Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 05:50 AM EDT

PDB ID	:	3SIC
Title	:	MOLECULAR RECOGNITION AT THE ACTIVE SITE OF SUBTILISIN BPN': CRYSTALLOGRAPHIC STUDIES USING GENETICALLY ENGINEERED PROTEINACEOUS INHIBITOR SSI (STREPTOMYCES SUBTILISIN INHIBITOR)
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Deposited on	:	1991-08-30
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
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:

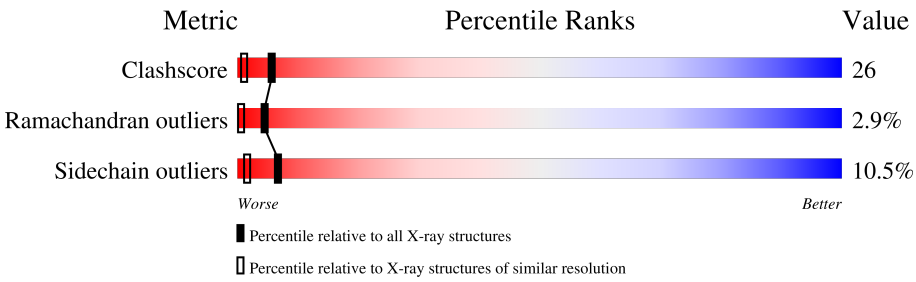
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 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))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	275	68% 27% 6%
2	I	107	31% 50% 15% 5%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2978 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 SUBTILISIN BPN'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	275	1938	1204	335	394	5	0	0	0

- Molecule 2 is a protein called STREPTOMYCES SUBTILISIN INHIBITOR (SSI).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	I	107	765	477	131	151	6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	73	LYS	MET	CONFLICT	UNP P01006

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	E	2	2	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	E	169	169	169	0	0
4	I	104	104	104	0	0

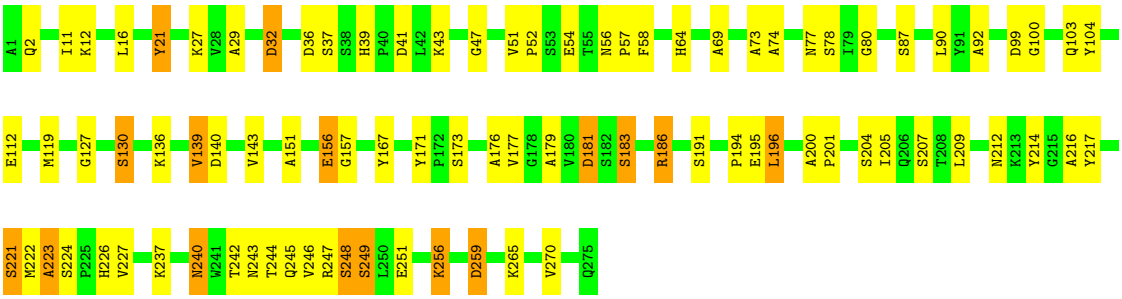
3 Residue-property plots (i)

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. 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. 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.

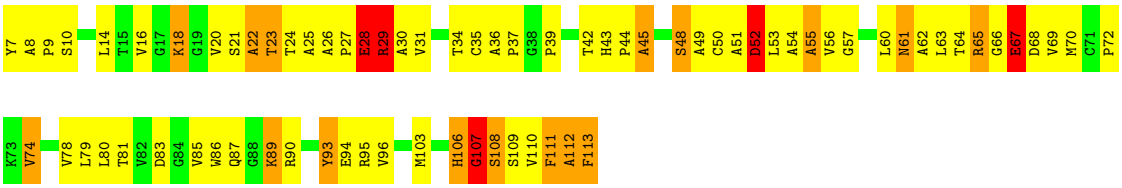
• Molecule 1: SUBTILISIN BPN'

Chain E: 68% 27% 6%



• Molecule 2: STREPTOMYCES SUBTILISIN INHIBITOR (SSI)

Chain I: 31% 50% 15% 5%



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	77.20Å 185.90Å 69.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.178 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2978	wwPDB-VP
Average B, all atoms ($Å^2$)	22.0	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: CA

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	1.04	0/1976	1.74	32/2697 (1.2%)
2	I	0.90	0/781	1.85	18/1066 (1.7%)
All	All	1.00	0/2757	1.77	50/3763 (1.3%)

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

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	23	THR	C-N-CA	20.91	173.97	121.70
1	E	181	ASP	CB-CG-OD1	14.01	130.91	118.30
1	E	99	ASP	CB-CG-OD2	-11.72	107.75	118.30
2	I	52	ASP	CB-CG-OD1	-10.76	108.61	118.30
1	E	196	LEU	CA-CB-CG	10.32	139.04	115.30
1	E	99	ASP	CB-CG-OD1	10.26	127.53	118.30
1	E	181	ASP	CB-CG-OD2	-9.26	109.97	118.30
1	E	77	ASN	CB-CA-C	9.04	128.48	110.40
1	E	36	ASP	CB-CG-OD2	-8.46	110.69	118.30
1	E	140	ASP	CB-CG-OD1	8.05	125.55	118.30
1	E	54	GLU	OE1-CD-OE2	8.00	132.90	123.30
1	E	240	ASN	CB-CA-C	8.00	126.39	110.40
2	I	29	ARG	NE-CZ-NH2	7.34	123.97	120.30
1	E	214	TYR	CB-CG-CD2	7.26	125.36	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	83	ASP	CB-CG-OD1	7.11	124.70	118.30
1	E	217	TYR	CA-CB-CG	6.83	126.38	113.40
1	E	2	GLN	O-C-N	6.67	133.37	122.70
1	E	54	GLU	CG-CD-OE2	-6.57	105.16	118.30
1	E	176	ALA	CB-CA-C	6.50	119.84	110.10
2	I	67	GLU	CA-CB-CG	6.44	127.56	113.40
1	E	41	ASP	CB-CG-OD2	6.42	124.08	118.30
2	I	112	ALA	CA-C-O	6.33	133.39	120.10
1	E	259	ASP	CB-CG-OD2	-6.30	112.63	118.30
2	I	94	GLU	CA-CB-CG	6.26	127.17	113.40
1	E	140	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	E	139	VAL	CB-CA-C	6.12	123.03	111.40
1	E	36	ASP	CB-CG-OD1	6.08	123.77	118.30
1	E	156	GLU	CG-CD-OE2	6.01	130.33	118.30
1	E	214	TYR	CB-CG-CD1	-6.01	117.39	121.00
1	E	32	ASP	CB-CG-OD2	5.99	123.69	118.30
2	I	112	ALA	CA-C-N	-5.96	104.08	117.20
1	E	221	SER	CA-CB-OG	5.82	126.92	111.20
2	I	112	ALA	C-N-CA	5.68	135.90	121.70
2	I	23	THR	O-C-N	-5.55	113.83	122.70
1	E	259	ASP	CB-CA-C	5.48	121.36	110.40
1	E	186	ARG	CD-NE-CZ	-5.43	115.99	123.60
1	E	156	GLU	CB-CA-C	5.43	121.25	110.40
1	E	112	GLU	OE1-CD-OE2	-5.38	116.84	123.30
1	E	207	SER	CB-CA-C	5.36	120.28	110.10
2	I	106	HIS	CA-CB-CG	-5.34	104.53	113.60
2	I	93	TYR	CA-CB-CG	5.29	123.45	113.40
1	E	249	SER	CA-CB-OG	-5.25	97.02	111.20
1	E	223	ALA	N-CA-CB	-5.22	102.79	110.10
2	I	107	GLY	C-N-CA	5.14	134.55	121.70
2	I	49	ALA	CB-CA-C	5.07	117.71	110.10
2	I	29	ARG	CD-NE-CZ	5.07	130.70	123.60
2	I	29	ARG	NE-CZ-NH1	-5.07	117.77	120.30
2	I	28	GLU	CG-CD-OE1	-5.04	108.22	118.30
2	I	83	ASP	CB-CG-OD2	-5.01	113.79	118.30
1	E	21	TYR	CB-CG-CD1	-5.01	118.00	121.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	186	ARG	Sidechain

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	1938	0	1899	53	1
2	I	765	0	742	94	1
3	E	2	0	0	0	0
4	E	169	0	0	12	1
4	I	104	0	0	12	2
All	All	2978	0	2641	136	4

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 (136) 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:E:177:VAL:HG22	4:E:623:HOH:O	1.33	1.29
2:I:28:GLU:HG3	2:I:29:ARG:HD3	1.42	1.01
4:E:660:HOH:O	2:I:74:VAL:HB	1.59	1.01
2:I:109:SER:HA	2:I:112:ALA:HB2	1.39	1.00
2:I:31:VAL:HB	2:I:42:THR:O	1.68	0.93
2:I:60:LEU:O	2:I:61:ASN:HB2	1.75	0.85
1:E:64:HIS:CD2	2:I:74:VAL:HG12	2.12	0.83
2:I:60:LEU:HD11	4:I:181:HOH:O	1.81	0.80
2:I:86:TRP:NE1	4:I:179:HOH:O	2.09	0.79
2:I:8:ALA:HB3	2:I:36:ALA:CB	2.13	0.78
4:E:600:HOH:O	2:I:74:VAL:HB	1.85	0.77
2:I:66:GLY:O	2:I:67:GLU:HB2	1.83	0.76
2:I:86:TRP:CD1	4:I:178:HOH:O	2.37	0.76
1:E:64:HIS:CD2	2:I:74:VAL:CG1	2.68	0.76
2:I:28:GLU:CG	2:I:29:ARG:HD3	2.16	0.76
1:E:64:HIS:HD2	2:I:74:VAL:HG12	1.53	0.74
2:I:29:ARG:HH11	2:I:29:ARG:HG2	1.54	0.72
2:I:20:VAL:HA	2:I:96:VAL:HG11	1.72	0.71
2:I:7:TYR:CE2	2:I:9:PRO:HG3	2.26	0.70
1:E:256:LYS:HD2	4:E:626:HOH:O	1.92	0.70
2:I:23:THR:O	4:I:203:HOH:O	2.10	0.69
2:I:21:SER:O	2:I:25:ALA:HB3	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:7:TYR:CG	2:I:7:TYR:O	2.47	0.67
2:I:79:LEU:HD12	2:I:96:VAL:HG13	1.75	0.66
2:I:64:THR:HG23	4:I:184:HOH:O	1.97	0.65
2:I:52:ASP:OD2	2:I:109:SER:OG	2.15	0.65
2:I:8:ALA:HB3	2:I:36:ALA:HB2	1.78	0.65
2:I:60:LEU:O	2:I:61:ASN:CB	2.45	0.63
2:I:60:LEU:CD1	4:I:181:HOH:O	2.41	0.63
2:I:103:MET:O	2:I:106:HIS:HB2	1.98	0.62
2:I:52:ASP:O	2:I:55:ALA:HB3	1.99	0.62
2:I:86:TRP:CE3	2:I:87:GLN:HB3	2.35	0.62
2:I:87:GLN:O	2:I:87:GLN:HG3	2.01	0.61
4:E:582:HOH:O	2:I:112:ALA:HB1	1.99	0.61
2:I:43:HIS:C	2:I:45:ALA:H	2.04	0.60
2:I:48:SER:O	2:I:51:ALA:HB3	2.01	0.60
2:I:14:LEU:HD12	2:I:14:LEU:N	2.18	0.59
1:E:47:GLY:HA3	1:E:92:ALA:O	2.02	0.59
1:E:64:HIS:HD2	2:I:74:VAL:CG1	2.08	0.58
1:E:242:THR:OG1	1:E:245:GLN:HG3	2.03	0.58
2:I:8:ALA:HB3	2:I:36:ALA:HB1	1.84	0.57
2:I:37:PRO:HD3	4:I:128:HOH:O	2.03	0.57
2:I:53:LEU:CD2	4:I:181:HOH:O	2.51	0.57
2:I:66:GLY:O	2:I:67:GLU:CB	2.52	0.56
2:I:20:VAL:HG22	4:I:170:HOH:O	2.06	0.56
1:E:156:GLU:O	1:E:157:GLY:C	2.44	0.55
1:E:69:ALA:HB1	1:E:90:LEU:HD21	1.88	0.55
1:E:151:ALA:O	1:E:177:VAL:HG23	2.05	0.55
2:I:29:ARG:HH11	2:I:29:ARG:CG	2.20	0.55
1:E:191:SER:O	4:E:627:HOH:O	2.18	0.54
2:I:109:SER:O	2:I:112:ALA:HB3	2.07	0.54
2:I:14:LEU:O	2:I:30:ALA:HA	2.08	0.54
2:I:109:SER:HA	2:I:112:ALA:CB	2.27	0.54
2:I:85:VAL:HA	2:I:89:LYS:O	2.08	0.54
1:E:21:TYR:CZ	1:E:237:LYS:HG3	2.42	0.53
2:I:87:GLN:O	2:I:87:GLN:CG	2.57	0.53
1:E:104:TYR:CZ	2:I:70:MET:CE	2.92	0.52
1:E:100:GLY:O	2:I:72:PRO:HD3	2.10	0.52
2:I:7:TYR:O	2:I:9:PRO:HD3	2.10	0.52
1:E:104:TYR:CZ	2:I:70:MET:HE2	2.45	0.52
2:I:22:ALA:HA	2:I:79:LEU:HD21	1.92	0.51
1:E:127:GLY:HA2	1:E:167:TYR:O	2.10	0.51
2:I:43:HIS:CD2	2:I:44:PRO:HD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:53:LEU:HD21	4:I:181:HOH:O	2.10	0.51
2:I:48:SER:O	2:I:52:ASP:N	2.32	0.51
2:I:14:LEU:HA	2:I:81:THR:O	2.11	0.50
2:I:86:TRP:HE3	2:I:87:GLN:HB3	1.75	0.50
2:I:10:SER:O	2:I:34:THR:HG23	2.12	0.50
1:E:11:ILE:O	1:E:270:VAL:HG12	2.12	0.50
1:E:194:PRO:HD2	1:E:195:GLU:OE1	2.11	0.50
1:E:130:SER:CB	2:I:67:GLU:OE1	2.60	0.49
1:E:227:VAL:HG21	4:E:623:HOH:O	2.12	0.49
1:E:58:PHE:N	1:E:58:PHE:CD1	2.80	0.49
2:I:21:SER:O	2:I:25:ALA:CB	2.61	0.49
2:I:89:LYS:HB2	2:I:89:LYS:NZ	2.27	0.49
2:I:56:VAL:HG11	2:I:62:ALA:HB3	1.93	0.49
2:I:7:TYR:O	2:I:7:TYR:CD1	2.66	0.48
2:I:43:HIS:HD2	2:I:45:ALA:H	1.62	0.48
1:E:212:ASN:CG	1:E:212:ASN:O	2.51	0.48
1:E:227:VAL:HG11	4:E:623:HOH:O	2.13	0.48
2:I:18:LYS:HB3	4:I:144:HOH:O	2.13	0.48
2:I:43:HIS:HD2	2:I:45:ALA:N	2.12	0.48
4:E:660:HOH:O	2:I:74:VAL:HA	2.13	0.48
4:E:660:HOH:O	2:I:74:VAL:CB	2.35	0.48
2:I:56:VAL:CG1	2:I:62:ALA:HB3	2.44	0.48
1:E:136:LYS:HG3	1:E:171:TYR:CE1	2.49	0.47
2:I:53:LEU:O	2:I:57:GLY:N	2.48	0.47
1:E:179:ALA:HA	1:E:200:ALA:O	2.15	0.47
1:E:247:ARG:NE	1:E:251:GLU:OE2	2.45	0.47
1:E:136:LYS:HG3	1:E:171:TYR:CD1	2.50	0.47
1:E:195:GLU:OE1	1:E:195:GLU:N	2.47	0.47
1:E:205:ILE:O	1:E:216:ALA:HA	2.14	0.47
2:I:16:VAL:HA	2:I:79:LEU:O	2.15	0.46
2:I:34:THR:O	2:I:39:PRO:HA	2.16	0.46
2:I:56:VAL:HG21	2:I:63:LEU:HD13	1.98	0.46
1:E:56:ASN:HA	1:E:57:PRO:HD2	1.82	0.46
2:I:54:ALA:O	2:I:55:ALA:C	2.54	0.45
2:I:43:HIS:HE1	2:I:110:VAL:O	2.00	0.45
1:E:130:SER:OG	2:I:67:GLU:OE1	2.30	0.45
2:I:80:LEU:HD21	2:I:111:PHE:CE1	2.51	0.45
1:E:177:VAL:HG21	1:E:224:SER:HA	1.99	0.45
2:I:63:LEU:HG	2:I:107:GLY:HA2	1.98	0.45
1:E:244:THR:O	1:E:248:SER:HB2	2.17	0.45
1:E:104:TYR:OH	2:I:70:MET:HE2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:61:ASN:ND2	2:I:93:TYR:CE1	2.85	0.44
2:I:53:LEU:O	2:I:54:ALA:C	2.55	0.44
1:E:181:ASP:OD1	1:E:183:SER:HB2	2.17	0.44
2:I:43:HIS:C	2:I:45:ALA:N	2.70	0.44
2:I:60:LEU:HD22	2:I:60:LEU:N	2.32	0.44
1:E:47:GLY:CA	1:E:92:ALA:O	2.66	0.43
1:E:29:ALA:HB2	1:E:119:MET:HG3	2.00	0.43
1:E:21:TYR:CE1	1:E:237:LYS:HG3	2.54	0.43
1:E:242:THR:O	1:E:246:VAL:HG23	2.18	0.43
4:E:660:HOH:O	2:I:74:VAL:CA	2.66	0.43
1:E:51:VAL:HA	1:E:52:PRO:HD3	1.90	0.43
2:I:48:SER:HA	2:I:51:ALA:HB3	2.00	0.43
1:E:181:ASP:OD1	1:E:183:SER:CB	2.67	0.43
1:E:181:ASP:C	1:E:183:SER:H	2.22	0.42
1:E:104:TYR:CZ	2:I:70:MET:HE3	2.54	0.42
1:E:16:LEU:HD12	1:E:16:LEU:HA	1.79	0.42
2:I:48:SER:HB3	2:I:109:SER:CB	2.50	0.42
2:I:26:ALA:HA	2:I:27:PRO:HD3	1.78	0.42
1:E:200:ALA:HA	1:E:201:PRO:HD3	1.90	0.42
2:I:35:CYS:SG	2:I:50:CYS:CB	3.08	0.42
2:I:113:PHE:CB	4:I:189:HOH:O	2.66	0.42
1:E:243:ASN:OD1	1:E:243:ASN:N	2.52	0.41
2:I:111:PHE:CD1	2:I:111:PHE:N	2.87	0.41
2:I:65:ARG:HG2	2:I:66:GLY:N	2.35	0.41
1:E:143:VAL:HG21	1:E:173:SER:HB2	2.02	0.41
1:E:223:ALA:O	1:E:226:HIS:HB2	2.20	0.41
1:E:80:GLY:CA	4:E:513:HOH:O	2.69	0.41
1:E:73:ALA:O	1:E:74:ALA:C	2.58	0.41
1:E:39:HIS:CD2	1:E:209:LEU:O	2.74	0.41
1:E:37:SER:OG	1:E:58:PHE:HB3	2.21	0.40
2:I:23:THR:HA	2:I:25:ALA:H	1.85	0.40
2:I:66:GLY:C	2:I:68:ASP:H	2.24	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:132:HOH:O	4:I:132:HOH:O[4_555]	1.39	0.81
2:I:23:THR:OG1	2:I:90:ARG:NE[2_555]	1.62	0.58
1:E:12:LYS:NZ	4:E:544:HOH:O[6_555]	2.03	0.17
4:I:122:HOH:O	4:I:122:HOH:O[3_555]	2.17	0.03

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	E	273/275 (99%)	260 (95%)	11 (4%)	2 (1%)	22 10
2	I	105/107 (98%)	79 (75%)	17 (16%)	9 (9%)	1 0
All	All	378/382 (99%)	339 (90%)	28 (7%)	11 (3%)	4 0

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	24	THR
2	I	65	ARG
2	I	61	ASN
2	I	108	SER
2	I	55	ALA
2	I	67	GLU
1	E	32	ASP
1	E	204	SER
2	I	22	ALA
2	I	107	GLY
2	I	45	ALA

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	E	205/205 (100%)	188 (92%)	17 (8%)	11 3
2	I	80/80 (100%)	67 (84%)	13 (16%)	2 0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	285/285 (100%)	255 (90%)	30 (10%)	7 1

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	27	LYS
1	E	43	LYS
1	E	78	SER
1	E	87	SER
1	E	103	GLN
1	E	130	SER
1	E	139	VAL
1	E	183	SER
1	E	196	LEU
1	E	221	SER
1	E	222	MET
1	E	240	ASN
1	E	248	SER
1	E	249	SER
1	E	256	LYS
1	E	259	ASP
1	E	265	LYS
2	I	18	LYS
2	I	28	GLU
2	I	29	ARG
2	I	48	SER
2	I	52	ASP
2	I	69	VAL
2	I	74	VAL
2	I	78	VAL
2	I	89	LYS
2	I	95	ARG
2	I	108	SER
2	I	111	PHE
2	I	113	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	59	GLN
1	E	271	GLN

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Mol	Chain	Res	Type
2	I	43	HIS
2	I	61	ASN

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)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.