A:243:THR:HG23	1.94	0.49
1:A:105:LYS:HE2	1:A:106:ASN:OD1	2.13	0.49
1:B:206:LEU:HD22	1:B:299:LEU:HD11	1.94	0.49
1:B:95:LEU:HD12	1:B:95:LEU:O	2.13	0.49
1:B:361:VAL:O	1:B:366:LYS:HE3	2.13	0.48
1:B:486:ASN:OD1	1:B:486:ASN:C	2.51	0.48
1:B:95:LEU:HD12	1:B:95:LEU:C	2.34	0.48
1:B:526:PHE:HB3	1:B:527:PRO:HD3	1.95	0.48
1:B:97:VAL:CG1	1:B:99:ILE:HD11	2.44	0.48
1:A:97:VAL:CG1	1:A:99:ILE:HD11	2.44	0.48
1:B:102:PRO:O	1:B:103:LYS:C	2.52	0.48
1:B:118:PHE:O	1:B:148:VAL:HB	2.14	0.48
1:B:502:THR:HG22	1:B:508:THR:HA	1.96	0.47
1:A:378:ASP:O	1:A:380:GLN:N	2.48	0.47
1:A:100:PRO:HG2	1:A:104:PRO:HG3	1.95	0.47
1:A:506:GLU:CG	1:A:507:SER:N	2.75	0.47
1:B:25:VAL:HG13	1:B:99:ILE:O	2.14	0.47
1:A:161:GLU:HB3	1:A:261:ILE:HG21	1.97	0.47
1:B:209:LEU:O	1:B:211:PRO:HD3	2.14	0.47
1:B:414:ASN:ND2	1:B:414:ASN:H	2.13	0.47
1:B:378:ASP:C	1:B:380:GLN:N	2.68	0.47
1:B:99:ILE:HD12	1:B:99:ILE:N	2.30	0.47
1:A:84:PRO:HG2	1:A:88:LEU:HD11	1.96	0.46
1:A:479:ASN:OD1	1:A:481:ASN:ND2	2.49	0.46
1:B:414:ASN:H	1:B:414:ASN:HD22	1.61	0.46
1:A:377:VAL:O	1:A:377:VAL:CG2	2.62	0.46
1:B:507:SER:O	1:B:508:THR:HG22	2.15	0.46
1:A:97:VAL:HG12	1:A:99:ILE:HD12	1.97	0.46
1:B:414:ASN:ND2	1:B:414:ASN:N	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:GLY:HA2	1:A:51:LYS:NZ	2.31	0.46
1:B:74:PRO:HA	1:B:80:GLU:OE2	2.16	0.46
1:A:27:ALA:HB1	1:A:29:LEU:HD13	1.98	0.45
1:A:110:LEU:HB3	1:A:195:PHE:CE2	2.52	0.45
1:A:137:GLU:OE2	1:A:469:LYS:HE2	2.15	0.45
1:B:348:LYS:O	1:B:352:GLU:HG2	2.17	0.45
1:B:24:THR:O	1:B:101:ALA:HB3	2.15	0.45
1:B:506:GLU:CG	1:B:507:SER:N	2.77	0.45
1:B:198:SER:HB2	1:B:438:HIS:CE1	2.51	0.45
1:A:274:LEU:HD23	1:A:274:LEU:O	2.17	0.45
1:A:99:ILE:HD12	1:A:99:ILE:N	2.32	0.44
1:A:449:PRO:HA	1:A:456:TYR:HD1	1.80	0.44
1:B:54:ASP:HB2	1:B:55:ILE:H	1.59	0.44
1:B:18:LEU:CD1	1:B:27:ALA:HB2	2.48	0.44
1:B:40:ARG:HA	1:B:265:ARG:NH2	2.31	0.44
1:B:261:ILE:O	1:B:265:ARG:HB2	2.17	0.44
1:A:502:THR:HG22	1:A:508:THR:HA	2.00	0.44
1:B:156:LEU:HD13	1:B:257:GLU:HG2	1.99	0.44
1:B:461:GLU:O	1:B:465:ARG:HB2	2.18	0.44
1:B:502:THR:HB	1:B:509:ARG:O	2.18	0.43
1:A:197:GLU:O	1:A:200:GLY:N	2.47	0.43
1:A:40:ARG:HB2	1:A:40:ARG:HH11	1.80	0.43
1:B:310:GLY:HA2	1:B:312:PHE:CE2	2.54	0.43
1:A:40:ARG:O	1:A:40:ARG:HG3	2.16	0.43
1:B:464:SER:O	1:B:468:VAL:HG23	2.19	0.43
1:A:308:GLU:O	1:A:308:GLU:HG3	2.17	0.43
1:B:113:ILE:O	1:B:200:GLY:HA3	2.19	0.43
1:B:105:LYS:NZ	1:B:106:ASN:H	2.16	0.43
1:B:125:LEU:HD12	1:B:128:TYR:CZ	2.53	0.43
1:B:201:ALA:HB1	1:B:225:GLY:O	2.19	0.43
1:B:227:PHE:C	1:B:227:PHE:CD1	2.91	0.43
1:B:164:GLY:CA	1:B:166:MET:CE	2.92	0.43
1:B:274:LEU:HD23	1:B:274:LEU:O	2.19	0.43
1:A:320:GLY:HA3	1:A:419:TYR:CE2	2.54	0.43
1:B:378:ASP:O	1:B:379:ASP:OD2	2.37	0.42
1:B:99:ILE:HG13	1:B:140:ILE:HG12	2.01	0.42
1:B:156:LEU:HD12	1:B:261:ILE:HD13	2.00	0.42
1:B:346:THR:O	1:B:347:ARG:C	2.58	0.42
1:B:519:CYS:O	1:B:523:THR:OG1	2.28	0.42
1:B:76:PHE:CE2	1:B:78:GLY:HA3	2.55	0.42
1:B:280:VAL:HG23	1:B:281:PRO:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:362:SER:C	1:B:364:PHE:N	2.72	0.42
1:A:280:VAL:HG23	1:A:281:PRO:HD2	2.02	0.42
1:B:449:PRO:HA	1:B:456:TYR:HD1	1.78	0.41
1:A:524:SER:O	1:A:528:LYS:HG2	2.20	0.41
1:B:445:VAL:HG13	1:B:471:TRP:CD1	2.56	0.41
1:A:154:LEU:O	1:A:166:MET:HE1	2.19	0.41
1:A:166:MET:CE	1:A:166:MET:H	2.33	0.41
1:A:378:ASP:C	1:A:380:GLN:H	2.22	0.41
1:B:195:PHE:HD2	1:B:195:PHE:H	1.69	0.41
1:B:428:LEU:HA	1:B:429:PRO:HD3	1.79	0.41
1:B:42:ARG:O	1:B:43:PHE:HB2	2.20	0.41
1:A:40:ARG:HA	1:A:265:ARG:NH2	2.34	0.41
1:A:320:GLY:HA3	1:A:419:TYR:CZ	2.56	0.41
1:A:526:PHE:HB3	1:A:527:PRO:HD3	2.02	0.41
1:B:80:GLU:HG2	1:B:83:ASN:HD22	1.86	0.41
1:A:40:ARG:HB2	1:A:40:ARG:CZ	2.50	0.41
1:A:167:GLY:O	1:A:170:ASP:HB2	2.21	0.41
1:A:195:PHE:HB3	1:A:221:ILE:HB	2.01	0.41
1:A:362:SER:C	1:A:364:PHE:N	2.74	0.41
1:B:195:PHE:HB3	1:B:221:ILE:HB	2.04	0.40
1:A:42:ARG:O	1:A:43:PHE:CB	2.69	0.40
1:B:200:GLY:O	1:B:204:VAL:HG23	2.20	0.40
1:A:428:LEU:HA	1:A:429:PRO:HD3	1.83	0.40
1:B:97:VAL:HG12	1:B:99:ILE:HD12	2.03	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	529/574 (92%)	477 (90%)	46 (9%)	6 (1%)	14 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	529/574 (92%)	477 (90%)	46 (9%)	6 (1%)	14	47
All	All	1058/1148 (92%)	954 (90%)	92 (9%)	12 (1%)	14	47

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	379	ASP
1	B	379	ASP
1	A	347	ARG
1	A	488	THR
1	B	105	LYS
1	B	363	GLU
1	B	488	THR
1	B	506	GLU
1	B	513	LYS
1	A	198	SER
1	A	506	GLU
1	A	513	LYS

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	455/494 (92%)	422 (93%)	33 (7%)	14	42
1	B	455/494 (92%)	415 (91%)	40 (9%)	10	34
All	All	910/988 (92%)	837 (92%)	73 (8%)	12	38

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	65	CYS
1	A	71	GLN
1	A	84	PRO

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Mol	Chain	Res	Type
1	A	92	CYS
1	A	93	LEU
1	A	103	LYS
1	A	105	LYS
1	A	166	MET
1	A	195	PHE
1	A	252	CYS
1	A	253	SER
1	A	262	LYS
1	A	284	THR
1	A	338	SER
1	A	363	GLU
1	A	364	PHE
1	A	374	THR
1	A	376	TRP
1	A	377	VAL
1	A	383	GLU
1	A	411	GLU
1	A	428	LEU
1	A	452	ARG
1	A	465	ARG
1	A	471	TRP
1	A	482	GLU
1	A	486	ASN
1	A	487	SER
1	A	495	SER
1	A	497	GLU
1	A	502	THR
1	A	533	THR
1	B	40	ARG
1	B	65	CYS
1	B	92	CYS
1	B	93	LEU
1	B	103	LYS
1	B	105	LYS
1	B	108	THR
1	B	166	MET
1	B	195	PHE
1	B	252	CYS
1	B	253	SER
1	B	262	LYS
1	B	265	ARG

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Mol	Chain	Res	Type
1	B	274	LEU
1	B	284	THR
1	B	302	MET
1	B	338	SER
1	B	363	GLU
1	B	364	PHE
1	B	368	SER
1	B	374	THR
1	B	376	TRP
1	B	377	VAL
1	B	383	GLU
1	B	408	LYS
1	B	410	SER
1	B	411	GLU
1	B	414	ASN
1	B	428	LEU
1	B	452	ARG
1	B	465	ARG
1	B	469	LYS
1	B	471	TRP
1	B	482	GLU
1	B	486	ASN
1	B	487	SER
1	B	495	SER
1	B	497	GLU
1	B	502	THR
1	B	533	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	351	GLN
1	B	96	ASN
1	B	172	GLN
1	B	351	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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	BEZ	B	999	-	9,9,9	1.07	0	11,11,11	1.05	1 (9%)
2	BEZ	A	999	-	9,9,9	0.79	0	11,11,11	0.79	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	BEZ	B	999	-	-	4/4/4/4	0/1/1/1
2	BEZ	A	999	-	-	1/4/4/4	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	999	BEZ	O2-C-O1	-2.68	117.59	123.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	999	BEZ	O2-C-C1-C2
2	B	999	BEZ	O2-C-C1-C6
2	B	999	BEZ	O1-C-C1-C2
2	B	999	BEZ	O1-C-C1-C6
2	A	999	BEZ	O2-C-C1-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	999	BEZ	1	0
2	A	999	BEZ	2	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, 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	531/574 (92%)	0.14	22 (4%)	37	22	34, 53, 79, 95	0
1	B	531/574 (92%)	0.09	23 (4%)	35	20	34, 53, 79, 94	0
All	All	1062/1148 (92%)	0.11	45 (4%)	36	21	34, 53, 79, 95	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	379	ASP	6.1
1	B	379	ASP	4.5
1	A	380	GLN	4.4
1	A	282	TYR	4.2
1	A	274	LEU	4.2
1	B	378	ASP	3.8
1	B	282	TYR	3.6
1	B	75	GLY	3.6
1	B	534	GLY	3.5
1	A	53	SER	3.5
1	B	380	GLN	3.2
1	A	378	ASP	3.2
1	B	40	ARG	3.1
1	B	244	LEU	3.1
1	A	256	ASN	3.0
1	B	377	VAL	3.0
1	B	281	PRO	3.0
1	A	237	TYR	3.0
1	B	201	ALA	2.9
1	B	237	TYR	2.9
1	A	51	LYS	2.9
1	B	196	GLY	2.8
1	B	342	ASN	2.7
1	A	255	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	55	ILE	2.6
1	A	382	PRO	2.6
1	A	143	SER	2.5
1	B	16	MET	2.5
1	B	348	LYS	2.5
1	B	344	ILE	2.4
1	A	196	GLY	2.4
1	A	271	GLU	2.3
1	A	22	GLY	2.2
1	B	484	GLN	2.2
1	A	52	TRP	2.2
1	B	340	ASP	2.2
1	A	257	GLU	2.2
1	B	80	GLU	2.2
1	B	224	SER	2.2
1	A	50	THR	2.2
1	A	488	THR	2.1
1	B	453	ARG	2.1
1	A	364	PHE	2.1
1	B	53	SER	2.0
1	A	259	GLU	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, 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	B-factors(Å^2)	Q<0.9
2	BEZ	A	999	9/9	0.89	0.26	70,73,75,76	0
2	BEZ	B	999	9/9	0.91	0.24	71,73,75,75	0

6.5 Other polymers (i)

There are no such residues in this entry.