

PREFERRED THERAPEUTIC FORM OF OAS1

SEQ ID NO: 1

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIIDIICGFLKERCFRGSSYPVCVSKVVK 60
61 GGSSGKGTTLRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRRQLEACQRERAF SVKFE 120
121 VQAPRWGNPRALS FVLSSLQLGEGVEFDVLPAPDALGQLTGSYKPNPQIYVKLIEECTDL 180
181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW 240
241 ERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYYDFKNPIIEKYLRRLTKPRPVILD 300
301 PADPTGNLGGDPK GWRQLAQEAEAWLNYPCKNWDGSPVSSWILL 346

FIGURE 2
LIST OF AMINO ACID SUBSTITUTIONS USEFUL IN THERAPEUTIC FORMS OF OAS1

Position	Amino Acid Substitutions
1	M or - (Deleted)
31	D or N
115	L or F
127	G or R
162	S or G
295	R or T
315	G or R

FIGURE 3
LIST OF PRIMATE AMINO ACID MODIFICATIONS USEFUL IN THERAPEUTIC FORMS
OF OAS1

Position	Amino Acid Substitutions
24	Lys or Thr
25	His or Cys
28	Thr or Lys or Met
36	Thr or Ile
47	Gln or Arg
53	Ala or Val
54	Arg or Cys
54	Arg or His or Cys
64	Phe or Ser
69	Ala or Thr
69	Ala or Ser or Thr
74	Ile or Ser
104	Lys or Arg
108	Val or Ala
112	Glu insertion
113	Ser or Arg
114	Ile or Ala
116	Arg or Ser or Ala
117	Glu or Val
118	Val or Lys
119	Termination or Phe
127	Asp or Gly
130	Cys or Arg
139	Phe or Leu
142	Arg or Gly
160	Ile or Thr
161	Asp or Gly
166	Asp or Asn
175	Lys or Glu
179	Tyr or Asp
200	Glu or Gln
226	Pro insertion
242	Gln or Arg
246	Glu or Lys
248	Asp or His
250	Ile or Asn
254	Glu or Gly
274	Val or Lys
279	Glu or Lys
282	Ser or Ile
284	Lys or Glu
288	Ser or Arg
289	Arg or Arg
292	Glu or Thr

292	Arg or Thr
292	Ser or Thr
314	Ile or Lys
335	Termination or Trp
347+	Thr or Ala
347^	Pro or Thr
349+	Ser or Ser
350+	Asp or Asn
352+	Gly or Glu or Ala
353+	Arg or Asp
354+	Termination or Asp
356+	Ser or Thr
357+	Tyr or Asp
361+	Met or Arg
361^	Glu or Gly
363*	Lys or Glu
363+	Pro or Gln
364+	Gln or Lys
364^	Val or Leu
365+	His or Tyr
369+	Gln or Arg or Gly
371+	Tyr or His
372^	Ala or Ala
373+	Cys or Tyr
374+	Ser or Pro
375+	Tyr or His
378+	Gln or His
379+	Ser or Arg
382+	Ile or Thr
384^	His or Gln
385 ^	Leu or Phe
388+	Ala or Thr
389+	Arg or Pro
394+	Asn or Asp
399^	Arg or Ser

* Positions indicated with * refer to forms of OAS1 that are carboxyl-terminus homologous to Genbank accession NP_002525.1 (for example SEQ ID NO:3).

+ Positions indicated with + refer to forms of OAS1 that are carboxyl-terminus homologous to Genbank accession NP_058132.1 (for example SEQ ID NO:2).

^ Positions indicated with ^ refer to forms of OAS1 that are carboxyl-terminus homologous to Genbank accession NP_001027581.1 (for example SEQ ID NO:4).

All other unmarked positions refer to all forms of OAS1.

[illegible]

[illegible]

Amino acid positions are with reference to all isoforms of OAS1 (for example, SEQ ID NO:1-4 and Genbank accessions NP_002525.1 and NP_058132.1) except where * indicates position relative to NP_002525.1 homologous forms only, + indicates position relative to NP_058132.1 homologous forms only, and ^ indicates position relative to NP_001027581.1 homologous forms only.

FIGURE 5
ADDITIONAL OAS1 ISOFORMS OF THE INVENTION

SEQ ID NO:2 (Human OAS1 Isoform E18/p46 from NT_009775.15 Chrom 12q24.1 with nucleotide endpoints 3914354,3926867)

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1  MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
61  GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
121 VQAPRWGNPRALSFVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIEECTDL
181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
241 ERGSMKTHFNTAQGFRTVLELVINYQQLCIYWKYYDFKNPIIEKYLRRQLTKPRPVILD
301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLAESNSADDETDDPR
361 RYQKYGYIGTHEYPHFSHRPSTLQAASTPQAEEDWTCTIL

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SEQ ID NO:3 (Human OAS1 Isoform E16/p40 from NT_009775.15 Chrom 12q24.1 with nucleotide endpoints 3914354,3925071)

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1  MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
61  GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
121 VQAPRWGNPRALSFVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIEECTDL
181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
241 ERGSMKTHFNTAQGFRTVLELVINYQQLCIYWKYYDFKNPIIEKYLRRQLTKPRPVILD
301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLVRPPASSLPFIPAP
361 LHEA

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SEQ ID NO:4 (Human OAS1 Isoform p48 from NT_009775.15 Chrom 12q24.1 with nucleotide endpoints 3914354,3927007)

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1  MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
61  GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
121 VQAPRWGNPRALSFVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIEECTDL
181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
241 ERGSMKTHFNTAQGFRTVLELVINYQQLCIYWKYYDFKNPIIEKYLRRQLTKPRPVILD
301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLTQHTPGSIHPTGRR
361 GLDLHHPLNASASWGKGLQCYLDQFLHFQVGLLIQRGQSSSVSWCIIQDRTQVS

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SEQ ID NO:5 (Gorilla gorilla OAS1 Isoform E18 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGKTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
 121 VQAPRWGNPCALS FVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIKECTYL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 EQGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLRRLRKPRPVILD
 301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLAESDSGR

SEQ ID NO:6 (Gorilla gorilla OAS1 Isoform E16 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGKTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
 121 VQAPRWGNPCALS FVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIKECTYL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 EQGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLRRLRKPRPVILD
 301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLVRPPASSLPFIPAP
 361 LHKA

SEQ ID NO:7 (Gorilla gorilla OAS1 Isoform p48 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRMQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGKTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRRQLEACQRERAFSVKFE
 121 VQAPRWGNPCALS FVLSSLQLGEGVEFDVLPAFDALGQLTGGYKPNPQIYVKLIKECTYL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 EQGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLRRLKPRPVILD
 301 PADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLTQHTPGSIHPTGRR
 361 GLDLHHPLNASASWGKGLQCYLDQFLHFQVGLLIQRGQSSSVSWCIIQDRTQVS

SEQ ID NO:8 (Pan paniscus OAS1 Isoform E18 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRTQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGTTLRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRRQLEVCQREERAFSVKFE
 121 EVQAPRWDNPRALS FVLSSLQLGEGVEFDVLPAFDALGQLIGGYKPDQIYVKLIEECTY

181 LQKEGEFSTCFTELQRDFLKERPTKLKSLIRLVKHWYQNCKKKLGLPPQYALELLTVYA
 241 WERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLSRQLEKPRPVIL
 301 DPADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKNXDGSPVSSWILLAESDSADDETDDP
 361 RRYQKYGYIGTHEYPHFSHRPSTLQAASAPQAEEDWTCTIL

SEQ ID NO:9 (Pan paniscus OAS1 Isoform E16 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRTQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEVCQREERAFSVKF
 121 EVQAPRWDNPRALS FVLSSLQLGEGVEFDVLPAFDALGQLIGGYKDPQIYVKLIEECTY
 181 LQKEGEFSTCFTELQRDFLKERPTKLKSLIRLVKHWYQNCKKKLGLPPQYALELLTVYA
 241 WERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLSRQLEKPRPVIL
 301 DPADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKNXDGSPVSSWILLVRPPASSLPFIPA
 361 PLHEA

SEQ ID NO:10 (Pan paniscus OAS1 Isoform p48 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTCFRKQINHAIDIICGFLKERCFRGSSYPVCVSKVVK
 61 GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEVCQREERAFSVKF
 121 EVQAPRWDNPRALS FVLSSLQLGEGVEFDVLPAFDALGQLIGGYKDPQIYVKLIEECTY
 181 LQKEGEFSTCFTELQRDFLKERPTKLKSLIRLVKHWYQNCKKKLGLPPQYALELLTVYA
 241 WERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIEKYLSRQLEKPRPVIL
 301 DPADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKNXDGSPVSSWILLTQHTPGSIRPTGR
 361 RGLDLHHPLNASASWGKGLQCYLDQFLHFQVGLLIQRGQSSSVSWCIIQDRTQVS

SEQ ID NO:11 (Pan troglodytes verus OAS1 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDKCFRKQINHAIDIICGFLKERCFQGSSYPVHVSKVVK
 61 GGSSGKGTTLRGRSDADLVVFLSPLTTFQDQLNRRGEFIQEIRRQLEACQREERAFSVKF
 121 EVQAPRWDNPRALS FVLSSLQLGEGVEFDVLPAFDALGQLTDGYKDPQIYVKLIEECTY
 181 LQKEGEFSTCFTELQRDFLQRPPTKLKSLIRLVKHWYQNCKKKLGLPPQYALELLTVYA
 241 WEQGSMTDFNTAQEFRTVLELVINYQQLCIYWTKYDFENPIIEKYLRRLTKPRPVIL
 301 DPADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKN

SEQ ID NO:12 (Pan troglodytes OAS1 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDKCFRKQINHAIDIICGFLKERCFQGSSYPVHVSKVVK
 61 GGSSGKGTTLRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRKQLEACQREERAFXVKF
 121 EVQAPRWDNPRALS FVLSSLQLGEGVEFDVLPAFDALGQLTDGYKDPDQIYVKLIEECTY
 181 LQKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYA
 241 WEQGSMTDFNTAQEFRTVLELVINYQQLCIYWTKYDFENPIIEKYLRRQLTKPRPVIL
 301 DPADPTGNLGGGDPKGWRQLAQEAEAWLNYPCKFN

SEQ ID NO:13 (Pongo pygmaeus abelii OAS1 Short Isoform)

1 MMDLRNTPAKSLDKFIEDYLLPDTHFRMQINHAIDTICGFLKERCFRGSSYPARVSKVVK
 61 GGSSGKGTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRKQLEACQRESIFREV

SEQ ID NO:14 (Pongo pygmaeus abelii OAS1 Isoform E18 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTHFRMQINHAIDTICGFLKERCFRGSSYPVHVSKVVK
 61 GGSSGKGTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRKQLEACQREXXFXXXXE
 121 VQAPRWDNPRALS FVLSSFQLXEGVEFDVLPAFDALGQLTGGYKDPDQIYVKLIEECTDL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 ERGSMKTHFNNTAQGFRTVLELVINYQQLCIYWTKYDFKNPIIKYLSRQLRKPRPVILD
 301 PADPTGNLGGGDPGWWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLAESDSEDDETYDPR
 361 MYXKYGYIRTHEYSHFSPSTLQAASTPQAEENWTCTIL

SEQ ID NO:15 (Pongo pygmaeus abelii OAS1 Isoform E16 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTHFRMQINHAIDTICGFLKERCFRGSSYPVHVSKVVK
 61 GGSSGKGTALRGRSDADLVVFLSPLTTTFQDQLNRRGEFIQEIRKQLEACQREXXFXXXXE
 121 VQAPRWDNPRALS FVLSSFQLXEGVEFDVLPAFDALGQLTGGYKDPDQIYVKLIEECTDL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 ERGSMKTHFNNTAQGFRTVLELVINYQQLCIYWTKYDFENPIIKYLSRQLRKPRPVILD
 301 PADPTGNLGGGDPGWWRQLAQEAEAWLNYPCKFNWDGSPVSSWILLVRPPASSLPFIPAP
 361 LHEA

SEQ ID NO:16 (Pongo pygmaeus abelii OAS1 Isoform p48 homolog)

1 MMDLRNTPAKSLDKFIEDYLLPDTHFRMQINHAIDTICGFLKERCFRGSSYPVHVSKVVK

61 GGSSGKGTALRGRSDADLVVFLSPLTTFQDQINRRGEFIQEIRKQLEACQREXXFXXXXE
 121 VQAPRWDNPRALSFVLSSFQLXEGVEFDVLPAPFDALGQLTGGYKPDQIYVKLIEECTDL
 181 QKEGEFSTCFTELQRDFLKQRPTKLKSLIRLVKHWYQNCKKKLGKLPPQYALELLTVYAW
 241 ERGSMKTHFNTAQGFRTVLELVINYQQLCIYWTKYDFENPIIKYLSRQLKKPRPVILD
 301 PADPTGNLGGGDPIGWRLAQEAELNYPCEKNWDGSPVSSWILLPQHPTGSIHPTGRR
 361 ELDVHHPLNASASWGKGLQCYLDHLLHFQVGLLIQRGQRSSVSWCIIQDRTQVS

In the foregoing sequences, X indicates a variant amino acid as described by the following table.

Sequence	Amino Acid Position	Alternate Amino Acids
SEQ ID NO:8	336	W or C
SEQ ID NO:9	336	W or C
SEQ ID NO:10	336	W or C
SEQ ID NO:12	117	S or A
SEQ ID NO:14	113	S or R
SEQ ID NO:15	113	S or R
SEQ ID NO:16	113	S or R
SEQ ID NO:14	114	I or A
SEQ ID NO:15	114	I or A
SEQ ID NO:16	114	I or A
SEQ ID NO:14	116	R or S
SEQ ID NO:15	116	R or S
SEQ ID NO:16	116	R or S
SEQ ID NO:14	117	E or V
SEQ ID NO:15	117	E or V
SEQ ID NO:16	117	E or V
SEQ ID NO:14	118	V or K
SEQ ID NO:15	118	V or K
SEQ ID NO:16	118	V or K
SEQ ID NO:14	119	Term or F
SEQ ID NO:15	119	Term or F
SEQ ID NO:16	119	Term or F
SEQ ID NO:14	142	R or G
SEQ ID NO:15	142	R or G
SEQ ID NO:16	142	R or G
SEQ ID NO:14	363	P or Q