Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 11:51 PM GMT

PDB ID	:	5ER1
Title	:	A rational approach to the design of antihypertensives. X-ray studies of complexes between aspartic proteinases and aminoalcohol renin inhibitors
Authors	:	Cooper, J.B.; Foundling, S.I.; Blundell, T.L.
Deposited on	:	1990-11-07
Resolution	:	2.00 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 (i) symbol.

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

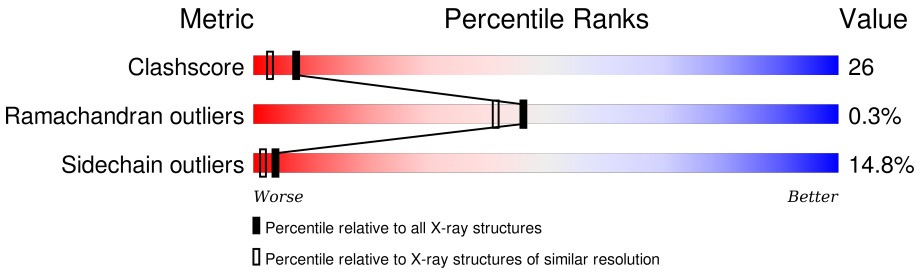
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.00 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	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

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 <=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	E	330	58% 31% 10% •

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	0HT	E	327	-	-	X	-

2 Entry composition

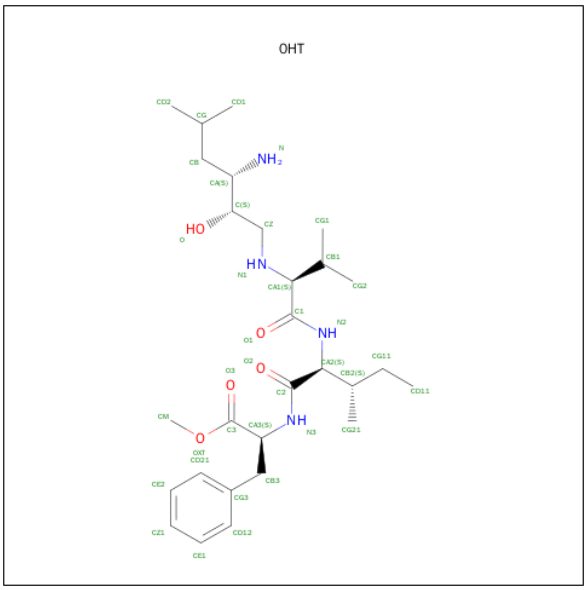
There are 3 unique types of molecules in this entry. The entry contains 2756 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDOTHIAPEPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	330	Total	C	N	O	S	0	0	0
			2389	1514	366	507	2			

- Molecule 2 is METHYL N-[(2S,3S)-3-AMINO-2-HYDROXY-5-METHYLHEXYL]-L-VALYL-L-ISOLEUCYL-L-PHENYLALANINATE (three-letter code: 0HT) (formula: $C_{28}H_{48}N_4O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	E	1	Total	C	N	O	0	0
			37	28	4	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	330	Total	O	0	0
			330	330		

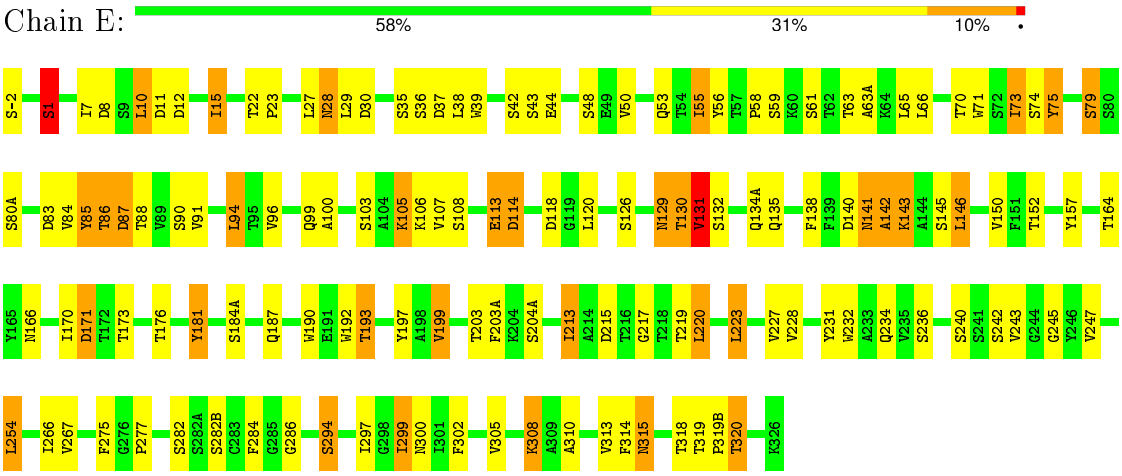
3 Residue-property plots (i)

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: ENDOTHIAPEPSIN

Chain E:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	53.50Å 73.90Å 45.70Å 90.00° 109.60° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.206 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2756	wwPDB-VP
Average B, all atoms (Å^2)	0.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 0HT

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	E	1.43	15/2445 (0.6%)	1.77	52/3345 (1.6%)

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	E	0	1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	35	SER	CA-CB	-7.23	1.42	1.52
1	E	192	TRP	NE1-CE2	-7.21	1.28	1.37
1	E	85	TYR	CD1-CE1	6.66	1.49	1.39
1	E	232	TRP	NE1-CE2	-6.64	1.28	1.37
1	E	141	ASN	CG-OD1	6.42	1.38	1.24
1	E	190	TRP	NE1-CE2	-6.32	1.29	1.37
1	E	134(A)	GLN	N-CA	5.86	1.58	1.46
1	E	39	TRP	NE1-CE2	-5.77	1.30	1.37
1	E	36	SER	CA-CB	-5.71	1.44	1.52
1	E	220	LEU	N-CA	5.66	1.57	1.46
1	E	59	SER	CA-CB	-5.53	1.44	1.52
1	E	28	ASN	CG-OD1	5.21	1.35	1.24
1	E	282	SER	CA-CB	-5.13	1.45	1.52
1	E	181	TYR	CE2-CZ	-5.09	1.31	1.38
1	E	1	SER	CB-OG	-5.09	1.35	1.42

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	275	PHE	CG-CD2-CE2	-11.11	108.58	120.80
1	E	157	TYR	CB-CG-CD1	10.21	127.13	121.00
1	E	267	VAL	CA-CB-CG2	9.94	125.81	110.90
1	E	215	ASP	CB-CG-OD2	9.82	127.14	118.30
1	E	227	VAL	CA-CB-CG2	9.63	125.34	110.90
1	E	75	TYR	CB-CG-CD2	-8.95	115.63	121.00
1	E	157	TYR	CB-CG-CD2	-8.06	116.16	121.00
1	E	275	PHE	CB-CG-CD2	-8.05	115.17	120.80
1	E	302	PHE	CB-CG-CD2	-8.04	115.17	120.80
1	E	107	VAL	CA-CB-CG2	7.29	121.84	110.90
1	E	275	PHE	CD1-CE1-CZ	-7.25	111.41	120.10
1	E	193	THR	CA-CB-CG2	-7.12	102.43	112.40
1	E	275	PHE	CZ-CE2-CD2	6.90	128.38	120.10
1	E	94	LEU	O-C-N	6.88	133.72	122.70
1	E	181	TYR	CG-CD2-CE2	-6.78	115.88	121.30
1	E	37	ASP	O-C-N	6.76	133.51	122.70
1	E	66	LEU	CB-CG-CD1	6.66	122.33	111.00
1	E	131	VAL	CA-CB-CG2	6.63	120.85	110.90
1	E	302	PHE	CB-CG-CD1	6.60	125.42	120.80
1	E	199	VAL	CA-CB-CG2	6.58	120.76	110.90
1	E	247	VAL	CA-CB-CG2	6.53	120.69	110.90
1	E	35	SER	N-CA-CB	6.44	120.16	110.50
1	E	91	VAL	CA-CB-CG2	6.36	120.43	110.90
1	E	164	THR	C-N-CA	6.32	137.49	121.70
1	E	197	TYR	CB-CG-CD2	-6.25	117.25	121.00
1	E	84	VAL	CA-CB-CG2	6.09	120.03	110.90
1	E	39	TRP	CG-CD2-CE3	5.99	139.29	133.90
1	E	199	VAL	C-N-CA	5.95	134.80	122.30
1	E	142	ALA	C-N-CA	5.90	136.44	121.70
1	E	39	TRP	CZ3-CH2-CZ2	-5.82	114.61	121.60
1	E	59	SER	CB-CA-C	5.82	121.16	110.10
1	E	75	TYR	CG-CD2-CE2	-5.81	116.65	121.30
1	E	275	PHE	CG-CD1-CE1	5.71	127.08	120.80
1	E	11	ASP	CB-CG-OD1	5.69	123.42	118.30
1	E	8	ASP	CB-CG-OD2	5.55	123.30	118.30
1	E	84	VAL	CG1-CB-CG2	5.49	119.69	110.90
1	E	30	ASP	CB-CG-OD2	5.42	123.18	118.30
1	E	42	SER	O-C-N	5.39	131.33	122.70
1	E	228	VAL	CA-CB-CG2	5.32	118.89	110.90
1	E	85	TYR	CG-CD1-CE1	-5.29	117.07	121.30
1	E	215	ASP	OD1-CG-OD2	-5.28	113.28	123.30
1	E	223	LEU	CB-CG-CD1	5.27	119.96	111.00
1	E	87	ASP	CB-CG-OD2	-5.26	113.57	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	234	GLN	N-CA-CB	5.24	120.03	110.60
1	E	220	LEU	C-N-CA	5.22	134.75	121.70
1	E	245	GLY	C-N-CA	5.13	134.52	121.70
1	E	164	THR	O-C-N	5.09	130.84	122.70
1	E	243	VAL	CA-CB-CG2	5.07	118.50	110.90
1	E	213	ILE	CA-C-O	5.07	130.74	120.10
1	E	181	TYR	CZ-CE2-CD2	5.06	124.35	119.80
1	E	203(A)	PHE	CD1-CE1-CZ	5.06	126.17	120.10
1	E	146	LEU	CB-CG-CD2	5.03	119.55	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	56	TYR	Mainchain

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	E	2389	0	2279	103	0
2	E	37	0	48	24	0
3	E	330	0	0	17	0
All	All	2756	0	2327	123	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 26.

All (123) 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)
2:E:327:0HT:CD21	2:E:327:0HT:HD21	0.97	1.15
2:E:327:0HT:HD12	2:E:327:0HT:CD11	0.97	1.10
2:E:327:0HT:HD14	2:E:327:0HT:CD12	0.97	1.09
2:E:327:0HT:CD11	2:E:327:0HT:HD11	0.97	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:327:0HT:CD11	2:E:327:0HT:HD13	0.97	1.04
1:E:7:ILE:HG22	1:E:15:ILE:HG12	1.49	0.95
2:E:327:0HT:CG3	2:E:327:0HT:CE2	2.43	0.93
1:E:1:SER:HB3	1:E:166:ASN:ND2	1.83	0.93
2:E:327:0HT:CE1	2:E:327:0HT:CG3	2.43	0.92
1:E:75:TYR:HD1	1:E:79:SER:HB3	1.35	0.91
1:E:217:GLY:O	2:E:327:0HT:HBA	1.73	0.88
1:E:71:TRP:HZ3	1:E:73:ILE:HD11	1.39	0.86
2:E:327:0HT:CE1	2:E:327:0HT:HD14	2.06	0.85
2:E:327:0HT:HD13	2:E:327:0HT:HD11	1.58	0.85
2:E:327:0HT:HD12	2:E:327:0HT:CG11	2.07	0.85
2:E:327:0HT:CG11	2:E:327:0HT:HD11	2.07	0.85
2:E:327:0HT:HD12	2:E:327:0HT:HD11	1.58	0.85
2:E:327:0HT:CG3	2:E:327:0HT:HD21	2.06	0.85
2:E:327:0HT:HD12	2:E:327:0HT:HD13	1.58	0.84
2:E:327:0HT:CG3	2:E:327:0HT:HD14	2.06	0.84
2:E:327:0HT:HD21	2:E:327:0HT:CE2	2.06	0.84
2:E:327:0HT:CG11	2:E:327:0HT:HD13	2.07	0.84
1:E:181:TYR:HD1	1:E:320:THR:HG23	1.43	0.82
1:E:75:TYR:CD1	1:E:79:SER:HB3	2.15	0.82
1:E:86:THR:HG22	3:E:454:HOH:O	1.82	0.80
1:E:75:TYR:HB2	1:E:79:SER:HB2	1.63	0.79
1:E:1:SER:HB3	1:E:166:ASN:HD22	1.46	0.78
1:E:299:ILE:HG12	3:E:509:HOH:O	1.84	0.77
1:E:10:LEU:N	1:E:10:LEU:HD23	1.99	0.76
1:E:315:ASN:HB2	1:E:320:THR:HG22	1.68	0.75
1:E:71:TRP:CZ3	1:E:73:ILE:HD11	2.22	0.73
1:E:171:ASP:OD2	1:E:173:THR:HB	1.91	0.71
1:E:152:THR:HG22	1:E:313:VAL:HG22	1.73	0.70
1:E:105:LYS:HB2	3:E:366:HOH:O	1.92	0.69
1:E:297:ILE:CG2	1:E:297:ILE:O	2.42	0.68
1:E:181:TYR:HD1	1:E:320:THR:CG2	2.07	0.67
1:E:181:TYR:CD1	1:E:320:THR:CG2	2.78	0.67
1:E:105:LYS:HD3	3:E:366:HOH:O	1.95	0.67
1:E:315:ASN:CB	1:E:320:THR:HG22	2.25	0.66
1:E:7:ILE:CG2	1:E:15:ILE:HG12	2.25	0.66
2:E:327:0HT:HMC1	3:E:462:HOH:O	1.95	0.65
1:E:71:TRP:HB2	1:E:130:THR:CG2	2.27	0.65
1:E:129:ASN:HD21	1:E:131:VAL:HB	1.60	0.65
1:E:113:GLU:HB2	3:E:620:HOH:O	1.95	0.65
1:E:297:ILE:HG22	1:E:297:ILE:O	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1:SER:CB	1:E:166:ASN:HD22	2.12	0.61
1:E:213:ILE:HD11	2:E:327:0HT:HG23	1.80	0.61
1:E:61:SER:HB3	1:E:63(A):ALA:HB2	1.81	0.61
1:E:130:THR:O	1:E:130:THR:HG23	1.99	0.61
1:E:318:THR:O	1:E:319(B):PRO:HD3	2.01	0.61
1:E:297:ILE:HD11	3:E:433:HOH:O	2.01	0.61
1:E:220:LEU:HD22	1:E:286:GLY:HA2	1.82	0.60
1:E:143:LYS:HA	1:E:146:LEU:HD12	1.83	0.59
1:E:113:GLU:HB3	3:E:621:HOH:O	2.02	0.59
1:E:176:THR:HG23	3:E:374:HOH:O	2.04	0.58
2:E:327:0HT:HG11	2:E:327:0HT:HE1	1.84	0.57
1:E:297:ILE:HG23	2:E:327:0HT:HZ	1.87	0.56
1:E:75:TYR:HB2	1:E:79:SER:CB	2.35	0.56
1:E:94:LEU:HD21	1:E:142:ALA:CB	2.35	0.56
2:E:327:0HT:CG1	2:E:327:0HT:HE1	2.36	0.55
1:E:152:THR:OG1	1:E:166:ASN:HB2	2.06	0.55
1:E:1:SER:CB	1:E:166:ASN:ND2	2.63	0.55
1:E:10:LEU:CD2	1:E:10:LEU:N	2.65	0.55
1:E:131:VAL:HG11	1:E:135:GLN:HG2	1.86	0.55
1:E:1:SER:HB3	1:E:166:ASN:HD21	1.71	0.55
1:E:135:GLN:NE2	3:E:543:HOH:O	2.40	0.54
1:E:315:ASN:HB2	1:E:320:THR:O	2.08	0.54
1:E:27:LEU:HD23	1:E:118:ASP:HB3	1.90	0.53
1:E:150:VAL:HG21	1:E:170:ILE:HD12	1.91	0.53
1:E:-2:SER:HB3	3:E:573:HOH:O	2.06	0.53
1:E:113:GLU:CB	3:E:621:HOH:O	2.57	0.52
1:E:181:TYR:CD1	1:E:320:THR:HG23	2.31	0.52
1:E:96:VAL:CG1	1:E:141:ASN:HB3	2.40	0.51
1:E:22:THR:HA	1:E:23:PRO:C	2.25	0.51
1:E:120:LEU:HD21	2:E:327:0HT:HD1A	1.92	0.51
1:E:71:TRP:HZ3	1:E:73:ILE:CD1	2.16	0.50
1:E:199:VAL:HG11	1:E:231:TYR:HA	1.93	0.50
1:E:43:SER:HB3	1:E:58:PRO:HD3	1.93	0.50
1:E:126:SER:HB2	1:E:140:ASP:OD1	2.13	0.49
1:E:100:ALA:HB2	1:E:135:GLN:HE21	1.77	0.49
1:E:71:TRP:HB2	1:E:130:THR:HG22	1.96	0.48
1:E:171:ASP:C	1:E:173:THR:H	2.16	0.48
1:E:314:PHE:CD1	1:E:314:PHE:N	2.81	0.48
1:E:94:LEU:HD21	1:E:142:ALA:HB1	1.95	0.48
1:E:28:ASN:C	1:E:29:LEU:HD23	2.34	0.48
1:E:220:LEU:HA	1:E:305:VAL:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:94:LEU:HD23	1:E:138:PHE:CZ	2.49	0.47
1:E:319:THR:O	1:E:319:THR:HG22	2.14	0.47
1:E:150:VAL:HG21	1:E:170:ILE:CD1	2.45	0.47
1:E:53:GLN:NE2	1:E:114:ASP:O	2.44	0.47
1:E:277:PRO:HA	1:E:282(B):SER:O	2.15	0.47
1:E:181:TYR:CD1	1:E:320:THR:HG21	2.49	0.46
1:E:242:SER:HA	3:E:545:HOH:O	2.15	0.45
1:E:113:GLU:CB	3:E:620:HOH:O	2.59	0.45
1:E:266:ILE:HG21	1:E:310:ALA:HB2	1.99	0.45
1:E:22:THR:HA	1:E:23:PRO:HA	1.77	0.45
1:E:131:VAL:HG12	1:E:131:VAL:O	2.14	0.45
1:E:220:LEU:HD11	1:E:284:PHE:HE2	1.82	0.45
1:E:94:LEU:HD21	1:E:142:ALA:HB2	1.97	0.45
1:E:318:THR:C	1:E:319(B):PRO:HD3	2.37	0.44
1:E:44:GLU:OE1	1:E:85:TYR:HE2	2.00	0.44
1:E:96:VAL:HG11	1:E:141:ASN:HB3	1.99	0.43
1:E:187:GLN:HG2	3:E:572:HOH:O	2.18	0.43
1:E:43:SER:CB	1:E:58:PRO:HD3	2.48	0.43
1:E:220:LEU:HA	1:E:305:VAL:CG2	2.48	0.43
1:E:44:GLU:OE2	1:E:83:ASP:OD1	2.35	0.43
1:E:75:TYR:N	1:E:79:SER:O	2.45	0.42
1:E:105:LYS:CB	3:E:366:HOH:O	2.60	0.42
1:E:294:SER:CB	1:E:300:ASN:HD22	2.31	0.42
1:E:73:ILE:CD1	1:E:80(A):SER:HB3	2.49	0.42
1:E:87:ASP:OD2	1:E:88:THR:N	2.51	0.42
1:E:129:ASN:ND2	1:E:131:VAL:HB	2.30	0.42
1:E:99:GLN:NE2	1:E:138:PHE:HA	2.35	0.42
1:E:219:THR:O	1:E:305:VAL:HG23	2.19	0.42
1:E:254:LEU:HD12	1:E:254:LEU:HA	1.77	0.41
1:E:113:GLU:O	1:E:113:GLU:HG3	2.20	0.41
1:E:44:GLU:OE1	1:E:85:TYR:CE2	2.73	0.41
1:E:73:ILE:HD12	1:E:80(A):SER:HB3	2.03	0.41
1:E:22:THR:CA	1:E:23:PRO:C	2.88	0.41
1:E:50:VAL:HG11	1:E:55:ILE:CD1	2.51	0.41
1:E:308:LYS:NZ	3:E:438:HOH:O	2.42	0.41
1:E:71:TRP:CZ3	1:E:80(A):SER:HB3	2.56	0.40
1:E:38:LEU:HD23	1:E:38:LEU:C	2.42	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	E	328/330 (99%)	314 (96%)	13 (4%)	1 (0%)	46 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	171	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	E	263/263 (100%)	224 (85%)	39 (15%)	4 1

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1	SER
1	E	10	LEU
1	E	12	ASP
1	E	15	ILE
1	E	48	SER
1	E	55	ILE
1	E	63	THR
1	E	65	LEU
1	E	70	THR
1	E	73	ILE

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Mol	Chain	Res	Type
1	E	74	SER
1	E	79	SER
1	E	86	THR
1	E	90	SER
1	E	103	SER
1	E	105	LYS
1	E	106	LYS
1	E	108	SER
1	E	113	GLU
1	E	114	ASP
1	E	129	ASN
1	E	130	THR
1	E	131	VAL
1	E	132	SER
1	E	143	LYS
1	E	145	SER
1	E	184(A)	SER
1	E	193	THR
1	E	203	THR
1	E	204(A)	SER
1	E	223	LEU
1	E	236	SER
1	E	240	SER
1	E	254	LEU
1	E	294	SER
1	E	299	ILE
1	E	308	LYS
1	E	315	ASN
1	E	320	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	19	GLN
1	E	28	ASN
1	E	99	GLN
1	E	129	ASN
1	E	134(A)	GLN
1	E	135	GLN
1	E	141	ASN
1	E	166	ASN
1	E	300	ASN

5.3.3 RNA

There are no RNA molecules 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

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	$\#\|Z\| > 2$
2	0HT	E	327	-	36,37,37	1.21	2 (5%)	44,49,49	1.11	5 (11%)

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	0HT	E	327	-	-	0/49/49/49	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	327	0HT	CZ-N1	-5.15	1.32	1.47
2	E	327	0HT	OXT-C3	3.62	1.42	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	327	0HT	CB1-CA1-C1	-2.71	104.21	111.31
2	E	327	0HT	CM-OXT-C3	-2.56	109.99	115.99
2	E	327	0HT	CG21-CB2-CG11	-2.34	105.92	111.87
2	E	327	0HT	OXT-C3-O3	-2.30	119.03	123.79
2	E	327	0HT	OXT-C3-CA3	3.27	120.00	111.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	327	0HT	24	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

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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