



Full wwPDB Geometry-Only Validation Report ⓘ

Mar 8, 2026 – 03:26 AM UTC

PDB ID : 3CHN / pdb_00003chn
Title : Solution structure of human secretory IgA1
Authors : Bonner, A.; Almogren, A.; Furtado, P.B.; Kerr, M.A.; Perkins, S.J.
Deposited on : 2008-03-10
Resolution : Not provided

This is a Full wwPDB Geometry-Only 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

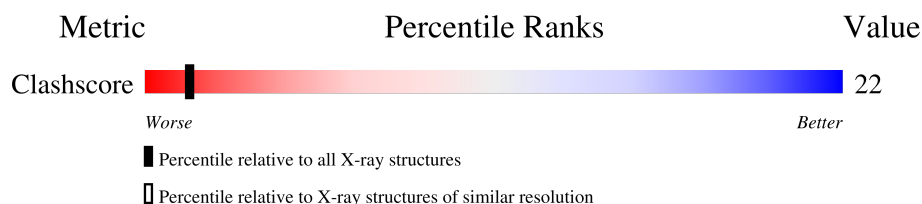
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION SCATTERING

The reported resolution of this entry is unknown.

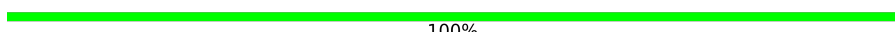
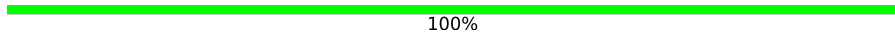
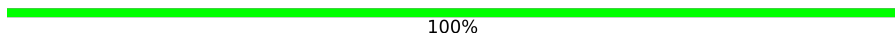
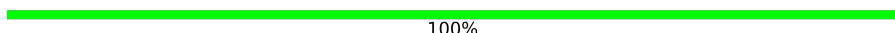
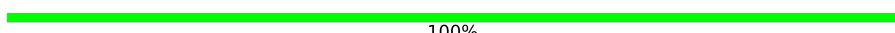
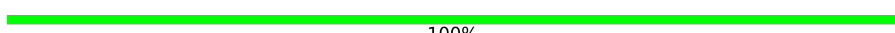
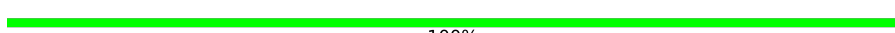
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	-

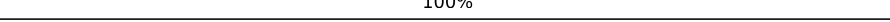
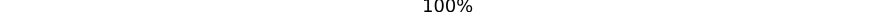
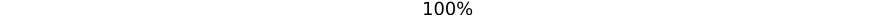
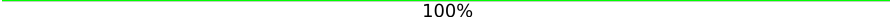
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1-L	214	 100%
1	1-M	214	 100%
1	1-N	214	 100%
1	1-O	214	 100%
1	10-L	214	 100%
1	10-M	214	 100%
1	10-N	214	 100%
1	10-O	214	 100%
1	2-L	214	 100%
1	2-M	214	 100%

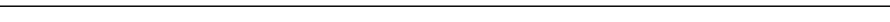
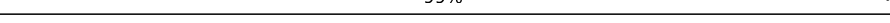
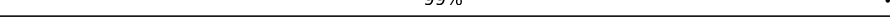
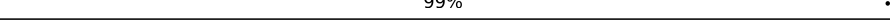
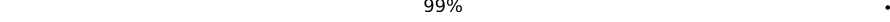
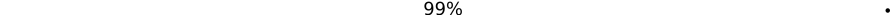
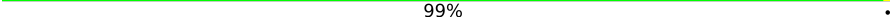
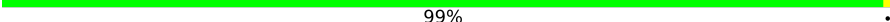
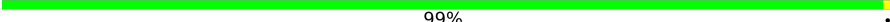
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Mol	Chain	Length	Quality of chain
1	2-N	214	 100%
1	2-O	214	 100%
1	3-L	214	 100%
1	3-M	214	 100%
1	3-N	214	 100%
1	3-O	214	 100%
1	4-L	214	 100%
1	4-M	214	 100%
1	4-N	214	 100%
1	4-O	214	 100%
1	5-L	214	 100%
1	5-M	214	 100%
1	5-N	214	 100%
1	5-O	214	 100%
1	6-L	214	 100%
1	6-M	214	 100%
1	6-N	214	 100%
1	6-O	214	 100%
1	7-L	214	 100%
1	7-M	214	 100%
1	7-N	214	 100%
1	7-O	214	 100%
1	8-L	214	 100%
1	8-M	214	 100%
1	8-N	214	 100%

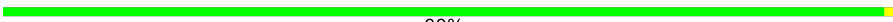
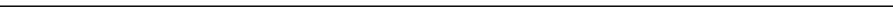
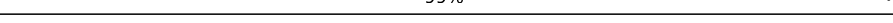
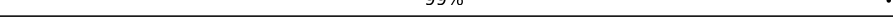
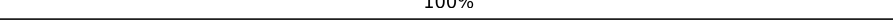
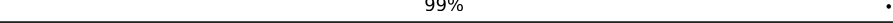
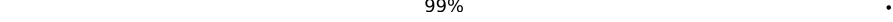
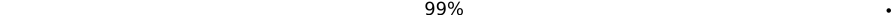
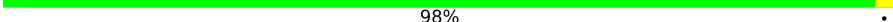
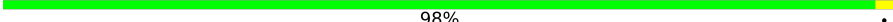
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Mol	Chain	Length	Quality of chain
1	8-O	214	 100%
1	9-L	214	 100%
1	9-M	214	 100%
1	9-N	214	 100%
1	9-O	214	 100%
2	1-A	475	 100%
2	1-B	475	 99% .
2	1-C	475	 99% .
2	1-D	475	 99% .
2	10-A	475	 100%
2	10-B	475	 99% .
2	10-C	475	 99% .
2	10-D	475	 99% .
2	2-A	475	 100%
2	2-B	475	 99% .
2	2-C	475	 99% .
2	2-D	475	 99% .
2	3-A	475	 100%
2	3-B	475	 99% .
2	3-C	475	 99% .
2	3-D	475	 99% .
2	4-A	475	 100%
2	4-B	475	 99% .
2	4-C	475	 99% .
2	4-D	475	 99% .

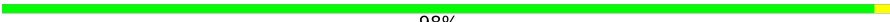
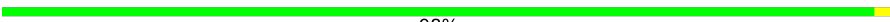
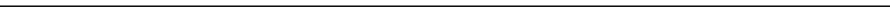
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Mol	Chain	Length	Quality of chain
2	5-A	475	 100%
2	5-B	475	 99%
2	5-C	475	 99%
2	5-D	475	 99%
2	6-A	475	 100%
2	6-B	475	 99%
2	6-C	475	 99%
2	6-D	475	 99%
2	7-A	475	 100%
2	7-B	475	 99%
2	7-C	475	 99%
2	7-D	475	 99%
2	8-A	475	 100%
2	8-B	475	 99%
2	8-C	475	 99%
2	8-D	475	 99%
2	9-A	475	 100%
2	9-B	475	 99%
2	9-C	475	 99%
2	9-D	475	 99%
3	1-J	106	 88% 12%
3	10-J	106	 91% 9%
3	2-J	106	 98%
3	3-J	106	 98%
3	4-J	106	 98%

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Mol	Chain	Length	Quality of chain
3	5-J	106	 98% .
3	6-J	106	 98% .
3	7-J	106	 98% .
3	8-J	106	 98% .
3	9-J	106	 93% 7%
4	1-S	585	 95% 5%
4	10-S	585	 93% 7%
4	2-S	585	 95% 5%
4	3-S	585	 90% 10%
4	4-S	585	 95% 5%
4	5-S	585	 95% 5%
4	6-S	585	 95% 5%
4	7-S	585	 89% 11%
4	8-S	585	 87% 13%
4	9-S	585	 88% 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 34470 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 Immunoglobulin kappa light chain.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	1-L	214	Total C 214 214	0	0	214
1	2-L	214	Total C 214 214	0	0	214
1	3-L	214	Total C 214 214	0	0	214
1	4-L	214	Total C 214 214	0	0	214
1	5-L	214	Total C 214 214	0	0	214
1	6-L	214	Total C 214 214	0	0	214
1	7-L	214	Total C 214 214	0	0	214
1	8-L	214	Total C 214 214	0	0	214
1	9-L	214	Total C 214 214	0	0	214
1	10-L	214	Total C 214 214	0	0	214
1	1-M	214	Total C 214 214	0	0	214
1	2-M	214	Total C 214 214	0	0	214
1	3-M	214	Total C 214 214	0	0	214
1	4-M	214	Total C 214 214	0	0	214
1	5-M	214	Total C 214 214	0	0	214
1	6-M	214	Total C 214 214	0	0	214

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	7-M	214	Total C 214 214	0	0	214
1	8-M	214	Total C 214 214	0	0	214
1	9-M	214	Total C 214 214	0	0	214
1	10-M	214	Total C 214 214	0	0	214
1	1-N	214	Total C 214 214	0	0	214
1	2-N	214	Total C 214 214	0	0	214
1	3-N	214	Total C 214 214	0	0	214
1	4-N	214	Total C 214 214	0	0	214
1	5-N	214	Total C 214 214	0	0	214
1	6-N	214	Total C 214 214	0	0	214
1	7-N	214	Total C 214 214	0	0	214
1	8-N	214	Total C 214 214	0	0	214
1	9-N	214	Total C 214 214	0	0	214
1	10-N	214	Total C 214 214	0	0	214
1	1-O	214	Total C 214 214	0	0	214
1	2-O	214	Total C 214 214	0	0	214
1	3-O	214	Total C 214 214	0	0	214
1	4-O	214	Total C 214 214	0	0	214
1	5-O	214	Total C 214 214	0	0	214
1	6-O	214	Total C 214 214	0	0	214
1	7-O	214	Total C 214 214	0	0	214

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	8-O	214	Total C 214 214	0	0	214
1	9-O	214	Total C 214 214	0	0	214
1	10-O	214	Total C 214 214	0	0	214

- Molecule 2 is a protein called Ig alpha-1 chain C region.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	1-A	475	Total C 475 475	452	0	475
2	2-A	475	Total C 475 475	452	0	475
2	3-A	475	Total C 475 475	452	0	475
2	4-A	475	Total C 475 475	452	0	475
2	5-A	475	Total C 475 475	452	0	475
2	6-A	475	Total C 475 475	452	0	475
2	7-A	475	Total C 475 475	452	0	475
2	8-A	475	Total C 475 475	452	0	475
2	9-A	475	Total C 475 475	452	0	475
2	10-A	475	Total C 475 475	452	0	475
2	1-B	475	Total C 475 475	451	0	475
2	2-B	475	Total C 475 475	451	0	475
2	3-B	475	Total C 475 475	451	0	475
2	4-B	475	Total C 475 475	451	0	475
2	5-B	475	Total C 475 475	451	0	475
2	6-B	475	Total C 475 475	451	0	475

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	7-B	475	Total C 475 475	451	0	475
2	8-B	475	Total C 475 475	451	0	475
2	9-B	475	Total C 475 475	451	0	475
2	10-B	475	Total C 475 475	451	0	475
2	1-D	475	Total C 475 475	451	0	475
2	2-D	475	Total C 475 475	451	0	475
2	3-D	475	Total C 475 475	451	0	475
2	4-D	475	Total C 475 475	451	0	475
2	5-D	475	Total C 475 475	451	0	475
2	6-D	475	Total C 475 475	451	0	475
2	7-D	475	Total C 475 475	451	0	475
2	8-D	475	Total C 475 475	451	0	475
2	9-D	475	Total C 475 475	451	0	475
2	10-D	475	Total C 475 475	451	0	475
2	1-C	475	Total C 475 475	451	0	475
2	2-C	475	Total C 475 475	451	0	475
2	3-C	475	Total C 475 475	451	0	475
2	4-C	475	Total C 475 475	451	0	475
2	5-C	475	Total C 475 475	451	0	475
2	6-C	475	Total C 475 475	451	0	475
2	7-C	475	Total C 475 475	451	0	475

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	8-C	475	Total C 475 475	451	0	475
2	9-C	475	Total C 475 475	451	0	475
2	10-C	475	Total C 475 475	451	0	475

There are 488 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLN	-	SEE REMARK 999	UNP P01876
A	2	VAL	-	SEE REMARK 999	UNP P01876
A	3	LYS	-	SEE REMARK 999	UNP P01876
A	4	LEU	-	SEE REMARK 999	UNP P01876
A	5	LEU	-	SEE REMARK 999	UNP P01876
A	6	GLU	-	SEE REMARK 999	UNP P01876
A	7	GLN	-	SEE REMARK 999	UNP P01876
A	8	SER	-	SEE REMARK 999	UNP P01876
A	9	GLY	-	SEE REMARK 999	UNP P01876
A	10	ALA	-	SEE REMARK 999	UNP P01876
A	11	GLU	-	SEE REMARK 999	UNP P01876
A	12	VAL	-	SEE REMARK 999	UNP P01876
A	13	LYS	-	SEE REMARK 999	UNP P01876
A	14	LYS	-	SEE REMARK 999	UNP P01876
A	15	PRO	-	SEE REMARK 999	UNP P01876
A	16	GLY	-	SEE REMARK 999	UNP P01876
A	17	ALA	-	SEE REMARK 999	UNP P01876
A	18	SER	-	SEE REMARK 999	UNP P01876
A	19	VAL	-	SEE REMARK 999	UNP P01876
A	20	LYS	-	SEE REMARK 999	UNP P01876
A	21	VAL	-	SEE REMARK 999	UNP P01876
A	22	SER	-	SEE REMARK 999	UNP P01876
A	23	CYS	-	SEE REMARK 999	UNP P01876
A	24	LYS	-	SEE REMARK 999	UNP P01876
A	25	ALA	-	SEE REMARK 999	UNP P01876
A	26	SER	-	SEE REMARK 999	UNP P01876
A	27	GLY	-	SEE REMARK 999	UNP P01876
A	28	TYR	-	SEE REMARK 999	UNP P01876
A	29	SER	-	SEE REMARK 999	UNP P01876
A	30	PHE	-	SEE REMARK 999	UNP P01876
A	31	THR	-	SEE REMARK 999	UNP P01876
A	32	SER	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
A	33	TYR	-	SEE REMARK 999	UNP P01876
A	34	GLY	-	SEE REMARK 999	UNP P01876
A	35	LEU	-	SEE REMARK 999	UNP P01876
A	36	HIS	-	SEE REMARK 999	UNP P01876
A	37	TRP	-	SEE REMARK 999	UNP P01876
A	38	VAL	-	SEE REMARK 999	UNP P01876
A	39	ARG	-	SEE REMARK 999	UNP P01876
A	40	GLN	-	SEE REMARK 999	UNP P01876
A	41	ALA	-	SEE REMARK 999	UNP P01876
A	42	PRO	-	SEE REMARK 999	UNP P01876
A	43	GLY	-	SEE REMARK 999	UNP P01876
A	44	GLN	-	SEE REMARK 999	UNP P01876
A	45	ARG	-	SEE REMARK 999	UNP P01876
A	46	LEU	-	SEE REMARK 999	UNP P01876
A	47	GLU	-	SEE REMARK 999	UNP P01876
A	48	TRP	-	SEE REMARK 999	UNP P01876
A	49	MET	-	SEE REMARK 999	UNP P01876
A	50	GLY	-	SEE REMARK 999	UNP P01876
A	51	TRP	-	SEE REMARK 999	UNP P01876
A	52	ILE	-	SEE REMARK 999	UNP P01876
A	53	SER	-	SEE REMARK 999	UNP P01876
A	54	ALA	-	SEE REMARK 999	UNP P01876
A	55	GLY	-	SEE REMARK 999	UNP P01876
A	56	THR	-	SEE REMARK 999	UNP P01876
A	57	GLY	-	SEE REMARK 999	UNP P01876
A	58	ASN	-	SEE REMARK 999	UNP P01876
A	59	THR	-	SEE REMARK 999	UNP P01876
A	60	LYS	-	SEE REMARK 999	UNP P01876
A	61	TYR	-	SEE REMARK 999	UNP P01876
A	62	SER	-	SEE REMARK 999	UNP P01876
A	63	GLN	-	SEE REMARK 999	UNP P01876
A	64	LYS	-	SEE REMARK 999	UNP P01876
A	65	PHE	-	SEE REMARK 999	UNP P01876
A	66	ARG	-	SEE REMARK 999	UNP P01876
A	67	GLY	-	SEE REMARK 999	UNP P01876
A	68	ARG	-	SEE REMARK 999	UNP P01876
A	69	VAL	-	SEE REMARK 999	UNP P01876
A	70	THR	-	SEE REMARK 999	UNP P01876
A	71	PHE	-	SEE REMARK 999	UNP P01876
A	72	THR	-	SEE REMARK 999	UNP P01876
A	73	ARG	-	SEE REMARK 999	UNP P01876
A	74	ASP	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
A	75	THR	-	SEE REMARK 999	UNP P01876
A	76	SER	-	SEE REMARK 999	UNP P01876
A	77	ALA	-	SEE REMARK 999	UNP P01876
A	78	THR	-	SEE REMARK 999	UNP P01876
A	79	THR	-	SEE REMARK 999	UNP P01876
A	80	ALA	-	SEE REMARK 999	UNP P01876
A	81	TYR	-	SEE REMARK 999	UNP P01876
A	82	MET	-	SEE REMARK 999	UNP P01876
A	83	GLY	-	SEE REMARK 999	UNP P01876
A	84	LEU	-	SEE REMARK 999	UNP P01876
A	85	SER	-	SEE REMARK 999	UNP P01876
A	86	SER	-	SEE REMARK 999	UNP P01876
A	87	LEU	-	SEE REMARK 999	UNP P01876
A	88	ARG	-	SEE REMARK 999	UNP P01876
A	89	PRO	-	SEE REMARK 999	UNP P01876
A	90	GLU	-	SEE REMARK 999	UNP P01876
A	91	ASP	-	SEE REMARK 999	UNP P01876
A	92	THR	-	SEE REMARK 999	UNP P01876
A	93	ALA	-	SEE REMARK 999	UNP P01876
A	94	VAL	-	SEE REMARK 999	UNP P01876
A	95	TYR	-	SEE REMARK 999	UNP P01876
A	96	TYR	-	SEE REMARK 999	UNP P01876
A	97	CYS	-	SEE REMARK 999	UNP P01876
A	98	ALA	-	SEE REMARK 999	UNP P01876
A	99	ARG	-	SEE REMARK 999	UNP P01876
A	100	ASP	-	SEE REMARK 999	UNP P01876
A	101	PRO	-	SEE REMARK 999	UNP P01876
A	102	TYR	-	SEE REMARK 999	UNP P01876
A	103	GLY	-	SEE REMARK 999	UNP P01876
A	104	GLY	-	SEE REMARK 999	UNP P01876
A	105	GLY	-	SEE REMARK 999	UNP P01876
A	106	LYS	-	SEE REMARK 999	UNP P01876
A	107	SER	-	SEE REMARK 999	UNP P01876
A	108	GLU	-	SEE REMARK 999	UNP P01876
A	109	PHE	-	SEE REMARK 999	UNP P01876
A	110	ASP	-	SEE REMARK 999	UNP P01876
A	111	TYR	-	SEE REMARK 999	UNP P01876
A	112	TRP	-	SEE REMARK 999	UNP P01876
A	113	GLY	-	SEE REMARK 999	UNP P01876
A	114	GLN	-	SEE REMARK 999	UNP P01876
A	115	GLY	-	SEE REMARK 999	UNP P01876
A	116	THR	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
A	117	LEU	-	SEE REMARK 999	UNP P01876
A	118	VAL	-	SEE REMARK 999	UNP P01876
A	119	THR	-	SEE REMARK 999	UNP P01876
A	120	VAL	-	SEE REMARK 999	UNP P01876
A	121	SER	-	SEE REMARK 999	UNP P01876
A	122	SER	-	SEE REMARK 999	UNP P01876
B	1	GLN	-	SEE REMARK 999	UNP P01876
B	2	VAL	-	SEE REMARK 999	UNP P01876
B	3	LYS	-	SEE REMARK 999	UNP P01876
B	4	LEU	-	SEE REMARK 999	UNP P01876
B	5	LEU	-	SEE REMARK 999	UNP P01876
B	6	GLU	-	SEE REMARK 999	UNP P01876
B	7	GLN	-	SEE REMARK 999	UNP P01876
B	8	SER	-	SEE REMARK 999	UNP P01876
B	9	GLY	-	SEE REMARK 999	UNP P01876
B	10	ALA	-	SEE REMARK 999	UNP P01876
B	11	GLU	-	SEE REMARK 999	UNP P01876
B	12	VAL	-	SEE REMARK 999	UNP P01876
B	13	LYS	-	SEE REMARK 999	UNP P01876
B	14	LYS	-	SEE REMARK 999	UNP P01876
B	15	PRO	-	SEE REMARK 999	UNP P01876
B	16	GLY	-	SEE REMARK 999	UNP P01876
B	17	ALA	-	SEE REMARK 999	UNP P01876
B	18	SER	-	SEE REMARK 999	UNP P01876
B	19	VAL	-	SEE REMARK 999	UNP P01876
B	20	LYS	-	SEE REMARK 999	UNP P01876
B	21	VAL	-	SEE REMARK 999	UNP P01876
B	22	SER	-	SEE REMARK 999	UNP P01876
B	23	CYS	-	SEE REMARK 999	UNP P01876
B	24	LYS	-	SEE REMARK 999	UNP P01876
B	25	ALA	-	SEE REMARK 999	UNP P01876
B	26	SER	-	SEE REMARK 999	UNP P01876
B	27	GLY	-	SEE REMARK 999	UNP P01876
B	28	TYR	-	SEE REMARK 999	UNP P01876
B	29	SER	-	SEE REMARK 999	UNP P01876
B	30	PHE	-	SEE REMARK 999	UNP P01876
B	31	THR	-	SEE REMARK 999	UNP P01876
B	32	SER	-	SEE REMARK 999	UNP P01876
B	33	TYR	-	SEE REMARK 999	UNP P01876
B	34	GLY	-	SEE REMARK 999	UNP P01876
B	35	LEU	-	SEE REMARK 999	UNP P01876
B	36	HIS	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
B	37	TRP	-	SEE REMARK 999	UNP P01876
B	38	VAL	-	SEE REMARK 999	UNP P01876
B	39	ARG	-	SEE REMARK 999	UNP P01876
B	40	GLN	-	SEE REMARK 999	UNP P01876
B	41	ALA	-	SEE REMARK 999	UNP P01876
B	42	PRO	-	SEE REMARK 999	UNP P01876
B	43	GLY	-	SEE REMARK 999	UNP P01876
B	44	GLN	-	SEE REMARK 999	UNP P01876
B	45	ARG	-	SEE REMARK 999	UNP P01876
B	46	LEU	-	SEE REMARK 999	UNP P01876
B	47	GLU	-	SEE REMARK 999	UNP P01876
B	48	TRP	-	SEE REMARK 999	UNP P01876
B	49	MET	-	SEE REMARK 999	UNP P01876
B	50	GLY	-	SEE REMARK 999	UNP P01876
B	51	TRP	-	SEE REMARK 999	UNP P01876
B	52	ILE	-	SEE REMARK 999	UNP P01876
B	53	SER	-	SEE REMARK 999	UNP P01876
B	54	ALA	-	SEE REMARK 999	UNP P01876
B	55	GLY	-	SEE REMARK 999	UNP P01876
B	56	THR	-	SEE REMARK 999	UNP P01876
B	57	GLY	-	SEE REMARK 999	UNP P01876
B	58	ASN	-	SEE REMARK 999	UNP P01876
B	59	THR	-	SEE REMARK 999	UNP P01876
B	60	LYS	-	SEE REMARK 999	UNP P01876
B	61	TYR	-	SEE REMARK 999	UNP P01876
B	62	SER	-	SEE REMARK 999	UNP P01876
B	63	GLN	-	SEE REMARK 999	UNP P01876
B	64	LYS	-	SEE REMARK 999	UNP P01876
B	65	PHE	-	SEE REMARK 999	UNP P01876
B	66	ARG	-	SEE REMARK 999	UNP P01876
B	67	GLY	-	SEE REMARK 999	UNP P01876
B	68	ARG	-	SEE REMARK 999	UNP P01876
B	69	VAL	-	SEE REMARK 999	UNP P01876
B	70	THR	-	SEE REMARK 999	UNP P01876
B	71	PHE	-	SEE REMARK 999	UNP P01876
B	72	THR	-	SEE REMARK 999	UNP P01876
B	73	ARG	-	SEE REMARK 999	UNP P01876
B	74	ASP	-	SEE REMARK 999	UNP P01876
B	75	THR	-	SEE REMARK 999	UNP P01876
B	76	SER	-	SEE REMARK 999	UNP P01876
B	77	ALA	-	SEE REMARK 999	UNP P01876
B	78	THR	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
B	79	THR	-	SEE REMARK 999	UNP P01876
B	80	ALA	-	SEE REMARK 999	UNP P01876
B	81	TYR	-	SEE REMARK 999	UNP P01876
B	82	MET	-	SEE REMARK 999	UNP P01876
B	83	GLY	-	SEE REMARK 999	UNP P01876
B	84	LEU	-	SEE REMARK 999	UNP P01876
B	85	SER	-	SEE REMARK 999	UNP P01876
B	86	SER	-	SEE REMARK 999	UNP P01876
B	87	LEU	-	SEE REMARK 999	UNP P01876
B	88	ARG	-	SEE REMARK 999	UNP P01876
B	89	PRO	-	SEE REMARK 999	UNP P01876
B	90	GLU	-	SEE REMARK 999	UNP P01876
B	91	ASP	-	SEE REMARK 999	UNP P01876
B	92	THR	-	SEE REMARK 999	UNP P01876
B	93	ALA	-	SEE REMARK 999	UNP P01876
B	94	VAL	-	SEE REMARK 999	UNP P01876
B	95	TYR	-	SEE REMARK 999	UNP P01876
B	96	TYR	-	SEE REMARK 999	UNP P01876
B	97	CYS	-	SEE REMARK 999	UNP P01876
B	98	ALA	-	SEE REMARK 999	UNP P01876
B	99	ARG	-	SEE REMARK 999	UNP P01876
B	100	ASP	-	SEE REMARK 999	UNP P01876
B	101	PRO	-	SEE REMARK 999	UNP P01876
B	102	TYR	-	SEE REMARK 999	UNP P01876
B	103	GLY	-	SEE REMARK 999	UNP P01876
B	104	GLY	-	SEE REMARK 999	UNP P01876
B	105	GLY	-	SEE REMARK 999	UNP P01876
B	106	LYS	-	SEE REMARK 999	UNP P01876
B	107	SER	-	SEE REMARK 999	UNP P01876
B	108	GLU	-	SEE REMARK 999	UNP P01876
B	109	PHE	-	SEE REMARK 999	UNP P01876
B	110	ASP	-	SEE REMARK 999	UNP P01876
B	111	TYR	-	SEE REMARK 999	UNP P01876
B	112	TRP	-	SEE REMARK 999	UNP P01876
B	113	GLY	-	SEE REMARK 999	UNP P01876
B	114	GLN	-	SEE REMARK 999	UNP P01876
B	115	GLY	-	SEE REMARK 999	UNP P01876
B	116	THR	-	SEE REMARK 999	UNP P01876
B	117	LEU	-	SEE REMARK 999	UNP P01876
B	118	VAL	-	SEE REMARK 999	UNP P01876
B	119	THR	-	SEE REMARK 999	UNP P01876
B	120	VAL	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
B	121	SER	-	SEE REMARK 999	UNP P01876
B	122	SER	-	SEE REMARK 999	UNP P01876
D	1	GLN	-	SEE REMARK 999	UNP P01876
D	2	VAL	-	SEE REMARK 999	UNP P01876
D	3	LYS	-	SEE REMARK 999	UNP P01876
D	4	LEU	-	SEE REMARK 999	UNP P01876
D	5	LEU	-	SEE REMARK 999	UNP P01876
D	6	GLU	-	SEE REMARK 999	UNP P01876
D	7	GLN	-	SEE REMARK 999	UNP P01876
D	8	SER	-	SEE REMARK 999	UNP P01876
D	9	GLY	-	SEE REMARK 999	UNP P01876
D	10	ALA	-	SEE REMARK 999	UNP P01876
D	11	GLU	-	SEE REMARK 999	UNP P01876
D	12	VAL	-	SEE REMARK 999	UNP P01876
D	13	LYS	-	SEE REMARK 999	UNP P01876
D	14	LYS	-	SEE REMARK 999	UNP P01876
D	15	PRO	-	SEE REMARK 999	UNP P01876
D	16	GLY	-	SEE REMARK 999	UNP P01876
D	17	ALA	-	SEE REMARK 999	UNP P01876
D	18	SER	-	SEE REMARK 999	UNP P01876
D	19	VAL	-	SEE REMARK 999	UNP P01876
D	20	LYS	-	SEE REMARK 999	UNP P01876
D	21	VAL	-	SEE REMARK 999	UNP P01876
D	22	SER	-	SEE REMARK 999	UNP P01876
D	23	CYS	-	SEE REMARK 999	UNP P01876
D	24	LYS	-	SEE REMARK 999	UNP P01876
D	25	ALA	-	SEE REMARK 999	UNP P01876
D	26	SER	-	SEE REMARK 999	UNP P01876
D	27	GLY	-	SEE REMARK 999	UNP P01876
D	28	TYR	-	SEE REMARK 999	UNP P01876
D	29	SER	-	SEE REMARK 999	UNP P01876
D	30	PHE	-	SEE REMARK 999	UNP P01876
D	31	THR	-	SEE REMARK 999	UNP P01876
D	32	SER	-	SEE REMARK 999	UNP P01876
D	33	TYR	-	SEE REMARK 999	UNP P01876
D	34	GLY	-	SEE REMARK 999	UNP P01876
D	35	LEU	-	SEE REMARK 999	UNP P01876
D	36	HIS	-	SEE REMARK 999	UNP P01876
D	37	TRP	-	SEE REMARK 999	UNP P01876
D	38	VAL	-	SEE REMARK 999	UNP P01876
D	39	ARG	-	SEE REMARK 999	UNP P01876
D	40	GLN	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
D	41	ALA	-	SEE REMARK 999	UNP P01876
D	42	PRO	-	SEE REMARK 999	UNP P01876
D	43	GLY	-	SEE REMARK 999	UNP P01876
D	44	GLN	-	SEE REMARK 999	UNP P01876
D	45	ARG	-	SEE REMARK 999	UNP P01876
D	46	LEU	-	SEE REMARK 999	UNP P01876
D	47	GLU	-	SEE REMARK 999	UNP P01876
D	48	TRP	-	SEE REMARK 999	UNP P01876
D	49	MET	-	SEE REMARK 999	UNP P01876
D	50	GLY	-	SEE REMARK 999	UNP P01876
D	51	TRP	-	SEE REMARK 999	UNP P01876
D	52	ILE	-	SEE REMARK 999	UNP P01876
D	53	SER	-	SEE REMARK 999	UNP P01876
D	54	ALA	-	SEE REMARK 999	UNP P01876
D	55	GLY	-	SEE REMARK 999	UNP P01876
D	56	THR	-	SEE REMARK 999	UNP P01876
D	57	GLY	-	SEE REMARK 999	UNP P01876
D	58	ASN	-	SEE REMARK 999	UNP P01876
D	59	THR	-	SEE REMARK 999	UNP P01876
D	60	LYS	-	SEE REMARK 999	UNP P01876
D	61	TYR	-	SEE REMARK 999	UNP P01876
D	62	SER	-	SEE REMARK 999	UNP P01876
D	63	GLN	-	SEE REMARK 999	UNP P01876
D	64	LYS	-	SEE REMARK 999	UNP P01876
D	65	PHE	-	SEE REMARK 999	UNP P01876
D	66	ARG	-	SEE REMARK 999	UNP P01876
D	67	GLY	-	SEE REMARK 999	UNP P01876
D	68	ARG	-	SEE REMARK 999	UNP P01876
D	69	VAL	-	SEE REMARK 999	UNP P01876
D	70	THR	-	SEE REMARK 999	UNP P01876
D	71	PHE	-	SEE REMARK 999	UNP P01876
D	72	THR	-	SEE REMARK 999	UNP P01876
D	73	ARG	-	SEE REMARK 999	UNP P01876
D	74	ASP	-	SEE REMARK 999	UNP P01876
D	75	THR	-	SEE REMARK 999	UNP P01876
D	76	SER	-	SEE REMARK 999	UNP P01876
D	77	ALA	-	SEE REMARK 999	UNP P01876
D	78	THR	-	SEE REMARK 999	UNP P01876
D	79	THR	-	SEE REMARK 999	UNP P01876
D	80	ALA	-	SEE REMARK 999	UNP P01876
D	81	TYR	-	SEE REMARK 999	UNP P01876
D	82	MET	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
D	83	GLY	-	SEE REMARK 999	UNP P01876
D	84	LEU	-	SEE REMARK 999	UNP P01876
D	85	SER	-	SEE REMARK 999	UNP P01876
D	86	SER	-	SEE REMARK 999	UNP P01876
D	87	LEU	-	SEE REMARK 999	UNP P01876
D	88	ARG	-	SEE REMARK 999	UNP P01876
D	89	PRO	-	SEE REMARK 999	UNP P01876
D	90	GLU	-	SEE REMARK 999	UNP P01876
D	91	ASP	-	SEE REMARK 999	UNP P01876
D	92	THR	-	SEE REMARK 999	UNP P01876
D	93	ALA	-	SEE REMARK 999	UNP P01876
D	94	VAL	-	SEE REMARK 999	UNP P01876
D	95	TYR	-	SEE REMARK 999	UNP P01876
D	96	TYR	-	SEE REMARK 999	UNP P01876
D	97	CYS	-	SEE REMARK 999	UNP P01876
D	98	ALA	-	SEE REMARK 999	UNP P01876
D	99	ARG	-	SEE REMARK 999	UNP P01876
D	100	ASP	-	SEE REMARK 999	UNP P01876
D	101	PRO	-	SEE REMARK 999	UNP P01876
D	102	TYR	-	SEE REMARK 999	UNP P01876
D	103	GLY	-	SEE REMARK 999	UNP P01876
D	104	GLY	-	SEE REMARK 999	UNP P01876
D	105	GLY	-	SEE REMARK 999	UNP P01876
D	106	LYS	-	SEE REMARK 999	UNP P01876
D	107	SER	-	SEE REMARK 999	UNP P01876
D	108	GLU	-	SEE REMARK 999	UNP P01876
D	109	PHE	-	SEE REMARK 999	UNP P01876
D	110	ASP	-	SEE REMARK 999	UNP P01876
D	111	TYR	-	SEE REMARK 999	UNP P01876
D	112	TRP	-	SEE REMARK 999	UNP P01876
D	113	GLY	-	SEE REMARK 999	UNP P01876
D	114	GLN	-	SEE REMARK 999	UNP P01876
D	115	GLY	-	SEE REMARK 999	UNP P01876
D	116	THR	-	SEE REMARK 999	UNP P01876
D	117	LEU	-	SEE REMARK 999	UNP P01876
D	118	VAL	-	SEE REMARK 999	UNP P01876
D	119	THR	-	SEE REMARK 999	UNP P01876
D	120	VAL	-	SEE REMARK 999	UNP P01876
D	121	SER	-	SEE REMARK 999	UNP P01876
D	122	SER	-	SEE REMARK 999	UNP P01876
C	1	GLN	-	SEE REMARK 999	UNP P01876
C	2	VAL	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
C	3	LYS	-	SEE REMARK 999	UNP P01876
C	4	LEU	-	SEE REMARK 999	UNP P01876
C	5	LEU	-	SEE REMARK 999	UNP P01876
C	6	GLU	-	SEE REMARK 999	UNP P01876
C	7	GLN	-	SEE REMARK 999	UNP P01876
C	8	SER	-	SEE REMARK 999	UNP P01876
C	9	GLY	-	SEE REMARK 999	UNP P01876
C	10	ALA	-	SEE REMARK 999	UNP P01876
C	11	GLU	-	SEE REMARK 999	UNP P01876
C	12	VAL	-	SEE REMARK 999	UNP P01876
C	13	LYS	-	SEE REMARK 999	UNP P01876
C	14	LYS	-	SEE REMARK 999	UNP P01876
C	15	PRO	-	SEE REMARK 999	UNP P01876
C	16	GLY	-	SEE REMARK 999	UNP P01876
C	17	ALA	-	SEE REMARK 999	UNP P01876
C	18	SER	-	SEE REMARK 999	UNP P01876
C	19	VAL	-	SEE REMARK 999	UNP P01876
C	20	LYS	-	SEE REMARK 999	UNP P01876
C	21	VAL	-	SEE REMARK 999	UNP P01876
C	22	SER	-	SEE REMARK 999	UNP P01876
C	23	CYS	-	SEE REMARK 999	UNP P01876
C	24	LYS	-	SEE REMARK 999	UNP P01876
C	25	ALA	-	SEE REMARK 999	UNP P01876
C	26	SER	-	SEE REMARK 999	UNP P01876
C	27	GLY	-	SEE REMARK 999	UNP P01876
C	28	TYR	-	SEE REMARK 999	UNP P01876
C	29	SER	-	SEE REMARK 999	UNP P01876
C	30	PHE	-	SEE REMARK 999	UNP P01876
C	31	THR	-	SEE REMARK 999	UNP P01876
C	32	SER	-	SEE REMARK 999	UNP P01876
C	33	TYR	-	SEE REMARK 999	UNP P01876
C	34	GLY	-	SEE REMARK 999	UNP P01876
C	35	LEU	-	SEE REMARK 999	UNP P01876
C	36	HIS	-	SEE REMARK 999	UNP P01876
C	37	TRP	-	SEE REMARK 999	UNP P01876
C	38	VAL	-	SEE REMARK 999	UNP P01876
C	39	ARG	-	SEE REMARK 999	UNP P01876
C	40	GLN	-	SEE REMARK 999	UNP P01876
C	41	ALA	-	SEE REMARK 999	UNP P01876
C	42	PRO	-	SEE REMARK 999	UNP P01876
C	43	GLY	-	SEE REMARK 999	UNP P01876
C	44	GLN	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
C	45	ARG	-	SEE REMARK 999	UNP P01876
C	46	LEU	-	SEE REMARK 999	UNP P01876
C	47	GLU	-	SEE REMARK 999	UNP P01876
C	48	TRP	-	SEE REMARK 999	UNP P01876
C	49	MET	-	SEE REMARK 999	UNP P01876
C	50	GLY	-	SEE REMARK 999	UNP P01876
C	51	TRP	-	SEE REMARK 999	UNP P01876
C	52	ILE	-	SEE REMARK 999	UNP P01876
C	53	SER	-	SEE REMARK 999	UNP P01876
C	54	ALA	-	SEE REMARK 999	UNP P01876
C	55	GLY	-	SEE REMARK 999	UNP P01876
C	56	THR	-	SEE REMARK 999	UNP P01876
C	57	GLY	-	SEE REMARK 999	UNP P01876
C	58	ASN	-	SEE REMARK 999	UNP P01876
C	59	THR	-	SEE REMARK 999	UNP P01876
C	60	LYS	-	SEE REMARK 999	UNP P01876
C	61	TYR	-	SEE REMARK 999	UNP P01876
C	62	SER	-	SEE REMARK 999	UNP P01876
C	63	GLN	-	SEE REMARK 999	UNP P01876
C	64	LYS	-	SEE REMARK 999	UNP P01876
C	65	PHE	-	SEE REMARK 999	UNP P01876
C	66	ARG	-	SEE REMARK 999	UNP P01876
C	67	GLY	-	SEE REMARK 999	UNP P01876
C	68	ARG	-	SEE REMARK 999	UNP P01876
C	69	VAL	-	SEE REMARK 999	UNP P01876
C	70	THR	-	SEE REMARK 999	UNP P01876
C	71	PHE	-	SEE REMARK 999	UNP P01876
C	72	THR	-	SEE REMARK 999	UNP P01876
C	73	ARG	-	SEE REMARK 999	UNP P01876
C	74	ASP	-	SEE REMARK 999	UNP P01876
C	75	THR	-	SEE REMARK 999	UNP P01876
C	76	SER	-	SEE REMARK 999	UNP P01876
C	77	ALA	-	SEE REMARK 999	UNP P01876
C	78	THR	-	SEE REMARK 999	UNP P01876
C	79	THR	-	SEE REMARK 999	UNP P01876
C	80	ALA	-	SEE REMARK 999	UNP P01876
C	81	TYR	-	SEE REMARK 999	UNP P01876
C	82	MET	-	SEE REMARK 999	UNP P01876
C	83	GLY	-	SEE REMARK 999	UNP P01876
C	84	LEU	-	SEE REMARK 999	UNP P01876
C	85	SER	-	SEE REMARK 999	UNP P01876
C	86	SER	-	SEE REMARK 999	UNP P01876

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Chain	Residue	Modelled	Actual	Comment	Reference
C	87	LEU	-	SEE REMARK 999	UNP P01876
C	88	ARG	-	SEE REMARK 999	UNP P01876
C	89	PRO	-	SEE REMARK 999	UNP P01876
C	90	GLU	-	SEE REMARK 999	UNP P01876
C	91	ASP	-	SEE REMARK 999	UNP P01876
C	92	THR	-	SEE REMARK 999	UNP P01876
C	93	ALA	-	SEE REMARK 999	UNP P01876
C	94	VAL	-	SEE REMARK 999	UNP P01876
C	95	TYR	-	SEE REMARK 999	UNP P01876
C	96	TYR	-	SEE REMARK 999	UNP P01876
C	97	CYS	-	SEE REMARK 999	UNP P01876
C	98	ALA	-	SEE REMARK 999	UNP P01876
C	99	ARG	-	SEE REMARK 999	UNP P01876
C	100	ASP	-	SEE REMARK 999	UNP P01876
C	101	PRO	-	SEE REMARK 999	UNP P01876
C	102	TYR	-	SEE REMARK 999	UNP P01876
C	103	GLY	-	SEE REMARK 999	UNP P01876
C	104	GLY	-	SEE REMARK 999	UNP P01876
C	105	GLY	-	SEE REMARK 999	UNP P01876
C	106	LYS	-	SEE REMARK 999	UNP P01876
C	107	SER	-	SEE REMARK 999	UNP P01876
C	108	GLU	-	SEE REMARK 999	UNP P01876
C	109	PHE	-	SEE REMARK 999	UNP P01876
C	110	ASP	-	SEE REMARK 999	UNP P01876
C	111	TYR	-	SEE REMARK 999	UNP P01876
C	112	TRP	-	SEE REMARK 999	UNP P01876
C	113	GLY	-	SEE REMARK 999	UNP P01876
C	114	GLN	-	SEE REMARK 999	UNP P01876
C	115	GLY	-	SEE REMARK 999	UNP P01876
C	116	THR	-	SEE REMARK 999	UNP P01876
C	117	LEU	-	SEE REMARK 999	UNP P01876
C	118	VAL	-	SEE REMARK 999	UNP P01876
C	119	THR	-	SEE REMARK 999	UNP P01876
C	120	VAL	-	SEE REMARK 999	UNP P01876
C	121	SER	-	SEE REMARK 999	UNP P01876
C	122	SER	-	SEE REMARK 999	UNP P01876

- Molecule 3 is a protein called Secretory component.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	1-J	106	Total C 106 106	0	0	106

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	2-J	106	Total C 106 106	0	0	106
3	3-J	106	Total C 106 106	0	0	106
3	4-J	106	Total C 106 106	0	0	106
3	5-J	106	Total C 106 106	0	0	106
3	6-J	106	Total C 106 106	0	0	106
3	7-J	106	Total C 106 106	0	0	106
3	8-J	106	Total C 106 106	0	0	106
3	9-J	106	Total C 106 106	0	0	106
3	10-J	106	Total C 106 106	0	0	106

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	347	SER	GLY	variant	UNP P01833

- Molecule 4 is a protein called Secretory component.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	1-S	585	Total C 585 585	0	0	585
4	2-S	585	Total C 585 585	0	0	585
4	3-S	585	Total C 585 585	0	0	585
4	4-S	585	Total C 585 585	0	0	585
4	5-S	585	Total C 585 585	0	0	585
4	6-S	585	Total C 585 585	0	0	585
4	7-S	585	Total C 585 585	0	0	585
4	8-S	585	Total C 585 585	0	0	585

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	9-S	585	Total C 585 585	0	0	585
4	10-S	585	Total C 585 585	0	0	585

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	347	SER	GLY	variant	UNP P01833

3 Residue-property plots

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: Immunoglobulin kappa light chain

Chain 1-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 1-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 1-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 1-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 2-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 2-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 2-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 2-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 3-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 3-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 3-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 3-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 4-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 4-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 4-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 4-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 5-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 5-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 5-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 5-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 6-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 6-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 6-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 6-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 7-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 7-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 7-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 7-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 8-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 8-M:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 8-N:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 8-O:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 9-L:  100%

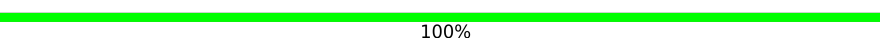
There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 9-M:  100%

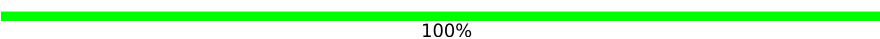
There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 9-N:  100%

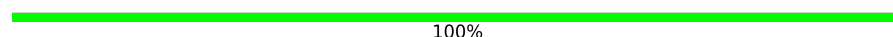
There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 9-O:  100%

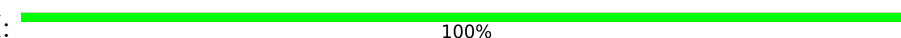
There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 10-L:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 10-M:  100%

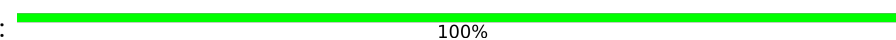
There are no outlier residues recorded for this chain.

- Molecule 1: Immunoglobulin kappa light chain

Chain 10-N:  100%

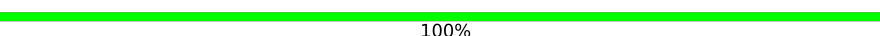
There are no outlier residues recorded for this chain.

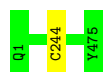
- Molecule 1: Immunoglobulin kappa light chain

Chain 10-O:  100%

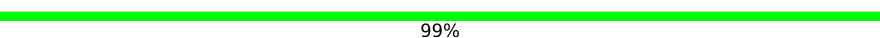
There are no outlier residues recorded for this chain.

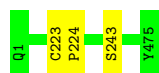
- Molecule 2: Ig alpha-1 chain C region

Chain 1-A:  100%

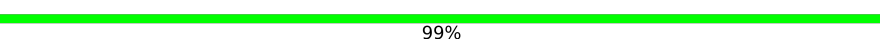


- Molecule 2: Ig alpha-1 chain C region

Chain 1-B:  99%

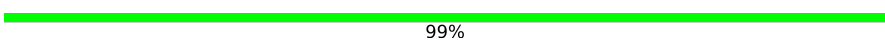


- Molecule 2: Ig alpha-1 chain C region

Chain 1-D:  99%

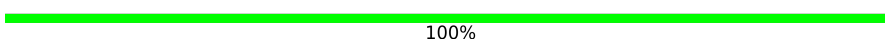


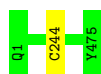
- Molecule 2: Ig alpha-1 chain C region

Chain 1-C:  99%

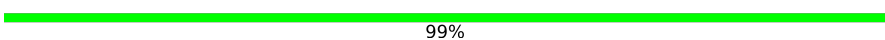


- Molecule 2: Ig alpha-1 chain C region

Chain 2-A:  100%

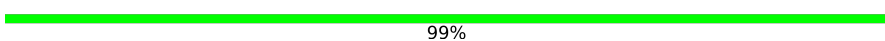


- Molecule 2: Ig alpha-1 chain C region

Chain 2-B:  99%

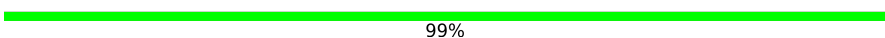


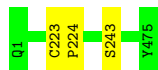
- Molecule 2: Ig alpha-1 chain C region

Chain 2-D:  99%

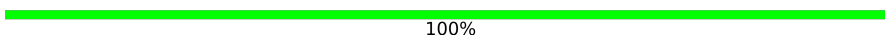


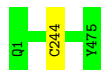
- Molecule 2: Ig alpha-1 chain C region

Chain 2-C:  99%

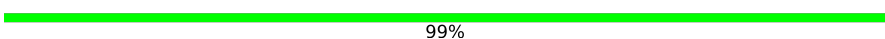


- Molecule 2: Ig alpha-1 chain C region

Chain 3-A:  100%

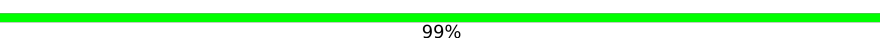


- Molecule 2: Ig alpha-1 chain C region

Chain 3-B:  99%

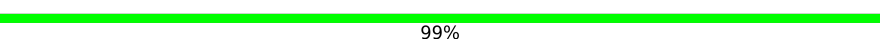


- Molecule 2: Ig alpha-1 chain C region

Chain 3-D:  99%

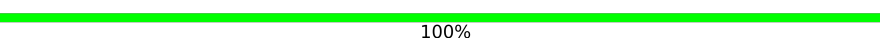


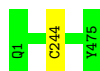
- Molecule 2: Ig alpha-1 chain C region

Chain 3-C:  99%

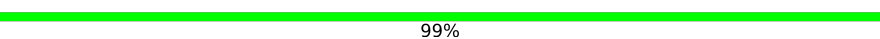


- Molecule 2: Ig alpha-1 chain C region

Chain 4-A:  100%

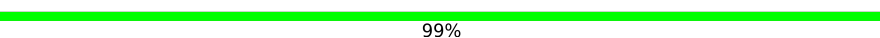


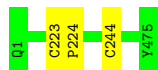
- Molecule 2: Ig alpha-1 chain C region

Chain 4-B:  99%

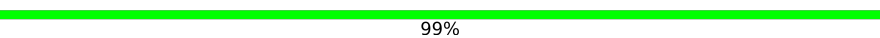


- Molecule 2: Ig alpha-1 chain C region

Chain 4-D:  99%

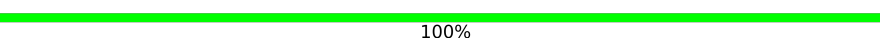


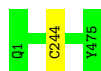
- Molecule 2: Ig alpha-1 chain C region

Chain 4-C:  99%

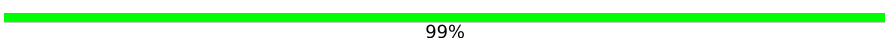


- Molecule 2: Ig alpha-1 chain C region

Chain 5-A:  100%

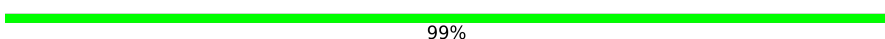


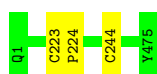
- Molecule 2: Ig alpha-1 chain C region

Chain 5-B:  99%

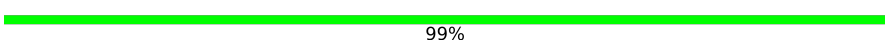


- Molecule 2: Ig alpha-1 chain C region

Chain 5-D:  99%

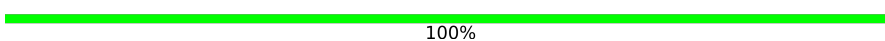


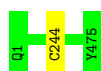
- Molecule 2: Ig alpha-1 chain C region

Chain 5-C:  99%

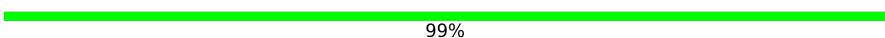


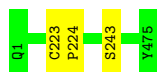
- Molecule 2: Ig alpha-1 chain C region

Chain 6-A:  100%

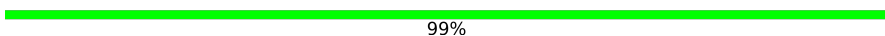


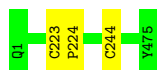
- Molecule 2: Ig alpha-1 chain C region

Chain 6-B:  99%

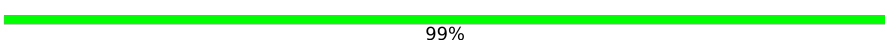


- Molecule 2: Ig alpha-1 chain C region

Chain 6-D:  99%



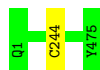
- Molecule 2: Ig alpha-1 chain C region

Chain 6-C:  99%



- Molecule 2: Ig alpha-1 chain C region

Chain 7-A:  100%



- Molecule 2: Ig alpha-1 chain C region

Chain 7-B:  99%



- Molecule 2: Ig alpha-1 chain C region

Chain 7-D:  99%



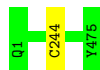
- Molecule 2: Ig alpha-1 chain C region

Chain 7-C:  99%



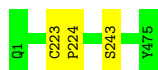
- Molecule 2: Ig alpha-1 chain C region

Chain 8-A:  100%



- Molecule 2: Ig alpha-1 chain C region

Chain 8-B:  99%

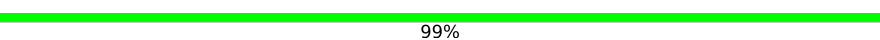


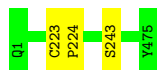
- Molecule 2: Ig alpha-1 chain C region

Chain 8-D:  99%

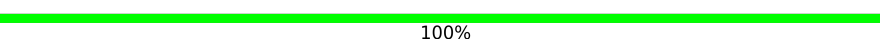


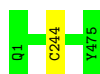
- Molecule 2: Ig alpha-1 chain C region

Chain 8-C:  99%

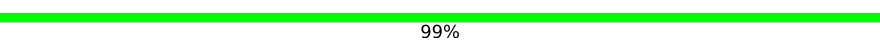


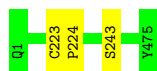
- Molecule 2: Ig alpha-1 chain C region

Chain 9-A:  100%

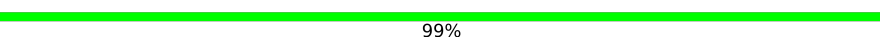


- Molecule 2: Ig alpha-1 chain C region

Chain 9-B:  99%

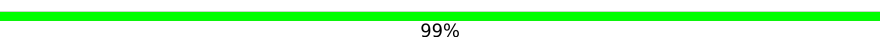


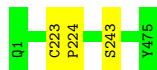
- Molecule 2: Ig alpha-1 chain C region

Chain 9-D:  99%

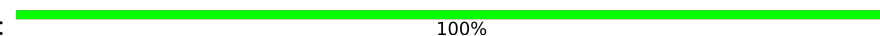


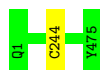
- Molecule 2: Ig alpha-1 chain C region

Chain 9-C:  99%

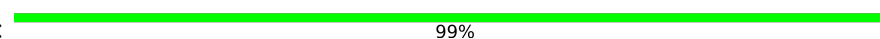


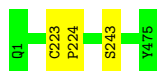
- Molecule 2: Ig alpha-1 chain C region

Chain 10-A:  100%



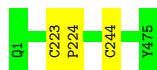
- Molecule 2: Ig alpha-1 chain C region

Chain 10-B:  99%



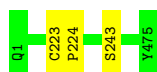
- Molecule 2: Ig alpha-1 chain C region

Chain 10-D: 99%



- Molecule 2: Ig alpha-1 chain C region

Chain 10-C: 99%



- Molecule 3: Secretory component

Chain 1-J: 88% 12%



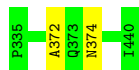
- Molecule 3: Secretory component

Chain 2-J: 98%



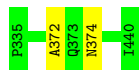
- Molecule 3: Secretory component

Chain 3-J: 98%



- Molecule 3: Secretory component

Chain 4-J: 98%



- Molecule 3: Secretory component

Chain 5-J: 98%



- Molecule 3: Secretory component

Chain 6-J: 98%



- Molecule 3: Secretory component

Chain 7-J: 98%



- Molecule 3: Secretory component

Chain 8-J: 98%



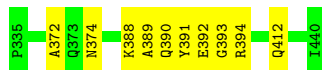
- Molecule 3: Secretory component

Chain 9-J: 93% 7%



- Molecule 3: Secretory component

Chain 10-J: 91% 9%



- Molecule 4: Secretory component

Chain 1-S: 95% 5%

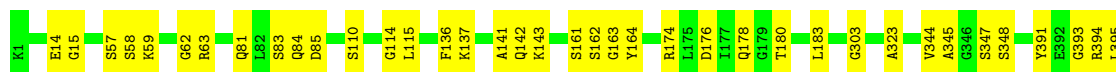


- Molecule 4: Secretory component

Chain 2-S: 95% 5%



- Molecule 4: Secretory component



- Molecule 4: Secretory component



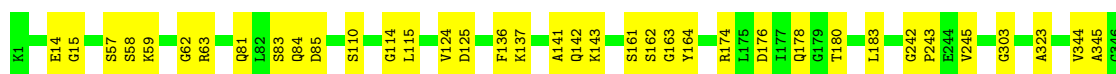
- Molecule 4: Secretory component



- Molecule 4: Secretory component

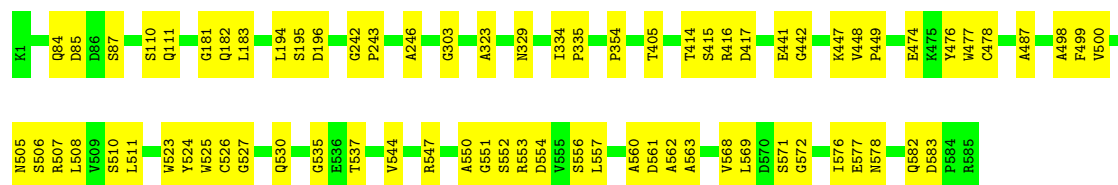


- Molecule 4: Secretory component



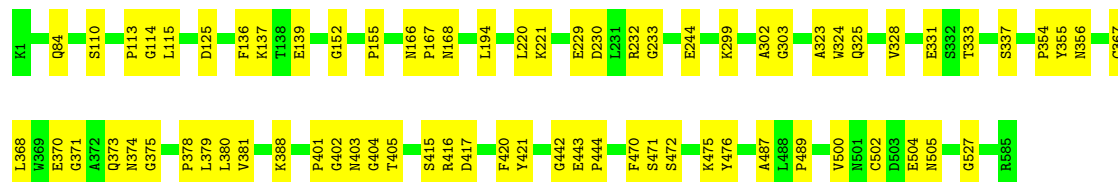
- Molecule 4: Secretory component





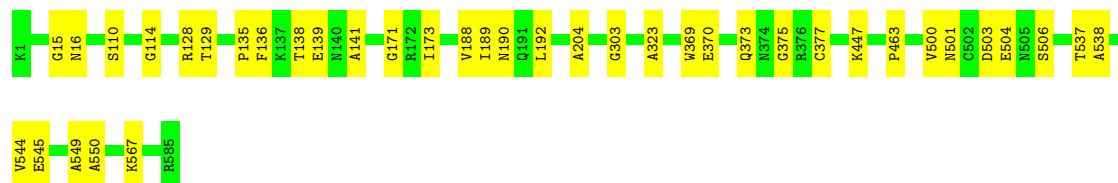
- Molecule 4: Secretory component

Chain 9-S: 88% 12%



- Molecule 4: Secretory component

Chain 10-S: 93% 7%



4 Model quality [i](#)

4.1 Standard geometry [i](#)

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	1-L	214	0	0	0	0
1	1-M	214	0	0	0	0
1	1-N	214	0	0	0	0
1	1-O	214	0	0	0	0
1	2-L	214	0	0	0	0
1	2-M	214	0	0	0	0
1	2-N	214	0	0	0	0
1	2-O	214	0	0	0	0
1	3-L	214	0	0	0	0
1	3-M	214	0	0	0	0
1	3-N	214	0	0	0	0
1	3-O	214	0	0	0	0
1	4-L	214	0	0	0	0
1	4-M	214	0	0	0	0
1	4-N	214	0	0	0	0
1	4-O	214	0	0	0	0
1	5-L	214	0	0	0	0
1	5-M	214	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5-N	214	0	0	0	0
1	5-O	214	0	0	0	0
1	6-L	214	0	0	0	0
1	6-M	214	0	0	0	0
1	6-N	214	0	0	0	0
1	6-O	214	0	0	0	0
1	7-L	214	0	0	0	0
1	7-M	214	0	0	0	0
1	7-N	214	0	0	0	0
1	7-O	214	0	0	0	0
1	8-L	214	0	0	0	0
1	8-M	214	0	0	0	0
1	8-N	214	0	0	0	0
1	8-O	214	0	0	0	0
1	9-L	214	0	0	0	0
1	9-M	214	0	0	0	0
1	9-N	214	0	0	0	0
1	9-O	214	0	0	0	0
1	10-L	214	0	0	0	0
1	10-M	214	0	0	0	0
1	10-N	214	0	0	0	0
1	10-O	214	0	0	0	0
2	1-A	475	0	0	1	0
2	1-B	475	0	0	2	0
2	1-C	475	0	0	2	0
2	1-D	475	0	0	2	0
2	2-A	475	0	0	1	0
2	2-B	475	0	0	2	0
2	2-C	475	0	0	2	0
2	2-D	475	0	0	2	0
2	3-A	475	0	0	1	0
2	3-B	475	0	0	2	0
2	3-C	475	0	0	2	0
2	3-D	475	0	0	2	0
2	4-A	475	0	0	1	0
2	4-B	475	0	0	2	0
2	4-C	475	0	0	2	0
2	4-D	475	0	0	2	0
2	5-A	475	0	0	1	0
2	5-B	475	0	0	2	0
2	5-C	475	0	0	2	0
2	5-D	475	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	6-A	475	0	0	1	0
2	6-B	475	0	0	2	0
2	6-C	475	0	0	2	0
2	6-D	475	0	0	2	0
2	7-A	475	0	0	1	0
2	7-B	475	0	0	2	0
2	7-C	475	0	0	2	0
2	7-D	475	0	0	2	0
2	8-A	475	0	0	1	0
2	8-B	475	0	0	2	0
2	8-C	475	0	0	2	0
2	8-D	475	0	0	2	0
2	9-A	475	0	0	1	0
2	9-B	475	0	0	2	0
2	9-C	475	0	0	2	0
2	9-D	475	0	0	2	0
2	10-A	475	0	0	1	0
2	10-B	475	0	0	2	0
2	10-C	475	0	0	2	0
2	10-D	475	0	0	2	0
3	1-J	106	0	0	15	0
3	2-J	106	0	0	2	0
3	3-J	106	0	0	2	0
3	4-J	106	0	0	2	0
3	5-J	106	0	0	2	0
3	6-J	106	0	0	2	0
3	7-J	106	0	0	2	0
3	8-J	106	0	0	2	0
3	9-J	106	0	0	10	0
3	10-J	106	0	0	12	0
4	1-S	585	0	0	27	0
4	2-S	585	0	0	18	0
4	3-S	585	0	0	41	0
4	4-S	585	0	0	20	0
4	5-S	585	0	0	17	0
4	6-S	585	0	0	16	0
4	7-S	585	0	0	44	0
4	8-S	585	0	0	50	0
4	9-S	585	0	0	49	0
4	10-S	585	0	0	30	0
All	All	34470	0	0	362	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 22.

All (362) 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)
3:J:391:TYR:CA	4:S:190:ASN:CA	1.74	1.64
4:S:58:SER:CA	4:S:164:TYR:CA	1.76	1.62
4:S:13:VAL:CA	4:S:181:GLY:CA	1.76	1.61
3:J:393:GLY:CA	4:S:188:VAL:CA	1.77	1.61
4:S:58:SER:CA	4:S:164:TYR:CA	1.76	1.59
4:S:507:ARG:CA	4:S:583:ASP:CA	1.81	1.56
4:S:449:PRO:CA	4:S:583:ASP:CA	1.74	1.56
4:S:375:GLY:CA	4:S:476:TYR:CA	1.79	1.56
4:S:391:TYR:CA	4:S:569:LEU:CA	1.87	1.52
3:J:392:GLU:CA	4:S:189:ILE:CA	1.87	1.52
4:S:108:GLU:CA	4:S:182:GLN:CA	1.89	1.50
4:S:114:GLY:CA	4:S:136:PHE:CA	1.90	1.49
4:S:124:VAL:CA	4:S:243:PRO:CA	1.85	1.49
4:S:348:SER:CA	4:S:502:CYS:CA	1.92	1.47
4:S:510:SER:CA	4:S:560:ALA:CA	1.92	1.47
4:S:463:PRO:CA	4:S:567:LYS:CA	1.91	1.46
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:C:223:CYS:CA	2:C:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
2:D:223:CYS:CA	2:D:224:PRO:CA	1.94	1.45
3:J:384:GLU:CA	4:S:167:PRO:CA	1.96	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
2:B:223:CYS:CA	2:B:224:PRO:CA	1.94	1.44
4:S:373:GLN:CA	4:S:487:ALA:CA	1.96	1.43
4:S:500:VAL:CA	4:S:563:ALA:CA	1.94	1.42
4:S:325:GLN:CA	4:S:405:THR:CA	1.95	1.42
4:S:87:SER:CA	4:S:181:GLY:CA	1.96	1.42
4:S:84:GLN:CA	4:S:139:GLU:CA	1.95	1.41
4:S:499:PHE:CA	4:S:562:ALA:CA	1.97	1.39
4:S:377:CYS:CA	4:S:504:GLU:CA	2.02	1.38
4:S:474:GLU:CA	4:S:568:VAL:CA	2.01	1.38
4:S:115:LEU:CA	4:S:136:PHE:CA	2.02	1.37
4:S:109:VAL:CA	4:S:182:GLN:CA	2.02	1.38
4:S:115:LEU:CA	4:S:136:PHE:CA	2.02	1.37
4:S:12:SER:CA	4:S:180:THR:CA	2.05	1.35
4:S:196:ASP:CA	4:S:243:PRO:CA	2.02	1.35
4:S:375:GLY:CA	4:S:501:ASN:CA	2.03	1.34
4:S:84:GLN:CA	4:S:182:GLN:CA	2.04	1.34
4:S:84:GLN:CA	4:S:110:SER:CA	2.04	1.34
3:J:388:LYS:CA	4:S:129:THR:CA	2.06	1.34
4:S:114:GLY:CA	4:S:137:LYS:CA	2.03	1.34
4:S:369:TRP:CA	4:S:503:ASP:CA	2.06	1.34
4:S:11:ASN:CA	4:S:181:GLY:CA	2.07	1.32
4:S:538:ALA:CA	4:S:559:LYS:CA	2.05	1.32
4:S:523:TRP:CA	4:S:550:ALA:CA	2.06	1.32
4:S:538:ALA:CA	4:S:559:LYS:CA	2.05	1.32
4:S:125:ASP:CA	4:S:242:GLY:CA	2.08	1.31
4:S:343:GLY:CA	4:S:441:GLU:CA	2.09	1.31
3:J:393:GLY:CA	4:S:149:LYS:CA	2.09	1.30
4:S:524:TYR:CA	4:S:550:ALA:CA	2.09	1.29
4:S:12:SER:CA	4:S:181:GLY:CA	2.08	1.29
4:S:195:SER:CA	4:S:242:GLY:CA	2.11	1.29
4:S:498:ALA:CA	4:S:561:ASP:CA	2.10	1.29
4:S:229:GLU:CA	4:S:356:ASN:CA	2.09	1.29
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
3:J:374:ASN:CA	4:S:303:GLY:CA	2.08	1.28
4:S:537:THR:CA	4:S:549:ALA:CA	2.12	1.27
4:S:114:GLY:CA	4:S:137:LYS:CA	2.13	1.27
4:S:447:LYS:CA	4:S:547:ARG:CA	2.12	1.26
4:S:415:SER:CA	4:S:442:GLY:CA	2.11	1.26
4:S:114:GLY:CA	4:S:137:LYS:CA	2.13	1.26
4:S:299:LYS:CA	4:S:326:LEU:CA	2.12	1.25
4:S:299:LYS:CA	4:S:326:LEU:CA	2.12	1.25
4:S:299:LYS:CA	4:S:326:LEU:CA	2.12	1.25
3:J:383:SER:CA	4:S:167:PRO:CA	2.14	1.25
4:S:15:GLY:CA	4:S:138:THR:CA	2.15	1.25
3:J:386:TRP:CA	4:S:168:ASN:CA	2.17	1.21
4:S:388:LYS:CA	4:S:505:ASN:CA	2.19	1.20
4:S:114:GLY:CA	4:S:136:PHE:CA	2.18	1.20
4:S:442:GLY:CA	4:S:535:GLY:CA	2.18	1.20
4:S:416:ARG:CA	4:S:444:PRO:CA	2.19	1.20
4:S:368:LEU:CA	4:S:471:SER:CA	2.20	1.20
3:J:388:LYS:CA	4:S:128:ARG:CA	2.18	1.20
4:S:110:SER:CA	4:S:139:GLU:CA	2.20	1.19
4:S:371:GLY:CA	4:S:527:GLY:CA	2.20	1.18
4:S:347:SER:CA	4:S:530:GLN:CA	2.21	1.18
4:S:14:GLU:CA	4:S:141:ALA:CA	2.21	1.18
4:S:441:GLU:CA	4:S:467:PRO:CA	2.21	1.18
4:S:347:SER:CA	4:S:530:GLN:CA	2.21	1.18
4:S:14:GLU:CA	4:S:141:ALA:CA	2.21	1.16
4:S:416:ARG:CA	4:S:443:GLU:CA	2.24	1.15
4:S:508:LEU:CA	4:S:576:ILE:CA	2.25	1.14
4:S:378:PRO:CA	4:S:500:VAL:CA	2.26	1.13
4:S:453:THR:CA	4:S:572:GLY:CA	2.27	1.13
4:S:441:GLU:CA	4:S:571:SER:CA	2.25	1.12
4:S:453:THR:CA	4:S:572:GLY:CA	2.27	1.11
4:S:507:ARG:CA	4:S:577:GLU:CA	2.28	1.10
4:S:11:ASN:CA	4:S:180:THR:CA	2.29	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:417:ASP:CA	4:S:469:LYS:CA	2.29	1.10
4:S:447:LYS:CA	4:S:545:GLU:CA	2.28	1.10
4:S:524:TYR:CA	4:S:551:GLY:CA	2.31	1.09
4:S:538:ALA:CA	4:S:549:ALA:CA	2.33	1.07
4:S:112:GLY:CA	4:S:184:LEU:CA	2.33	1.07
4:S:538:ALA:CA	4:S:549:ALA:CA	2.33	1.06
3:J:393:GLY:CA	4:S:148:TYR:CA	2.34	1.05
4:S:124:VAL:CA	4:S:242:GLY:CA	2.33	1.05
4:S:63:ARG:CA	4:S:176:ASP:CA	2.34	1.05
4:S:487:ALA:CA	4:S:553:ARG:CA	2.34	1.05
4:S:63:ARG:CA	4:S:176:ASP:CA	2.34	1.04
4:S:538:ALA:CA	4:S:549:ALA:CA	2.33	1.04
4:S:232:ARG:CA	4:S:331:GLU:CA	2.33	1.04
4:S:342:LYS:CA	4:S:441:GLU:CA	2.35	1.03
4:S:451:ASN:CA	4:S:570:ASP:CA	2.37	1.02
4:S:451:ASN:CA	4:S:570:ASP:CA	2.37	1.02
3:J:395:LEU:CA	4:S:156:VAL:CA	2.36	1.02
4:S:127:GLY:CA	4:S:245:VAL:CA	2.38	1.02
4:S:57:SER:CA	4:S:163:GLY:CA	2.39	1.00
4:S:57:SER:CA	4:S:163:GLY:CA	2.39	1.00
4:S:380:LEU:CA	4:S:502:CYS:CA	2.40	1.00
4:S:449:PRO:CA	4:S:546:GLU:CA	2.39	0.99
4:S:507:ARG:CA	4:S:576:ILE:CA	2.39	0.99
4:S:114:GLY:CA	4:S:136:PHE:CA	2.41	0.99
3:J:384:GLU:CA	4:S:167:PRO:CA	2.41	0.98
3:J:385:GLY:CA	4:S:168:ASN:CA	2.41	0.98
4:S:128:ARG:CA	4:S:244:GLU:CA	2.41	0.97
4:S:537:THR:CA	4:S:545:GLU:CA	2.43	0.97
4:S:233:GLY:CA	4:S:333:THR:CA	2.42	0.97
3:J:386:TRP:CA	4:S:168:ASN:CA	2.43	0.97
4:S:537:THR:CA	4:S:545:GLU:CA	2.43	0.96
3:J:372:ALA:CA	4:S:401:PRO:CA	2.43	0.95
4:S:417:ASP:CA	4:S:443:GLU:CA	2.45	0.95
4:S:537:THR:CA	4:S:545:GLU:CA	2.43	0.95
4:S:190:ASN:CA	4:S:244:GLU:CA	2.46	0.94
4:S:373:GLN:CA	4:S:500:VAL:CA	2.46	0.94
4:S:345:ALA:CA	4:S:506:SER:CA	2.46	0.94
4:S:539:ALA:CA	4:S:560:ALA:CA	2.46	0.94
4:S:112:GLY:CA	4:S:134:CYS:CA	2.46	0.94
4:S:538:ALA:CA	4:S:550:ALA:CA	2.46	0.94
4:S:112:GLY:CA	4:S:134:CYS:CA	2.46	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:539:ALA:CA	4:S:560:ALA:CA	2.46	0.93
4:S:112:GLY:CA	4:S:133:ASN:CA	2.47	0.93
4:S:112:GLY:CA	4:S:133:ASN:CA	2.47	0.93
4:S:112:GLY:CA	4:S:133:ASN:CA	2.47	0.93
4:S:421:TYR:CA	4:S:472:SER:CA	2.47	0.93
4:S:115:LEU:CA	4:S:136:PHE:CA	2.47	0.92
4:S:112:GLY:CA	4:S:134:CYS:CA	2.46	0.92
4:S:324:TRP:CA	4:S:404:GLY:CA	0.92	0.92
4:S:194:LEU:CA	4:S:221:LYS:CA	2.47	0.91
4:S:417:ASP:CA	4:S:547:ARG:CA	2.49	0.91
3:J:385:GLY:CA	4:S:167:PRO:CA	2.48	0.91
4:S:478:CYS:CA	4:S:552:SER:CA	2.50	0.90
4:S:450:GLY:CA	4:S:547:ARG:CA	0.89	0.89
4:S:450:GLY:CA	4:S:547:ARG:CA	0.89	0.89
4:S:129:THR:CA	4:S:243:PRO:CA	2.50	0.89
4:S:450:GLY:CA	4:S:547:ARG:CA	0.89	0.89
4:S:530:GLN:CA	4:S:569:LEU:CA	2.52	0.88
4:S:115:LEU:CA	4:S:136:PHE:CA	2.52	0.88
4:S:450:GLY:CA	4:S:546:GLU:CA	2.52	0.87
4:S:511:LEU:CA	4:S:560:ALA:CA	2.52	0.87
4:S:115:LEU:CA	4:S:136:PHE:CA	2.52	0.87
4:S:115:LEU:CA	4:S:136:PHE:CA	2.52	0.87
3:J:396:SER:CA	4:S:156:VAL:CA	2.53	0.87
3:J:393:GLY:CA	4:S:155:PRO:CA	2.52	0.87
4:S:450:GLY:CA	4:S:546:GLU:CA	2.53	0.86
4:S:125:ASP:CA	4:S:245:VAL:CA	2.53	0.86
4:S:329:ASN:CA	4:S:354:PRO:CA	2.52	0.86
4:S:345:ALA:CA	4:S:534:TYR:CA	2.54	0.85
4:S:345:ALA:CA	4:S:534:TYR:CA	2.54	0.85
4:S:450:GLY:CA	4:S:546:GLU:CA	2.53	0.85
4:S:539:ALA:CA	4:S:559:LYS:CA	2.56	0.84
4:S:111:GLN:CA	4:S:183:LEU:CA	2.56	0.83
4:S:11:ASN:CA	4:S:182:GLN:CA	2.55	0.83
4:S:506:SER:CA	4:S:578:ASN:CA	2.57	0.83
4:S:539:ALA:CA	4:S:559:LYS:CA	2.56	0.83
4:S:110:SER:CA	4:S:204:ALA:CA	2.56	0.82
4:S:418:ALA:CA	4:S:469:LYS:CA	2.58	0.82
4:S:374:ASN:CA	4:S:489:PRO:CA	2.57	0.82
4:S:194:LEU:CA	4:S:220:LEU:CA	2.58	0.81
4:S:127:GLY:CA	4:S:245:VAL:CA	2.59	0.80
4:S:15:GLY:CA	4:S:183:LEU:CA	2.60	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:346:GLY:CA	4:S:507:ARG:CA	2.60	0.80
4:S:15:GLY:CA	4:S:183:LEU:CA	2.60	0.79
4:S:452:VAL:CA	4:S:571:SER:CA	0.79	0.79
4:S:452:VAL:CA	4:S:571:SER:CA	0.79	0.79
3:J:412:GLN:CA	4:S:171:GLY:CA	2.62	0.78
4:S:85:ASP:CA	4:S:182:GLN:CA	2.62	0.78
4:S:15:GLY:CA	4:S:180:THR:CA	2.64	0.76
4:S:151:ILE:CA	4:S:244:GLU:CA	2.63	0.76
3:J:390:GLN:CA	4:S:190:ASN:CA	2.64	0.76
4:S:15:GLY:CA	4:S:180:THR:CA	2.64	0.76
4:S:112:GLY:CA	4:S:183:LEU:CA	2.64	0.75
4:S:229:GLU:CA	4:S:355:TYR:CA	2.64	0.75
4:S:84:GLN:CA	4:S:110:SER:CA	2.63	0.75
4:S:347:SER:CA	4:S:501:ASN:CA	2.65	0.75
4:S:395:LEU:CA	4:S:483:THR:CA	2.65	0.74
3:J:394:ARG:CA	4:S:149:LYS:CA	2.65	0.74
4:S:476:TYR:CA	4:S:554:ASP:CA	2.65	0.74
4:S:508:LEU:CA	4:S:585:ARG:CA	2.66	0.74
4:S:395:LEU:CA	4:S:483:THR:CA	2.66	0.73
4:S:329:ASN:CA	4:S:404:GLY:CA	0.72	0.72
4:S:302:ALA:CA	4:S:402:GLY:CA	0.73	0.72
4:S:194:LEU:CA	4:S:242:GLY:CA	2.68	0.72
4:S:498:ALA:CA	4:S:562:ALA:CA	2.68	0.71
4:S:299:LYS:CA	4:S:403:ASN:CA	2.69	0.70
4:S:381:VAL:CA	4:S:504:GLU:CA	2.70	0.70
4:S:299:LYS:CA	4:S:325:GLN:CA	2.70	0.69
4:S:14:GLU:CA	4:S:180:THR:CA	2.70	0.69
4:S:452:VAL:CA	4:S:572:GLY:CA	2.70	0.69
3:J:389:ALA:CA	4:S:196:ASP:CA	2.71	0.69
4:S:14:GLU:CA	4:S:180:THR:CA	2.70	0.69
4:S:452:VAL:CA	4:S:572:GLY:CA	2.70	0.69
4:S:59:LYS:CA	4:S:162:SER:CA	2.71	0.68
4:S:59:LYS:CA	4:S:162:SER:CA	2.71	0.68
3:J:394:ARG:CA	4:S:152:GLY:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68
3:J:372:ALA:CA	4:S:323:ALA:CA	2.71	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:505:ASN:CA	4:S:578:ASN:CA	2.79	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
2:D:244:CYS:CA	2:C:243:SER:CA	2.80	0.60
4:S:441:GLU:CA	4:S:549:ALA:CA	2.80	0.59
4:S:85:ASP:CA	4:S:143:LYS:CA	2.81	0.59
4:S:16:ASN:CA	4:S:139:GLU:CA	2.81	0.59
4:S:85:ASP:CA	4:S:143:LYS:CA	2.81	0.58
4:S:418:ALA:CA	4:S:555:VAL:CA	2.82	0.58
4:S:84:GLN:CA	4:S:110:SER:CA	2.82	0.58
4:S:84:GLN:CA	4:S:110:SER:CA	2.82	0.57
4:S:344:VAL:CA	4:S:533:PHE:CA	2.83	0.56
4:S:453:THR:CA	4:S:573:PHE:CA	2.83	0.56
4:S:344:VAL:CA	4:S:533:PHE:CA	2.84	0.56
3:J:389:ALA:CA	4:S:192:LEU:CA	2.84	0.56
4:S:15:GLY:CA	4:S:139:GLU:CA	2.83	0.56
4:S:334:ILE:CA	4:S:335:PRO:CA	2.84	0.56
4:S:453:THR:CA	4:S:573:PHE:CA	2.83	0.56
4:S:420:PHE:CA	4:S:470:PHE:CA	2.85	0.55
4:S:370:GLU:CA	4:S:475:LYS:CA	2.85	0.54
4:S:370:GLU:CA	4:S:506:SER:CA	2.85	0.54
4:S:537:THR:CA	4:S:544:VAL:CA	2.85	0.54
4:S:115:LEU:CA	4:S:136:PHE:CA	2.86	0.53
4:S:329:ASN:CA	4:S:405:THR:CA	2.87	0.53
4:S:539:ALA:CA	4:S:547:ARG:CA	2.87	0.53
4:S:11:ASN:CA	4:S:179:GLY:CA	2.86	0.53
4:S:416:ARG:CA	4:S:525:TRP:CA	2.87	0.53
4:S:415:SER:CA	4:S:470:PHE:CA	2.86	0.53
4:S:195:SER:CA	4:S:246:ALA:CA	2.87	0.53
4:S:478:CYS:CA	4:S:553:ARG:CA	2.87	0.52
4:S:539:ALA:CA	4:S:547:ARG:CA	2.87	0.52
4:S:539:ALA:CA	4:S:547:ARG:CA	2.87	0.52
4:S:16:ASN:CA	4:S:138:THR:CA	2.89	0.50
4:S:346:GLY:CA	4:S:506:SER:CA	2.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:S:448:VAL:CA	4:S:582:GLN:CA	2.89	0.50
4:S:526:CYS:CA	4:S:557:LEU:CA	2.90	0.50
3:J:394:ARG:CA	4:S:173:ILE:CA	2.91	0.49
4:S:107:LEU:CA	4:S:178:GLN:CA	2.90	0.49
4:S:379:LEU:CA	4:S:502:CYS:CA	2.91	0.48
3:J:393:GLY:CA	4:S:189:ILE:CA	2.91	0.48
4:S:510:SER:CA	4:S:561:ASP:CA	2.91	0.48
4:S:325:GLN:CA	4:S:354:PRO:CA	2.92	0.48
3:J:392:GLU:CA	4:S:149:LYS:CA	2.91	0.48
4:S:113:PRO:CA	4:S:183:LEU:CA	2.92	0.47
3:J:389:ALA:CA	4:S:197:ALA:CA	2.92	0.47
4:S:114:GLY:CA	4:S:135:PRO:CA	2.93	0.47
4:S:447:LYS:CA	4:S:582:GLN:CA	2.93	0.47
4:S:525:TRP:CA	4:S:551:GLY:CA	2.94	0.46
3:J:385:GLY:CA	4:S:168:ASN:CA	2.94	0.46
4:S:113:PRO:CA	4:S:137:LYS:CA	2.94	0.46
4:S:394:ARG:CA	4:S:486:GLN:CA	2.94	0.45
4:S:394:ARG:CA	4:S:486:GLN:CA	2.94	0.45
4:S:347:SER:CA	4:S:531:GLY:CA	2.95	0.45
4:S:415:SER:CA	4:S:554:ASP:CA	0.45	0.45
4:S:347:SER:CA	4:S:531:GLY:CA	2.95	0.45
4:S:114:GLY:CA	4:S:136:PHE:CA	2.96	0.44
4:S:58:SER:CA	4:S:163:GLY:CA	2.96	0.44
4:S:114:GLY:CA	4:S:136:PHE:CA	2.96	0.44
4:S:58:SER:CA	4:S:163:GLY:CA	2.96	0.43
4:S:81:GLN:CA	4:S:178:GLN:CA	2.97	0.43
4:S:414:THR:CA	4:S:547:ARG:CA	2.96	0.43
4:S:81:GLN:CA	4:S:178:GLN:CA	2.97	0.43
3:J:385:GLY:CA	4:S:166:ASN:CA	2.96	0.42
4:S:348:SER:CA	4:S:530:GLN:CA	2.97	0.42
4:S:579:LYS:CA	4:S:580:ALA:CA	2.98	0.42
4:S:15:GLY:CA	4:S:141:ALA:CA	2.98	0.42
4:S:348:SER:CA	4:S:530:GLN:CA	2.97	0.41
4:S:579:LYS:CA	4:S:580:ALA:CA	2.98	0.41
4:S:110:SER:CA	4:S:183:LEU:CA	2.98	0.41
4:S:126:LEU:CA	4:S:220:LEU:CA	2.99	0.41
4:S:126:LEU:CA	4:S:220:LEU:CA	2.99	0.41

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

4.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

4.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.